

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: December 12, 2005, 20:43:06 ; Search time 112.667 Seconds  
(without alignments)  
58.497 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPFQTDQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	8	ADRI0601 Dog IGE e
2	53	65.4	15	8	ADRI0607 Pig IGE e
3	48	59.3	15	8	ADRI0602 Cat IGE e
4	41	50.6	15	8	ADRI0603 Horse IGE
5	34	42.0	15	7	ADRI0603 Horse IGE
6	32	39.5	10	5	ABG98754 F protein
7	32	39.5	10	5	ABG98755 F protein
8	32	39.5	13	2	AAR79898 Fusion pr
9	31	38.3	14	2	AAM35339 Rat GDNF
10	31	38.3	14	2	AAM84178 Rat GDNF
11	30	37.0	14	4	AAM98177 Human pep
12	30	35.8	10	3	AAY51451 AAV VP3 d
13	29	35.8	10	4	AAB46909 AAV mutan
14	29	35.8	10	8	ADG94454 Human JAM
15	29	35.8	10	8	ADG94454 Human JAM
16	29	35.8	10	8	ADP87029 Junctiona
17	29	35.8	10	8	ADRI0604 Sheep IGE
18	28	34.6	8	7	ADJ72341 Streptomy
19	28	34.6	8	8	ADG94478 Human JAM
20	28	34.6	8	8	ADI46877 Permeabil
21	28	34.6	8	8	ADP87053 Junctiona
22	28	34.6	10	6	ABJ19566 Neuronal
23	28	34.6	10	8	ABY01523 SARS coro
24	28	34.6	10	8	ABY01210 SARS coro

25	28	34.6	10	9	ADZ86156 SARS coro
26	28	34.6	10	9	AEE45250 Apolipop
27	28	34.6	14	4	AEE05129 Peptide #
28	28	34.6	15	9	ADV51735 SARS-Cov
29	28	34.6	15	9	ADV51737 SARS-Cov
30	28	34.6	15	9	ADV51734 SARS-Cov
31	28	34.6	15	9	ADV51736 SARS-Cov
32	28	34.6	15	9	ADV51733 SARS-Cov
33	28	34.6	15	9	ADV51739 SARS-Cov
34	28	34.6	15	9	ADV51743 SARS-Cov
35	28	34.6	15	9	ADV51738 SARS-Cov
36	28	34.6	15	9	ADV51740 SARS-Cov
37	28	34.6	15	9	ADV51741 SARS-Cov
38	28	34.6	15	9	ADV51742 SARS-Cov
39	27	33.3	9	9	ADM23315 SARS coro
40	27	33.3	9	9	ADM23310 SARS coro
41	27	33.3	9	9	ADM23329 SARS coro
42	27	33.3	10	5	ABG98753 F protein
43	27	33.3	10	5	AU72805 TRA-8 hea
44	27	33.3	10	6	AAO29873 Mouse ant
45	27	33.3	10	7	ADJ79791 TRA-8 hea

## ALIGNMENTS

RESULT 1  
ADRI0601 standard, peptide, 15 AA.

ADRI0601;  
21-OCT-2004 (first entry)

Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

Antiasthmatic; Antiallergic; Immunosuppressive; IGF; dog; asthma;  
anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

Canis familiaris.  
WO2004065936-A2.  
05-AUG-2004.  
15-JAN-2004; 2004WO-US003566.  
16-JAN-2003; 2003US-0440472P.  
(UNNC-) UNIV NORTH CAROLINA STATE.  
Hammerberg B;  
WPI; 2004-593545/57.

Novel antibody that specifically binds to mammalian IGE epitope, useful  
for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (I) that  
specifically binds to a mammalian IGE epitope, where the epitope is  
between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
(I) is useful for testing an allergen reactivity of an IGE sample. The  
allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
and corn allergens. The sample is a biological sample collected from a  
dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
antibodies recognise epitopes on canine IGE corresponding to amino acid  
residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.  
 XX

Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RNDSPICQDQYTTTG 15  
 |||||  
 Db 1 RNDSPICQDQYTTTG 15

RESULT 2

ADRI0607  
 ID ADRI0607 standard; peptide; 15 AA.

AC ADRI0607;

DT 21-OCT-2004 (first entry)

DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KM pig.

XX Sue scrofa.

OS WO2004065936-A2.

PN 05-AUG-2004.

PD 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC pig IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 65.4%; Score 53; DB 8; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 0.042;  
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RNDSPICQDQYTTT 14  
 |||||  
 Db 1 RNDAPVQADRHSTT 14

RESULT 3

ADRI0602  
 ID ADRI0602 standard; peptide; 15 AA.

AC ADRI0602;

DT 21-OCT-2004 (first entry)

DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KM cat.

XX Felis catus.

OS WO2004065936-A2.

PN 05-AUG-2004.

PD 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC cat IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 59.3%; Score 48; DB 8; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 0.31;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSPIQDQYTTT 14  
 |||||  
 Db 2 NDSPIQDQYTTT 14

RESULT 4

ADRI0603  
 ID ADRI0603 standard; peptide; 15 AA.

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XX AC ADR10603;
XX XX
XX DT 21-OCT-2004 (first entry)
XX XX
DE Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.
XX
XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX horse.
XX
XX OS Equus caballus.
XX PN WO2004065936-A2.
XX PD 05-AUG-2004.
XX
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hammerberg B;
XX DR WPI; 2004-593545/57.
XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX or treating asthma or anaphylactic shock.
XX
XX PS Example 6; Page 9; 14pp; English.
XX
XX CC The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX of IGE from cat and horse, but did not exhibit cross-reactivity with
XX either pig or human epsilon-chains of IGE. The present sequence is the
XX horse IGE 5.91 recognition site.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 50.6%; Score 41; DB 8; Length 15;
XX Best Local Similarity 64.3%; Pred. No. 5.1;
XX Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 RNDSPQTQDYTTT 14
XX ||:|||||
XX 1 RNNVLIQTDOQATT 14
XX
XX
XX RESULT 5
XX ADR10603 standard; peptide; 15 AA.
XX
XX AC ADR10603;
XX XX
XX DT 21-OCT-2004 (first entry)
XX XX
DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.
XX
XX XX Horse; immunoglobulin E; IGE, heavy chain; immunogen; allergy.
XX
XX

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OS OS Equus caballus.
XX PN US2003087314-A1.
XX PD 08-MAY-2003.
XX
XX PF 08-NOV-2001; 2001US-00052788.
XX PR 08-NOV-2001; 2001US-00052788.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Gershwin LJ, Pettigrew HD, Kalina WV;
XX DR WPI; 2003-765437/72.
XX
XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
XX polypeptide that induces production of antibodies which specifically bind
XX to equine immunoglobulin E.
XX
XX PS Example 1; Page 8; 14pp; English.
XX
XX CC The invention relates to an immunogenic composition comprising an
XX isolated polypeptide having an amino acid sequence that is at least 80%
XX identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
XX equine immunoglobulin E (the composition induces production of an
XX antibody that specifically binds to equine immunoglobulin (IgE), the six
XX polypeptides are not explicitly identified in the specification. Also
XX included are a composition comprising an antibody that specifically binds
XX to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
XX specifically binds to equine IGE made by the process of immunising an
XX animal with a polypeptide at least 80% identical to (S1)-(S6), making an
XX animal with a composition further comprising an isolated polypeptide (the
XX amino acid sequence of the polypeptide is at least 80% identical to (S1)-
XX (S6)), and collecting antiserum from the animal) and a kit for detection
XX of equine IGE in a biological sample comprising the antibody and means
XX for detecting specific binding of the antibody to equine IGE. The
XX antibody is useful for detecting equine IGE protein in a biological
XX sample (serum) which involves contacting the sample with the antibody,
XX thus forming an antigen/antibody complex, and detecting the presence or
XX absence of the antigen/antibody complex. The antibody and antigen are
XX immobilised on a solid surface. The antibody is labelled such that the
XX complex can be detected. The complex is detected using a second labelled
XX antibody. The peptides are useful for generating antibodies specific for
XX IGE which can serve as a diagnostic test for allergy. The present
XX sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
XX peptide from the early portion of the C4 region.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 42.0%; Score 34; DB 7; Length 15;
XX Best Local Similarity 77.8%; Pred. No. 85;
XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6 IOTDQYTTT 14
XX |||||
XX 1 IOTDQQATT 9
XX
XX
XX RESULT 6
XX ABG98754 standard; peptide; 10 AA.
XX
XX AC ABG98754;
XX XX
XX DT 13-JAN-2003 (first entry)
XX XX
DE F protein decapetide #241.
XX
XX XX F protein; RSV; decapetide; negative sense single stranded RNA virus;
XX viral F protein; F protein mediated host cell virion fusion; virucide;
XX F protein mediated host cell virion budding.
XX
XX

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XX OS Respiratory syncytial virus.  
XX PN WO200242326-A1.  
XX PD 30-MAY-2002.  
XX PR 22-NOV-2000; 2001WO-AU001517.  
XX PF 22-NOV-2001; 2001WO-AU001517.  
XX PR 22-NOV-2000; 2000US-0252767P.  
XX PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.  
XX PI Mason AJ, Tucker SP, Young PR;  
XX DR WPI; 2002-599372/64.  
XX PT Facilitating production of a protein for analyzing, designing and/or  
PT modifying an agent that can interact with a viral F protein, comprises  
PT expressing a nucleic acid optimized for expression of the protein, using  
PT a eukaryotic cell.  
XX PS Claim 42; Page 102; 367pp; English.  
XX CC The invention relates to a method for facilitating production of a  
CC protein or its derivative from a negative sense single stranded RNA  
CC virus, by expressing a nucleic acid molecule encoding the protein in a  
CC host cell, where the nucleic acid is optimised for expression by a  
CC eukaryotic cell. The protein, especially F protein, is useful for  
CC analysing, designing and/or modifying an agent capable of interacting  
CC with a viral F protein or its derivative and modulating a functional  
CC activity associated with the protein, by contacting the protein with a  
CC putative agent and assessing the degree of interactive complementarity of  
CC the agent with the protein. An optimised nucleic acid or its derivative,  
CC equivalent, analogue or mimetic is useful for interacting with a viral F  
CC protein, for use in the manufacture of a medicament utilised in the  
CC therapeutic and/or prophylactic treatment of conditions characterised by  
CC infection with a negative sense single stranded RNA virus, and for  
CC modulating a functional activity associated with a viral F protein in a  
CC subject, preferably a mammal, especially a human, where the functional  
CC activity is F protein mediated host cell virion fusion and/or virion  
CC budding and the modulating is down regulation. Sequences ABG98514-  
CC ABG99058 represent F protein decapeptides of the invention  
CC  
XX Sequence 10 AA;  
SQ

Query Match 39.5%; Score 32; DB 5; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDO 10  
Db 2 NDMPTINDQ 10

RESULT 7  
ABG98755  
ID ABG98755 standard; peptide; 10 AA.  
XX AC ABG98755;  
XX DT 13-JAN-2003 (first entry)  
XX DE F protein decapeptide #242.  
XX KW F protein; RSV; decapeptide; negative sense single stranded RNA virus;  
KW viral F protein; F protein mediated host cell virion fusion; virucide;  
XX F protein mediated host cell virion budding.  
XX OS Respiratory syncytial virus.  
XX PN WO200242326-A1.

XX PD 30-MAY-2002.  
XX PF 22-NOV-2001; 2001WO-AU001517.  
XX PR 22-NOV-2000; 2000US-0252767P.  
XX PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.  
XX PI Mason AJ, Tucker SP, Young PR;  
XX DR WPI; 2002-599372/64.  
XX PT Facilitating production of a protein for analyzing, designing and/or  
PT modifying an agent that can interact with a viral F protein, comprises  
PT expressing a nucleic acid optimized for expression of the protein, using  
PT a eukaryotic cell.  
XX PS Claim 42; Page 102; 367pp; English.  
XX CC The invention relates to a method for facilitating production of a  
CC protein or its derivative from a negative sense single stranded RNA  
CC virus, by expressing a nucleic acid molecule encoding the protein in a  
CC host cell, where the nucleic acid is optimised for expression by a  
CC eukaryotic cell. The protein, especially F protein, is useful for  
CC analysing, designing and/or modifying an agent capable of interacting  
CC with a viral F protein or its derivative and modulating a functional  
CC activity associated with the protein, by contacting the protein with a  
CC putative agent and assessing the degree of interactive complementarity of  
CC the agent with the protein. An optimised nucleic acid or its derivative,  
CC equivalent, analogue or mimetic is useful for interacting with a viral F  
CC protein and modulating a functional activity associated with the viral  
CC protein, for use in the manufacture of a medicament utilised in the  
CC therapeutic and/or prophylactic treatment of conditions characterised by  
CC infection with a negative sense single stranded RNA virus, and for  
CC modulating a functional activity associated with a viral F protein in a  
CC subject, preferably a mammal, especially a human, where the functional  
CC activity is F protein mediated host cell virion fusion and/or virion  
CC budding and the modulating is down regulation. Sequences ABG98514-  
CC ABG99058 represent F protein decapeptides of the invention  
CC  
XX Sequence 10 AA;  
SQ

Query Match 39.5%; Score 32; DB 5; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDO 10  
Db 1 NDMPTINDQ 9

RESULT 8  
AAR79898  
ID AAR79898 standard; peptide; 13 AA.  
XX AC AAR79898;  
XX DT 25-MAR-2003 (revised)  
XX DT 25-APR-1996 (first entry)  
XX DE Fusion protein synthetic fragment SP4.  
XX KW Respiratory syncytial virus; RS virus; fusion protein; antibody; vaccine;  
KW human; therapy; diagnosis; immunoassay.  
XX OS Synthetic.  
XX PN CA1336955-C.  
XX PD 12-SEP-1995.  
XX PF 20-SEP-1989; 89CA-00612131.



XX 20-SEP-1988; 88US-00247017.  
 PR 20-SEP-1989; 89US-00409915.  
 XX  
 PA (PRAK-) PRAKIS BIOLOGICS INC.  
 XX  
 PI Paradise PR, Hu BT, Arumugham R, Hildreth SW, Martin-Gallardo A;  
 PI Walsh BE;  
 XX  
 DR WPI; 1995-328674/43.  
 XX  
 PT Sub-unit vaccine against respiratory syncytial virus - contains  
 PT polypeptide related to neutralising epitope on G protein, opt. also  
 PT polypeptide from F protein.  
 XX  
 PS Disclosure; Fig 3; 119pp; English.  
 XX  
 CC The sequences represented by AAR79895-R79899 are synthetic peptides  
 CC corresponding to regions of the respiratory syncytial (RS) virus fusion  
 CC protein (see AAR79894). This sequence corresponds to residues 261-273.  
 CC These fragments were used to create antibodies. The DNA encoding these  
 CC fragments is inserted into expression vectors and used to transform cell  
 CC cultures, the expressed protein is then isolated and purified. These  
 CC peptide fragments are then used in a vaccine. Alternatively, the  
 CC antibodies against these fragments could be used to confer short-term  
 CC protection against the RS virus. The vaccine can then be used to protect  
 CC humans and animals (for animals, the RS sequence used is from the RS  
 CC virus of that species). The dose of the vaccine is 0.1-100 micro grammes  
 CC per kg body weight. The vaccine can also be used in diagnosis, such as  
 CC immunoassays. The DNA encoding this sequence can be used in hybridisation  
 CC tests to detect RS virus in blood. The antibodies can be used to identify  
 CC viral epitopes. The advantage with using this methodology is that there  
 CC is no enhancement/potentiation of the disease seen with current  
 CC treatments. (Updated on 25-MAR-2003 to correct PF field.)  
 CC  
 SQ Sequence 13 AA;  
 XX  
 Query Match 39.5%; Score 32; DB 2; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 NDSPIQTQD 10  
 DB 2 NDMPTINDQ 10  
 XX  
 RESULT 9  
 AAM35339  
 ID AAM35339 standard; peptide; 14 AA.  
 XX  
 AC AAM35339;  
 XX  
 DT 01-MAY-1998 (first entry)  
 XX  
 DE Rat GDNF receptor residues 356-369.  
 XX  
 KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;  
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;  
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;  
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;  
 KW gene therapy.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO9740152-A1.  
 XX  
 PD 30-OCT-1997.  
 XX  
 PF 15-APR-1997; 97WO-US006281.  
 XX  
 PR 22-APR-1996; 96US-0015907P.  
 PR 09-MAY-1996; 96US-0017221P.  
 PR 14-APR-1997; 97US-00837199.

XX (AMGE-) AMGEN INC.  
 PA  
 XX  
 PI Fox GM, Men D, Jing S;  
 XX  
 DR WPI; 1997-535836/49.  
 XX  
 PT Glial cell line derived neurotrophic factor receptor - useful to treat  
 PT dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's  
 PT disease.  
 XX  
 PS Disclosure; Page 21; 196pp; English.  
 XX  
 CC The present peptide is derived from rat glial cell line-derived  
 CC neurotrophic factor (GDNF) receptor, which can be used to treat  
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's  
 CC disease or amyotrophic lateral sclerosis, complications of diabetes and  
 CC Huntington's disease and (optionally in combination with GDNF) glaucoma,  
 CC retinal degeneration and hearing loss caused by injury to inner ear  
 CC sensory neurons. The receptor can also be used to block unwanted GDNF  
 CC activity, analyse GDNF related molecules and stabilise GDNF in  
 CC pharmaceutical formulations. Receptor expressing cells, preferably  
 CC transfected ex vivo, can be used similarly by implantation, and the use  
 CC of the receptor cDNA in gene therapy is also contemplated. Probes based  
 CC on the cDNA can be used to identify GDNF responsive cells and tissues,  
 CC e.g. to identify patients who would benefit from GDNF therapy, and  
 CC abnormalities in receptor expression, and to isolate molecules that form  
 CC a complex with the cDNA or are homologous/cross-reactive with the cDNA.  
 CC Anti-receptor antibodies, oligonucleotides derived from the cDNA and  
 CC animal models that overexpress the receptor can be used to study the  
 CC biological function of GDNF, knockout transgenic animals can be used to  
 CC detect GDNF dependent neurons or processes and the antibody can be used  
 CC in immunoassays for the receptor. The receptor binds GDNF specifically  
 CC and with high affinity, acting as part of a complex that  
 CC mediates/enhances signal transduction by GDNF, i.e. increasing dopamine  
 CC uptake in dopaminergic cells  
 CC  
 SQ Sequence 14 AA;  
 XX  
 Query Match 38.3%; Score 31; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 PIQDQYTTT 14  
 DB 4 PVQITTTATT 13  
 XX  
 RESULT 10  
 AAM84178  
 ID AAM84178 standard; peptide; 14 AA.  
 XX  
 AC AAM84178;  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX  
 DE Rat GDNFR-alpha derived peptide.  
 XX  
 KW Rat; glial cell line derived neurotrophic factor receptor-alpha;  
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;  
 KW neurotrophin; signal transduction; dopaminergic nerve cell;  
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;  
 KW neurological disorder; diabetes; glaucoma; sensory neuron;  
 KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;  
 KW gene therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9854213-A2.  
 XX  
 PD 03-DEC-1998.  
 XX

```

PF 27-APR-1998; 98WO-US008486.
XX
XX 30-MAY-1997; 97US-00866354.
XX
XX (AMGE-) AMGEN INC.
XX
XX Fox GM, Jing S, Wen D;
XX
XX WPI; 1999-080806/07.
XX
XX New isolated glial cell line-derived neurotrophic factor receptors - used
PT to develop products for treating e.g. improperly functioning dopaminergic
PT nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
PT lateral sclerosis.
XX
XX Disclosure; Page 24; 318pp; English.
XX
XX The present peptide is derived from rat glial cell-line derived
CC neurotrophic factor receptor-alpha (GDNFR-alpha) amino acids 356-369. It
CC is used to raise antibodies against GDNFR-alpha. The peptide may also
CC possess an activity of GDNFR-alpha. The GDNFR-alpha protein is capable of
CC complexing with glial cell line-derived neurotrophic factor (GDNF) and
CC mediating cell response to GDNF. GDNFR-alpha proteins are functionally
CC characterised by the ability to bind GDNF and/or neurotrophin specifically,
CC and to act as part of a molecular complex which mediates or enhances the
CC signal transduction affects of GDNF and/or neurotrophin. The proteins can be
CC used for treating improperly functioning dopaminergic nerve cells,
CC Parkinson's disease, Alzheimer's disease or amyotrophic lateral
CC sclerosis. They can also be used for treating neurological disorders
CC associated with diabetes, glaucoma or other diseases and conditions
CC involving retinal ganglion cell degeneration, sensory neuropathy caused
CC by injury to, insults to, or degeneration of, sensory neurons,
CC pathological conditions, or disease or injury-related retinopathies. The
CC products can also be used for detection, diagnosis, drug screening and
CC gene therapy
XX
XX Sequence 14 AA;
SQ
Query Match 38.3%; Score 31; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 PLOTDOYTTT 14
|:|:|:|:|
DB 4 PVQTTATTTT 13

RESULT 11
AAM98177
ID AAM98177 standard; peptide; 14 AA.
XX
XX AAM98177;
AC
XX
XX 24-JAN-2002 (first entry)
XX
XX Human peptide #1452 encoded by a SNP oligonucleotide.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease.
XX
XX Homo sapiens.
XX
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.

```

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XX
XX 28-DEC-1999; 99US-0173419P.
XX
XX 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
XX Disclosure; Page 3986; 4143pp; English.
XX
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesin, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
XX Sequence 14 AA;
SQ
Query Match 37.0%; Score 30; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 6 IOTDOYTTT 14
|:|:|:|:|
DB 5 VQTDKVTSTT 13

RESULT 12
AAV51451
ID AAV51451 standard; peptide; 10 AA.
XX
XX AAV51451;
AC
XX
XX 11-MAY-2000 (first entry)
XX
XX AAV VP3 derived peptide fragment #6.
XX
XX VP3; structural protein; capsid; tropism; diagnosis; gene therapy.
XX
XX Adeno-associated virus.
XX
XX WO9967393-A2.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-EP004288.
XX
XX 19-JUN-1998; 98DE-01027457.
XX
XX (MEDT-) MEDIGENE AG.
XX
XX Haljek M, Ried M, Deleage G, Girod A;
XX
XX WPI; 2000-160586/14.
XX
XX Structure proteins of adeno-associated virus with at least one mutation
PT

```

PT have increased infectiveness.  
XX  
PS  
XX Example 2; Page 42; 43pp; German.  
XX  
CC This invention describes novel structural proteins of adeno-associated virus (AAV) especially AAV-capsids with at least one mutation and which have an increased infectiveness. The structural proteins are used to alter the tropism of AAV, to transform cells, for diagnosis and for effectivity studies for gene therapy and/or for genomic targeting.  
CC AAY51446-Y51467 represent AAV derived peptides used to illustrate the method of the invention  
CC  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 35.8%; Score 29; DB 3; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
XX  
OY 4 SPIQTDQY 11  
:|:|:|:|  
1 NPVATEQY 8  
XX  
DB 1 NPVATEQY 8  
XX  
RESULT 13  
AAB46909  
ID AAB46909 standard; peptide; 10 AA.  
XX  
XX AAB46909;  
XX  
XX 04-MAY-2001 (first entry)  
XX  
XX AAV mutant VP3 derived peptide SEQ ID 14.  
DE  
XX  
XX VP3 protein; structural protein; chromatography; tropism; antigenicity;  
XX  
XX genomic targeting; gene therapy; purification; affinity tag.  
OS  
XX Adeno associated virus.  
XX  
XX DE19933719-A1.  
XX  
XX 25-JAN-2001.  
PD  
XX  
XX 19-JUL-1999; 99DE-01033719.  
PF  
XX  
XX 19-JUL-1999; 99DE-01033719.  
PR  
XX  
XX (MED1-) MEDIGENE AG.  
PA  
XX  
XX Hallek M, Girod A, Ried M, Koerner C;  
PI  
XX  
XX WPI; 2001-203661/21.  
DR  
XX  
XX  
XX New mutant adeno-associated virus structural protein with altered  
PT chromatographic properties, useful in preparation of gene therapy  
PT vectors.  
XX  
XX Example 1; Page 15; 20pp; German.  
PS  
XX  
XX This invention describes a novel structural protein (I) of adeno-associated virus (AAV) which has at least one mutation that alters the  
CC chromatographic properties of the virus. The invention also describes (1)  
CC a nucleic acid (II) that encodes (1); (2) a cell (III) containing (II);  
CC and (3) producing (I) comprising culturing (III). (I), (II) and (III) are  
CC used to purify AAV and its particles, to alter the tropism or  
CC antigenicity of AAV, to transform cells, for genomic targeting, for  
CC diagnosis, for examination of activity and/or gene therapy. Altering the  
CC chromatographic properties improves purification, especially  
CC concentration of virus and produces viral particles to a higher titre or  
CC higher purity and/or provides more efficient purification (fewer steps,  
CC and a quicker and less expensive process). Particularly, mutated (I)  
CC result in viruses that are eluted at a different (higher or lower) salt  
CC concentration than the wild type, which tends to co-elute with other  
CC viruses, serum proteins and cellular debris, or that include a specific

CC affinity tag. Mutation may also allow targeting of cells, e.g.  
CC hematopoietic cells, that are not normally targets for AAV  
XX  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 35.8%; Score 29; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
XX  
OY 4 SPIQTDQY 11  
:|:|:|:|  
1 NPVATEQY 8  
XX  
DB 1 NPVATEQY 8  
XX  
RESULT 14  
ADG94454  
ID ADG94454 standard; peptide; 10 AA.  
XX  
XX ADG94454;  
XX  
XX 25-MAR-2004 (first entry)  
XX  
XX  
XX Human JAM-1 permeabilising peptide SEQ ID NO:433.  
DE  
XX  
XX human; permeabilising; interferon-beta; IFN-beta; mucosal delivery;  
XX immunosuppressive; virucide; autoimmune disease; viral disease;  
XX multiple sclerosis; chronic hepatitis B; condyloma acuminata;  
XX papilloma virus; childhood viral encephalitis; wart.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004002404-A2.  
XX  
XX  
XX 08-JAN-2004.  
PD  
XX  
XX 18-JUN-2003; 2003WO-US019261.  
PF  
XX  
XX 28-JUN-2002; 2002US-0393066P.  
PR  
XX  
XX (MAST-) MASTECH PHARM CO INC.  
PA  
XX  
XX Quay SC, Gupta M, De Weireles JC, Abd El- Shafy M;  
PI  
XX  
XX WPI; 2004-122360/12.  
DR  
XX  
XX  
XX Stable pharmaceutical composition comprising interferon compound(s)  
PT formulated for mucosal delivery to mammalian subjects in combination with  
PT mucosal delivery-enhancing agent (s).  
XX  
XX  
XX Disclosure; SEQ ID NO 433; 353pp; English.  
PS  
XX  
XX The invention relates to a novel stable pharmaceutical composition  
CC comprising one or more interferon (IFN)-beta compound(s) formulated for  
CC mucosal delivery to a mammalian subject in combination with one or more  
CC mucosal delivery-enhancing agent (s), where the composition following  
CC mucosal administration to the subject yields enhanced mucosal delivery of  
CC the one or more IFN-beta compound(s). A composition of the invention has  
CC immunosuppressive and virucide activity. The composition is useful for  
CC treating autoimmune diseases, viral disease, for alleviating one or more  
CC symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma  
CC acuminata, papilloma virus warts of the larynx or skin or childhood viral  
CC encephalitis in the subject without unacceptable adverse side effects.  
CC The composition can be delivered intranasally which reduces or eliminates  
CC compliance problems and side effects that attend delivery by injection.  
CC The sequences shown in ADG94022-ADG94810 represent permeabilising  
CC peptides used in a composition of the invention.  
XX  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 35.8%; Score 29; DB 8; Length 10;  
Best Local Similarity 62.5%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPLOTD 9  
 ||| : |||  
 Db 1 NDVPLPTD 8

## RESULT 15

ADI46852  
 ID ADI46852 standard; peptide; 10 AA.

XX  
 AC ADI46852;

XX  
 DT 06-MAY-2004 (first entry)

XX  
 DE Permeabilising peptide of human JAM-2 SegID561.

XX  
 KW mucosal delivery; permeabilising peptide;

KW mucosal epithelial paracellular transport; epithelial junction;

KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;

KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;

XX  
 OS female sexual dysfunction; human.

XX  
 PN Homo sapiens.

XX  
 PD WO2004003145-A2.

XX  
 PF 08-JAN-2004.

XX  
 PR 24-JUN-2003; 2003WO-US019994.

XX  
 PR 28-JUN-2002; 2002US-0392512P.

PA (NAST-) NASTECH PHARM CO INC.

PI Quay SC;

XX  
 DR WPI; 2004-091087/09.

PT Composition comprising biologically active agent and permeabilizing  
 PT peptide that reversibly enhances mucosal epithelial paracellular  
 PT transport by modulating epithelial junctional structure and/or physiology  
 PT in mammal.

PS Disclosure; SEQ ID NO 561; 426bp; English.

XX  
 CC This invention relates to a novel composition comprising a biologically  
 CC active agent and mucosal delivery-enhancing effective amount of  
 CC permeabilising peptide that reversibly enhances mucosal epithelial  
 CC paracellular transport by modulating epithelial junctional structure  
 CC and/or physiology in a mammal. The agent of the invention inhibits  
 CC homotypic binding of epithelial membrane adhesive protein chosen  
 CC junctional adhesion molecule (JAM), occludin and claudin. The  
 CC biologically active agent is effective for treatment of sexual  
 CC dysfunction, for example male erectile sexual dysfunction or female  
 CC sexual dysfunction. The present sequence is that of a permeabilising  
 CC peptide of human JAM-2 which may be used during the production of the  
 CC composition of the invention.

XX  
 SQ Sequence 10 AA;

Query Match 35.8%; Score 29; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPLOTD 9  
 ||| : |||  
 Db 1 NDVPLPTD 8

Search completed: December 12, 2005, 21:11:34  
 Job time : 114.667 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:30:45 / Search time 92.6667 Seconds  
(without alignments)  
67.634 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPIQTDQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	US-10-758-165-1	Sequence 1, Appl1
2	53	65.4	15	US-10-758-165-7	Sequence 7, Appl1
3	48	59.3	15	US-10-758-165-2	Sequence 2, Appl1
4	41	50.6	15	US-10-758-165-3	Sequence 3, Appl1
5	34	42.0	15	US-10-052-788-4	Sequence 4, Appl1
6	32	39.5	10	US-10-432-234A-249	Sequence 249, App
7	32	39.5	10	US-10-432-234A-250	Sequence 250, App
8	31	38.3	14	US-10-155-693-29	Sequence 29, Appl
9	31	38.3	14	US-10-872-161-29	Sequence 29, Appl
10	29	35.8	10	US-10-462-452-433	Sequence 433, App
11	29	35.8	10	US-10-601-953-561	Sequence 561, App
12	29	35.8	10	US-10-322-266-434	Sequence 434, App
13	29	35.8	12	US-09-990-832C-108	Sequence 108, Appl
14	29	35.8	15	US-10-758-165-4	Sequence 4, Appl1
15	28	34.6	8	US-10-462-452-457	Sequence 457, App
16	28	34.6	8	US-10-601-953-566	Sequence 566, App
17	28	34.6	8	US-10-322-266-458	Sequence 458, App
18	28	34.6	10	US-10-475-049A-24	Sequence 24, Appl
19	28	34.6	10	US-10-936-237-18	Sequence 18, Appl
20	28	34.6	11	US-10-378-173-28	Sequence 28, Appl
21	27	33.3	10	US-10-281-479A-27	Sequence 27, Appl
22	27	33.3	10	US-10-281-479A-27	Sequence 27, Appl
23	27	33.3	10	US-10-286-132A-27	Sequence 27, Appl
24	27	33.3	10	US-10-432-234A-248	Sequence 248, App
25	27	33.3	13	US-10-948-707-846	Sequence 846, App
26	27	33.3	13	US-10-948-707-949	Sequence 949, App
27	27	33.3	15	US-10-080-608A-161	Sequence 161, App

28	27	33.3	15	4	US-10-370-685-70	Sequence 70, Appl
29	26	32.1	10	3	US-10-428-335-103	Sequence 103, App
30	26	32.1	10	4	US-09-572-404B-1728	Sequence 1728, App
31	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
32	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, App
33	26	32.1	10	4	US-10-149-138-1502	Sequence 1502, App
34	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
35	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, App
36	26	32.1	10	4	US-10-149-138-1902	Sequence 1902, App
37	26	32.1	10	4	US-10-432-234A-251	Sequence 251, App
38	26	32.1	10	5	US-10-475-049A-15	Sequence 15, Appl
39	26	32.1	12	4	US-10-078-968-5	Sequence 5, Appl1
40	26	32.1	12	4	US-10-279-991-13	Sequence 13, Appl1
41	26	32.1	13	5	US-10-948-707-1324	Sequence 1324, App
42	26	32.1	14	3	US-09-826-290-126	Sequence 126, App
43	26	32.1	14	4	US-10-264-309-71	Sequence 71, Appl
44	26	32.1	14	5	US-10-264-309-71	Sequence 71, Appl
45	26	32.1	15	3	US-09-903-327A-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-10-758-165-1  
; Sequence 1, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-758-165-1

Query Match 100.0%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNDSPIQTDQYTTTG 15  
DB 1 RNDSPIQTDQYTTTG 15

RESULT 2  
US-10-758-165-7  
; Sequence 7, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-7

Query Match 65.4%; Score 53; DB 5; Length 15;

Best Local Similarity 57.1%; Pred. No. 0.035;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 1 RNDSP1QTDQYTTT 14  
|||:|:|:|:|  
Db 1 RNDAPVQADRHSTT 14

RESULT 3  
US-10-758-165-2  
; Sequence 2, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-2

Query Match 59.3%; Score 48; DB 5; Length 15;  
Best Local Similarity 61.5%; Pred. No. 0.26;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSP1QTDQYTTT 14  
|||:|:|:|:|  
Db 2 NDSPVTEQQAAT 14

RESULT 4  
US-10-758-165-3  
; Sequence 3, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Equus caballus  
US-10-758-165-3

Query Match 50.6%; Score 41; DB 5; Length 15;  
Best Local Similarity 64.3%; Pred. No. 4.2;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14  
|||:|:|:|:|  
Db 1 RNNVLIQTDQAAT 14

RESULT 5  
US-10-052-788-4  
; Sequence 4, Application US/10052788  
; Publication No. US20030087314A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerahwin, Laurel J.  
; APPLICANT: Pettigrew, Howard David

; APPLICANT: Kalina, Warren V.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for  
; FILE REFERENCE: 023070-121000US  
; CURRENT APPLICATION NUMBER: US/10/052,788  
; CURRENT FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:epitope peptide  
; OTHER INFORMATION: P4, early portion of C4 of equine IGF epsilon  
US-10-052-788-4

Query Match 42.0%; Score 34; DB 4; Length 15;  
Best Local Similarity 77.8%; Pred. No. 68;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDQYTTT 14  
|||:|:|:|:|  
Db 1 IQTDQAAT 9

RESULT 6  
US-10-432-234A-249  
; Sequence 249, Application US/10432234A  
; Publication No. US20040161846A1  
; GENERAL INFORMATION:  
; APPLICANT: Bioca Scientific Management Pty Ltd  
; TITLE OF INVENTION: A method of expression and agents identified thereby  
; FILE REFERENCE: 12084720/TDO  
; CURRENT APPLICATION NUMBER: US/10/432,234A  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US 60/252767  
; PRIOR FILING DATE: 2000-11-22  
; NUMBER OF SEQ ID NOS: 574  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 249  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: respiratory syncytial virus  
US-10-432-234A-249

Query Match 39.5%; Score 32; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 97;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSP1QTDQ 10  
|||:|:|:|:|  
Db 2 NDMPITNDQ 10

RESULT 7  
US-10-432-234A-250  
; Sequence 250, Application US/10432234A  
; Publication No. US20040161846A1  
; GENERAL INFORMATION:  
; APPLICANT: Bioca Scientific Management Pty Ltd  
; TITLE OF INVENTION: A method of expression and agents identified thereby  
; FILE REFERENCE: 12084720/TDO  
; CURRENT APPLICATION NUMBER: US/10/432,234A  
; CURRENT FILING DATE: 2003-05-22  
; PRIOR APPLICATION NUMBER: US 60/252767  
; PRIOR FILING DATE: 2000-11-22  
; NUMBER OF SEQ ID NOS: 574  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 250  
; LENGTH: 10

TYPE: PRT  
ORGANISM: respiratory syncytial virus  
US-10-432-234A-250

Query Match 39.5%; Score 32; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 97;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDQ 10  
DB 1 NDMPIITNDQ 9

RESULT 8  
US-10-155-693-29

Sequence 29, Application US/10155693  
Publication No. US20030175876A1  
GENERAL INFORMATION:  
APPLICANT: FOX, GARY M.  
APPLICANT: JING, SHUOJIAN  
APPLICANT: MEN, DUANZHI  
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR  
FILE REFERENCE: A-401C  
CURRENT APPLICATION NUMBER: US/10/155,693  
CURRENT FILING DATE: 2002-05-24  
PRIOR APPLICATION NUMBER: US/08/837,199  
PRIOR FILING DATE: 1997-04-14  
PRIOR APPLICATION NUMBER: US 60/015,907  
PRIOR FILING DATE: 1996-04-22  
PRIOR APPLICATION NUMBER: US 60/017,221  
PRIOR FILING DATE: 1996-05-09  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29  
LENGTH: 14  
TYPE: PRT  
ORGANISM: RAT  
US-10-155-693-29

Query Match 38.3%; Score 31; DB 4; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14  
DB 4 PVQTTTATTT 13

RESULT 9  
US-10-872-161-29

Sequence 29, Application US/10872161  
Publication No. US20040235714A1  
GENERAL INFORMATION:  
APPLICANT: FOX, GARY M.  
APPLICANT: JING, SHUOJIAN  
APPLICANT: MEN, DUANZHI  
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR  
FILE REFERENCE: A-401D  
CURRENT APPLICATION NUMBER: US/10/872,161  
CURRENT FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: US/08/866,354  
PRIOR FILING DATE: 1997-05-30  
PRIOR APPLICATION NUMBER: US 60/015,907  
PRIOR FILING DATE: 1996-04-22  
PRIOR APPLICATION NUMBER: US 60/017,221  
PRIOR FILING DATE: 1996-05-09  
PRIOR APPLICATION NUMBER: US 08/837,199  
PRIOR FILING DATE: 1997-04-14  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 29  
LENGTH: 14  
TYPE: PRT

ORGANISM: RAT  
US-10-872-161-29

Query Match 38.3%; Score 31; DB 5; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14  
DB 4 PVQTTTATTT 13

RESULT 10  
US-10-462-452-433

Sequence 433, Application US/10462452  
Publication No. US20040037809A1  
GENERAL INFORMATION:  
APPLICANT: Quay, Steven  
APPLICANT: El Shafy, Mohammed Abd  
APPLICANT: Gupta, Malini  
APPLICANT: de Meireles, Jorge  
TITLE OF INVENTION: Compositions and Methods for Enhanced  
TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta  
FILE REFERENCE: 02-0205  
CURRENT APPLICATION NUMBER: US/10/462,452  
CURRENT FILING DATE: 2003-06-16  
PRIOR APPLICATION NUMBER: 60/393,066  
PRIOR FILING DATE: 2002-06-28  
NUMBER OF SEQ ID NOS: 790  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 433  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-462-452-433

Query Match 35.8%; Score 29; DB 4; Length 10;  
Best Local Similarity 62.5%; Pred. No. 3.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTD 9  
DB 1 NDVPLPTD 8

RESULT 11  
US-10-601-953-561

Sequence 561, Application US/10601953  
Publication No. US2004007540A1  
GENERAL INFORMATION:  
APPLICANT: Quay, Steven C.  
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial  
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of  
TITLE OF INVENTION: Therapeutic Compounds  
FILE REFERENCE: 02-0305  
CURRENT APPLICATION NUMBER: US/10/601,953  
CURRENT FILING DATE: 2003-06-24  
PRIOR APPLICATION NUMBER: 60/392,512  
PRIOR FILING DATE: 2002-06-28  
NUMBER OF SEQ ID NOS: 900  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 561  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-10-601-953-561

Query Match 35.8%; Score 29; DB 4; Length 10;  
Best Local Similarity 62.5%; Pred. No. 3.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9  
||: ||  
Db 1 NDVPLPTD 8

## RESULT 12

US-10-322-266-434  
; Sequence 434, Application US/10322266  
; Publication No. US20040115135A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven C.  
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide  
; TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity  
; FILE REFERENCE: NPEI0567  
; CURRENT APPLICATION NUMBER: US/10/322,266  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 797  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 434  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-322-266-434

Query Match 35.8%; Score 29; DB 4; Length 10;  
Best Local Similarity 62.5%; Pred. No. 3.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9  
||: ||  
Db 1 NDVPLPTD 8

## RESULT 13

US-09-990-832C-108  
; Sequence 108, Application US/09990832C  
; Publication No. US20030149235A1  
; GENERAL INFORMATION:  
; APPLICANT: University Court of the University of Glasgow  
; TITLE OF INVENTION: Targeting peptides  
; FILE REFERENCE: PC/MC/JM/F11910US  
; CURRENT APPLICATION NUMBER: US/09/990,832C  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-108

Query Match 35.8%; Score 29; DB 3; Length 12;  
Best Local Similarity 62.5%; Pred. No. 3.9e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 SPIOTDXY 11  
: ||: ||  
Db 2 TPIDSTOY 9

## RESULT 14

US-10-758-165-4  
; Sequence 4, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165

; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Ovis aries  
US-10-758-165-4

Query Match 35.8%; Score 29; DB 5; Length 15;  
Best Local Similarity 42.9%; Pred. No. 5e+02;  
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 RNDSPIDQYTTT 14  
||: ||: ||  
Db 1 RNKELMREGQHTTT 14

## RESULT 15

US-10-462-452-457  
; Sequence 457, Application US/10462452  
; Publication No. US20040037809A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven  
; APPLICANT: El Shafy, Mohammed Abd  
; APPLICANT: Gupta, Malini  
; APPLICANT: de Meireles, Jorge  
; TITLE OF INVENTION: Compositions and Methods for Enhanced  
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta  
; FILE REFERENCE: 02-020US  
; CURRENT APPLICATION NUMBER: US/10/462,452  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: 60/393,066  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 790  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-462-452-457

Query Match 34.6%; Score 28; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNDSPIDQYTTT 8  
||: ||: ||  
Db 1 RNDVPLPTD 8

Search completed: December 12, 2005, 21:05:28  
Job time : 93.6667 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:20:00 ; Search time 27 Seconds  
(without alignments)  
45.931 Million cell updates/sec

Title: US-10-758-165a-1  
Perfect score: 81  
Sequence: 1 RNDSPIDQDTTGTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5 COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/6 COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/7 COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/8 COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/9 COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/10 COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	39.5	13	6	5223254-6
2	31	38.3	14	2	US-08-837-199A-29
3	27	33.3	9	2	US-09-341-982-75
4	27	33.3	12	1	US-08-479-233-8
5	27	33.3	13	4	PCT-US93-00643-8
6	27	33.3	13	1	US-08-209-525-50
7	27	33.3	15	2	US-09-914-259-161
8	26	32.1	12	1	US-08-423-441-4
9	26	32.1	12	2	US-09-514-739-5
10	26	32.1	12	2	US-09-517-866-13
11	26	32.1	15	2	US-10-378-707-1
12	25	30.9	8	1	US-08-413-708B-4
13	25	30.9	11	1	US-08-077-939-2
14	25	30.9	11	1	US-08-461-599-2
15	25	30.9	11	1	US-07-949-812-24
16	25	30.9	11	1	US-08-461-621-2
17	25	30.9	11	1	US-08-465-334-2
18	25	30.9	12	1	US-07-756-230-12
19	25	30.9	12	1	US-08-634-060-37
20	25	30.9	12	2	US-09-534-717-212
21	25	30.9	13	1	US-08-218-608-5
22	25	30.9	13	1	US-08-162-081B-7
23	25	30.9	13	1	US-08-780-872-7
24	25	30.9	13	1	US-08-747-137-23
25	25	30.9	13	2	US-09-205-680A-9
26	25	30.9	13	2	US-09-085-957-7
27	25	30.9	13	2	US-09-623-548A-1363

28	25	30.9	13	2	US-09-657-276-1363	Sequence 1363, App1
29	25	30.9	14	2	US-09-252-404A-15	Sequence 15, App1
30	25	30.9	14	2	US-08-851-567B-4	Sequence 4, App1
31	25	30.9	15	1	US-08-945-168-117	Sequence 117, App1
32	25	30.9	15	2	US-08-743-168B-17	Sequence 17, App1
33	25	30.9	15	2	US-09-306-998-4	Sequence 4, App1
34	25	30.9	15	2	US-09-233-086-6	Sequence 6, App1
35	25	30.9	15	2	US-09-117-860-11	Sequence 11, App1
36	25	30.9	15	4	PCT-US96-10435-17	Sequence 17, App1
37	24.5	30.2	14	1	US-08-162-402B-26	Sequence 26, App1
38	24.5	30.2	15	6	5204326-74	Patent No. 5204326
39	24	29.6	7	2	US-09-147-993-15	Sequence 15, App1
40	24	29.6	9	2	US-09-341-982-73	Sequence 73, App1
41	24	29.6	9	2	US-09-341-982-74	Sequence 74, App1
42	24	29.6	10	2	US-08-986-659B-16	Sequence 16, App1
43	24	29.6	12	2	US-09-349-661-4	Sequence 4, App1
44	24	29.6	12	2	US-09-341-982-79	Sequence 79, App1
45	24	29.6	13	2	US-09-680-728-9	Sequence 9, App1

## ALIGNMENTS

RESULT 1  
5223254-6  
; Patent No. 5223254  
; APPLICANT: PARADISO, PETER R.; HILDBRETH, STEPHEN W.; HU,  
; BRANDA, T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA  
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES  
; NUMBER OF SEQUENCES: 17  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/247,017  
; FILING DATE: 20-SEP-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 102,180  
; FILING DATE: 29-SEP-1987  
; SEQ ID NO: 6:  
; LENGTH: 13  
5223254-6

Query Match 39.5%; Score 32; DB 6; Length 13;  
Best Local Similarity 66.7%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	2	NDSPIQDTQ	10
DB	2	NDSPIQDTQ	10

RESULT 2  
US-08-837-199A-29  
; Sequence 29, Application US/08837199A  
; Patent No. 6455277  
; GENERAL INFORMATION:  
; APPLICANT: FOX, GARY M.  
; APPLICANT: JING, SHUOJIAN  
; APPLICANT: MEN, DUNZHUI  
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR  
; FILE REFERENCE: A-401C  
; CURRENT APPLICATION NUMBER: US/08/837,199A  
; CURRENT FILING DATE: 1997-04-14  
; PRIOR APPLICATION NUMBER: US 60/015,907  
; PRIOR FILING DATE: 1996-04-22  
; PRIOR APPLICATION NUMBER: US 60/017,221  
; PRIOR FILING DATE: 1996-05-09  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 29  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: RAT  
; US-08-837-199A-29

Query Match 38.3%; Score 31; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 53;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 5 PLOTQDTT 14  
|:|:|:|:  
DB 4 PVQTTATT 13

RESULT 3  
US-09-341-982-75  
; Sequence 75, Application US/09341982  
; Patent No. 6558671  
; GENERAL INFORMATION:  
; APPLICANT: SLINGLUFF, Craig L.  
; APPLICANT: HUNT, Donald F.  
; APPLICANT: ENGELHARD, Victor H.  
; APPLICANT: KITTELSEN, David  
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED  
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
; FILE REFERENCE: SLINGLUFF-3B  
; CURRENT FILING DATE: 1999-09-20  
; EARLIER APPLICATION NUMBER: PCT/US98/01592  
; EARLIER FILING DATE: 1998-01-29  
; EARLIER APPLICATION NUMBER: 60/037,781  
; EARLIER FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
US-09-341-982-75

Query Match 33.3%; Score 27; DB 2; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11  
|:|:|:|:  
DB 2 SDISTDY 9

RESULT 4  
US-08-479-233-8  
; Sequence 8, Application US/08479233  
; Patent No. 559679  
; GENERAL INFORMATION:  
; APPLICANT: Baylink, David J.  
; APPLICANT: Linkhart, Susan  
; TITLE OF INVENTION: AMINO PROCOLLAGEN 1(I) PEPTIDE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Stuart Street Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,233  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/829,142  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14508-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-479-233-8

Query Match 33.3%; Score 27; DB 1; Length 12;  
Best Local Similarity 58.3%; Pred. No. 2.2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 NDSPIQTDQYTT 13  
::|:|:|:|:  
DB 3 SESE--TDQYTT 12

RESULT 5  
PCT-US93-00643-8  
; Sequence 8, Application PC/TUS9300643  
; GENERAL INFORMATION:  
; APPLICANT: Baylink, David J.  
; APPLICANT: Linkhart, Susan  
; TITLE OF INVENTION: AMINO PROCOLLAGEN 1(I) PEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Stuart Street Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/00643  
; FILING DATE: 19930125  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14508-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-00643-8

Query Match 33.3%; Score 27; DB 4; Length 12;  
Best Local Similarity 58.3%; Pred. No. 2.2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 NDSPIQTDQYTT 13  
::|:|:|:|:

Db 3 SESP--TDOETT 12

## RESULT 6

US-08-209-525-50  
; Sequence 50, Application US/08209525  
; Patent No. 5571681

## GENERAL INFORMATION:

APPLICANT: Janda, Kim D.  
TITLE OF INVENTION: Chemical Event Selection By Suicide  
SUBSTRATE CONJUGATES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSER: The Scripps Research Institute  
STREET: 10566 No. 5571681th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CaliforniaCOUNTRY: US  
ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/209,525

FILING DATE: 10-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lewis, Donald G.

REGISTRATION NUMBER: 28,636

REFERENCE/DOCKET NUMBER: SCRF 408.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

US-08-209-525-50

Query Match 33.3%; Score 27; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 10 QYTTT 14  
| | | | |  
| | | | |  
Db 2 QYTTT 6

## RESULT 7

US-09-914-259-161  
; Sequence 161, Application US/09914259  
; Patent No. 6495336

## GENERAL INFORMATION:

APPLICANT: Makowski, Lee

APPLICANT: Hyman, Paul

TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

FILE REFERENCE: 8471-010-999

CURRENT APPLICATION NUMBER: US/09/914,259

NUMBER OF SEQ ID NOS: 180

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 161

LENGTH: 15

TYPE: PRT

ORGANISM: Murine sarcoma virus

US-09-914-259-161

Query Match 33.3%; Score 27; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;Qy 9 DQYTTG 15  
| | | | |  
| | | | |  
Db 8 DQYRTG 14

## RESULT 8

US-08-423-441-4  
; Sequence 4, Application US/08423441  
; Patent No. 5529926

## GENERAL INFORMATION:

APPLICANT: MAAT, JAN

APPLICANT: MUSTERS, WOUTER

APPLICANT: STAM, HEIN

APPLICANT: SCHAP, PETER J.

APPLICANT: VAN DE VONDERVOORT, PETER J.

APPLICANT: VISSER, JACOB

APPLICANT: VERBAKEL, JOHANNES M.

TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA ENCODING A

TITLE OF INVENTION: RIBOSOMAL FORM OF A POLYPEPTIDE HAVING SULFHYDRYL OXIDASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSER: CUSHMAN, DARBY &amp; CUSHMAN

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/423,441

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/044,620

FILING DATE: 09-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16773

REFERENCE/DOCKET NUMBER: 202744/T7019(V)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

TELEX: 248453CUSH

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-423-441-4

Query Match 32.1%; Score 26; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;Qy 3 DQPIQDQYT 12  
| | | | |  
| | | | |  
Db 2 DQKIDTDTYT 11

## RESULT 9

US-09-514-739-5  
; Sequence 5, Application US/09514739



FILING DATE: 16-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: GOES-3A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-413-708B-4

Query Match 30.9%; Score 25; DB 1; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQDPQYT 12  
:|:|:|:  
Db 2 VTIDNYT 8

RESULT 13  
US-08-077-939-2  
Sequence 2, Application US/08077939  
Patent No. 5521088  
GENERAL INFORMATION:  
APPLICANT: FUJII, Toshio  
APPLICANT: IWAMATSU, Akihiro  
APPLICANT: YOSHIMOTO, Hiroyuki  
APPLICANT: MINETOKI, Toshitaka  
APPLICANT: BOGAKI, Takayuki  
APPLICANT: NAGASAWA, Naoshi  
TITLE OF INVENTION: ALCOHOL ACETYLTRANSFERASE GENES AND USE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077, 939  
FILING DATE: 18-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 184328/1992  
FILING DATE: 18-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 62997/1993  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 49441/101 KYPA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
US-08-077-939-2

Query Match 30.9%; Score 25; DB 1; Length 11;  
Best Local Similarity 33.3%; Pred. No. 4.4e+02;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPIQDT 9  
:|:|:|:  
Db 1 KNQAPVQGE 9

RESULT 14  
US-08-461-599-2  
Sequence 2, Application US/08461599  
Patent No. 5658777  
GENERAL INFORMATION:  
APPLICANT: FUJII, Toshio  
APPLICANT: IWAMATSU, Akihiro  
APPLICANT: YOSHIMOTO, Hiroyuki  
APPLICANT: MINETOKI, Toshitaka  
APPLICANT: BOGAKI, Takayuki  
APPLICANT: NAGASAWA, Naoshi  
TITLE OF INVENTION: ALCOHOL ACETYLTRANSFERASE GENES AND USE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,599  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077, 939  
FILING DATE: 18-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 62997/1993  
FILING DATE: 26-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 184328/1992  
FILING DATE: 18-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 49441/105 KYPA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-461-599-2

Query Match 30.9%; Score 25; DB 1; Length 11;  
Best Local Similarity 33.3%; Pred. No. 4.4e+02;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPIQDT 9  
:|:|:|:  
Db 1 KNQAPVQGE 9

RESULT 15  
US-07-949-812-24  
; Sequence 24, Application US/07949812  
; Patent No. 5668007  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: RECOMBINANT 21KD COCOA PROTEIN AND PRECURSOR  
; NUMBER OF SEQUENCES: 28  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/949,812  
; FILING DATE: 27-JAN-1993  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-949-812-24

Query Match 30.9%; Score 25; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 4.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 DSPIC1D 9  
: ||: ||  
Db 2 NSPLD1D 8

Search completed: December 12, 2005, 21:00:45  
Job time : 28 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:00:56 ; Search time 4.66667 Seconds  
(without alignments)  
17.950 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPICRQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 8641

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	30.9	13	6	US-10-969-314-9
2	23	28.4	15	6	US-10-503-575-78
3	22	27.2	6	7	US-11-176-868-2
4	22	27.2	7	7	US-11-056-825-11
5	22	27.2	12	6	US-10-997-066-26
6	21	25.9	10	7	US-11-105-268-1
7	21	25.9	12	6	US-10-467-657-8983
8	21	25.9	14	6	US-10-524-643-51
9	21	25.9	15	7	US-11-022-562-119
10	20	24.7	7	7	US-11-096-706-58
11	20	24.7	8	6	US-10-989-226-49
12	20	24.7	9	6	US-10-989-226-50
13	20	24.7	9	6	US-10-491-096-94
14	20	24.7	9	7	US-11-010-748A-473
15	20	24.7	9	7	US-11-010-748A-479
16	20	24.7	10	6	US-10-491-096-95
17	20	24.7	12	7	US-11-016-706-14
18	20	24.7	13	6	US-10-511-559-117
19	20	24.7	13	6	US-10-511-559-118
20	20	24.7	13	6	US-10-511-559-304
21	20	24.7	13	6	US-10-511-559-305
22	20	24.7	13	6	US-10-511-559-628
23	20	24.7	15	6	US-10-511-559-77
24	20	24.7	15	7	US-11-022-562-120
25	19	23.5	9	7	US-11-010-748A-482

26	19	23.5	9	7	US-11-097-864-17	Sequence 17, Appl
27	19	23.5	9	7	US-11-097-912-17	Sequence 17, Appl
28	19	23.5	10	7	US-11-097-864-53	Sequence 53, Appl
29	19	23.5	10	7	US-11-097-912-53	Sequence 53, Appl
30	19	23.5	13	6	US-10-511-559-429	Sequence 429, Appl
31	19	23.5	13	6	US-10-511-559-430	Sequence 430, Appl
32	19	23.5	13	6	US-10-511-559-700	Sequence 700, Appl
33	19	23.5	13	6	US-10-511-559-702	Sequence 702, Appl
34	19	23.5	13	6	US-10-511-559-802	Sequence 802, Appl
35	19	23.5	13	6	US-10-511-559-803	Sequence 803, Appl
36	19	23.5	13	6	US-10-511-559-1080	Sequence 1080, Appl
37	19	23.5	13	6	US-10-989-226-22	Sequence 22, Appl
38	19	23.5	13	7	US-11-054-515-3054	Sequence 3054, Appl
39	19	23.5	14	6	US-10-494-781-12	Sequence 12, Appl
40	19	23.5	14	6	US-10-939-890-65	Sequence 65, Appl
41	19	23.5	14	7	US-11-054-515-2445	Sequence 2445, Appl
42	19	23.5	15	6	US-10-614-599-19	Sequence 19, Appl
43	19	23.5	15	6	US-10-989-226-54	Sequence 54, Appl
44	18.5	22.8	11	6	US-10-467-657-8862	Sequence 8862, Appl
45	18	22.2	7	6	US-10-467-657-7712	Sequence 7712, Appl

## ALIGNMENTS

RESULT 1  
US-10-969-314-9  
Sequence 9, Application US/10969314  
Publication No. US20050249719A1  
GENERAL INFORMATION:  
APPLICANT: SHAN, LU  
APPLICANT: BETHUNE, MICHAEL  
APPLICANT: KHOSLA, CHARITAN  
APPLICANT: GASS, JONATHAN  
APPLICANT: PYLE, GAIL G.  
APPLICANT: ISAACS, INDU  
APPLICANT: STROHMEIER, GREGG  
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR  
FILE REFERENCE: STAN-361  
CURRENT FILING DATE: US/10/969,314  
PRIORITY FILING DATE: 2004-10-19  
PRIORITY APPLICATION NUMBER: 60/565,668  
PRIORITY FILING DATE: 2004-04-26  
PRIORITY APPLICATION NUMBER: 10/367,405  
PRIORITY FILING DATE: 2003-02-14  
PRIORITY APPLICATION NUMBER: 60/357,238  
PRIORITY FILING DATE: 2002-02-14  
PRIORITY APPLICATION NUMBER: 60/380,761  
PRIORITY FILING DATE: 2002-05-14  
PRIORITY APPLICATION NUMBER: 60/392,782  
PRIORITY FILING DATE: 2002-06-28  
PRIORITY APPLICATION NUMBER: 60/422,933  
PRIORITY FILING DATE: 2002-10-31  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 13  
TYPE: PR  
ORGANISM: Trifolium aestivum  
US-10-969-314-9

Query Match 30.9%; Score 25; DB 6; Length 13;  
Best Local Similarity 40.0%; Pred. No. 27;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 IQTDQYTTTG 15  
|:|:|:|:|:  
Db 4 IEDNEYTARG 13

RESULT 2

US-10-503-575-78  
; Sequence 78, Application US/10503575  
; Publication No. US20050244823A1  
; GENERAL INFORMATION:  
; APPLICANT: Drifhout, Jan Mouter  
; APPLICANT: van Veele, Petrus Antonius  
; APPLICANT: Koning, Frits  
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD  
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS  
; FILE REFERENCE: 2799/72843-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/503,575  
; CURRENT FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: EP 02075456.0  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 78  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-575-78

Query Match 28.4%; Score 23; DB 6; Length 15;  
Best Local Similarity 57.1%; Pred. No. 75;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLOTDOY 11  
| | | |  
| | | |  
DB 3 PLOTDOY 9

RESULT 3  
US-11-176-868-2  
; Sequence 2, Application US/11176868  
; Publication No. US20050245454A1  
; GENERAL INFORMATION:  
; APPLICANT: Goldstein, Gideon  
; TITLE OF INVENTION: Methods and Compositions for Impairing Multiplication of HIV-1  
; FILE REFERENCE: GGG3USA  
; CURRENT APPLICATION NUMBER: US/11/176,868  
; CURRENT FILING DATE: 2005-07-08  
; PRIOR APPLICATION NUMBER: US/10/323,013  
; PRIOR FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US/10/114,176  
; PRIOR FILING DATE: 2002-04-02  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-11-176-868-2

Query Match 27.2%; Score 22; DB 7; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2.8e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP 5  
| | | |  
| | | |  
DB 2 RGDSP 6

RESULT 4  
US-11-056-825-11  
; Sequence 11, Application US/11056825  
; Publication No. US20050255109A1  
; GENERAL INFORMATION:  
; APPLICANT: Felding-Habermann, Brunhilde  
; APPLICANT: Janda, Kim D.  
; APPLICANT: Saven, Alan  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS

; FILE REFERENCE: SCP-0042  
; CURRENT APPLICATION NUMBER: US/11/056,825  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: US 60/626,726  
; PRIOR FILING DATE: 2004-11-10  
; PRIOR APPLICATION NUMBER: US 60/544,807  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-11-056-825-11

Query Match 27.2%; Score 22; DB 7; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2.8e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP 5  
| | | |  
| | | |  
DB 2 RGDSP 6

RESULT 5  
US-10-997-066-26  
; Sequence 26, Application US/10997066  
; Publication No. US20050244891A1  
; GENERAL INFORMATION:  
; APPLICANT: GRAHAM, RONALD J.  
; APPLICANT: LEE, HONGYE  
; APPLICANT: SUN, LINDA G.  
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF  
; FILE REFERENCE: 375461-011US  
; CURRENT APPLICATION NUMBER: US/10/997,066  
; CURRENT FILING DATE: 2004-11-24  
; PRIOR APPLICATION NUMBER: 60/525,492  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/628,509  
; PRIOR FILING DATE: 2004-11-15  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 26  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (8)  
; OTHER INFORMATION: Ser(PO4)  
US-10-997-066-26

Query Match 27.2%; Score 22; DB 6; Length 12;  
Best Local Similarity 44.4%; Pred. No. 89;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPQTD 9  
| | | |  
| | | |  
DB 1 RHSSPHQSE 9

RESULT 6  
US-11-105-268-1  
; Sequence 1, Application US/11105268  
; Publication No. US20050260204A1  
; GENERAL INFORMATION:  
; APPLICANT: Allan, Christian  
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF



```

; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-105-268-1

Query Match
Best Local Similarity 25.9%; Score 21; DB 7; Length 10;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTTTG 15
DB 2 YTFGTG 6

RESULT 7
US-10-467-657-8983
; Sequence 8983, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 8983
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-8983

Query Match
Best Local Similarity 25.9%; Score 21; DB 6; Length 12;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QTDQYTTT 14
DB 4 RTQYTTT 11

RESULT 8
US-10-524-643-51
; Sequence 51, Application US/10524643
; Publication No. US20050261215A1
; GENERAL INFORMATION:
; APPLICANT: GARREN, Hideki
; APPLICANT: HO, Peggy P.
; APPLICANT: STEINMAN, Lawrence
; TITLE OF INVENTION: METHODS AND IMMUNE MODULATORY NUCLEIC ACID COMPOSITIONS FOR
; TITLE OF INVENTION: PREVENTING AND TREATING DISEASE
; FILE REFERENCE: 022259-001010US
; CURRENT APPLICATION NUMBER: US/10/524,643
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: PCT/US2003/037157
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
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```

; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide antigen
; US-10-524-643-51

Query Match
Best Local Similarity 25.9%; Score 21; DB 6; Length 14;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IQTDQYT 12
DB 7 IETDKAT 13

RESULT 9
US-11-022-562-119
; Sequence 119, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Rupprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
; US-11-022-562-119

Query Match
Best Local Similarity 25.9%; Score 21; DB 7; Length 15;
Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 RNDSPIQDQYTTT 14
DB 2 QKQEPIDKELYPLT 15

RESULT 10
US-11-096-706-58
; Sequence 58, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: Region)
```

US-11-096-706-58

Query Match 24.7%; Score 20; DB 7; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNDSP1 6  
Db 1 RNDNR1 6

RESULT 11

US-10-989-226-49  
; Sequence 49, Application US/10989226  
; Publication No. US20050255491A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Xun  
; APPLICANT: Afeyan, Noubar B.  
; TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND  
; FILE REFERENCE: EPTM-P01-005  
; CURRENT APPLICATION NUMBER: US/10/989,226  
; CURRENT FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/519,530  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/532,687  
; PRIOR FILING DATE: 2003-12-24  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-989-226-49

Query Match 24.7%; Score 20; DB 6; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NDSP 5  
Db 2 NDAP 5

RESULT 12

US-10-989-226-50  
; Sequence 50, Application US/10989226  
; Publication No. US20050255491A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Xun  
; APPLICANT: Afeyan, Noubar B.  
; TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND  
; FILE REFERENCE: EPTM-P01-005  
; CURRENT APPLICATION NUMBER: US/10/989,226  
; CURRENT FILING DATE: 2004-11-15  
; PRIOR APPLICATION NUMBER: US 60/519,530  
; PRIOR FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/532,687  
; PRIOR FILING DATE: 2003-12-24  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 50  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-989-226-50

Query Match 24.7%; Score 20; DB 6; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NDSP 5  
Db 2 NDAP 5

RESULT 13

US-10-491-096-94  
; Sequence 94, Application US/10491096  
; Publication No. US20050267020A1  
; GENERAL INFORMATION:  
; APPLICANT: FAURE, OLIVIER  
; APPLICANT: KOSMATOPOULOS, KONSTANTINOS  
; TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM INDUCIBLE HSP70 AND PHARMACEUTICAL  
; FILE REFERENCE: 0508-1098  
; CURRENT APPLICATION NUMBER: US/10/491,096  
; CURRENT FILING DATE: 2004-03-29  
; PRIOR APPLICATION NUMBER: PCT/EP02/10821  
; PRIOR FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: FR 01402496.2  
; PRIOR FILING DATE: 2001-09-27  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 94  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-491-096-94

Query Match 24.7%; Score 20; DB 6; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+04;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 DSP1QTD 9  
Db 1 DAVQSD 7

RESULT 14

US-11-010-748A-473  
; Sequence 473, Application US/11010748A  
; Publication No. US20050244421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMATTER, Wolfgang  
; APPLICANT: WOLZ, Heidrun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 473  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 471  
US-11-010-748A-473

Query Match 24.7%; Score 20; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 10 QYTTG 15

Db 3 RYTSAG 8

RESULT 15

US-11-010-748A-479  
 ; Sequence 479, Application US/11010748A  
 ; Publication No. US20050244421A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck Patent GmbH  
 ; APPLICANT: STRITTMAYER, Wolfgang  
 ; APPLICANT: MOUL, Heidrun  
 ; APPLICANT: SCHARF, Burkhard  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
 ; FILE REFERENCE: MER-136  
 ; CURRENT APPLICATION NUMBER: US/11/010,748A  
 ; PRIORITY FILING DATE: 2004-12-13  
 ; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
 ; PRIOR FILING DATE: 2003-06-13  
 ; PRIOR APPLICATION NUMBER: EP02013423.5  
 ; PRIOR FILING DATE: 2002-06-13  
 ; NUMBER OF SEQ ID NOS: 926  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 479  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HLA-binding peptide of Seq. No. 471  
 US-11-010-748A-479

Query Match 24.7%; Score 20; DB 7; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 QYTTG 15  
 :||:|  
 Db 3 RYTSAG 8

Search completed: December 12, 2005, 21:17:40  
 Job time : 4.66667 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:05:42 / Search time 18 Seconds  
(without alignments)  
80.181 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPRQDTQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	34.6	14	2	Ig heavy chain DJ
2	26	32.1	11	2	amine oxidase (cop
3	24	29.6	14	2	porin - rice (stra
4	22	27.2	14	2	Ig heavy chain DJ
5	21	25.9	11	2	PSO259
6	21	25.9	13	2	H56046
7	20.5	25.3	13	2	S47376
8	20	24.7	11	2	S04875
9	20	24.7	11	2	A26120
10	20	24.7	11	2	S05002
11	20	24.7	12	2	PH0771
12	20	24.7	13	2	PN0125
13	20	24.7	14	2	PH1347
14	19	23.5	10	1	GMROL2
15	19	23.5	10	1	B60656
16	19	23.5	11	2	S58244
17	19	23.5	13	2	B61458
18	19	23.5	14	2	A61458
19	19	23.5	14	2	PH1705
20	19	23.5	14	2	S50900
21	19	23.5	15	2	S42741
22	19	23.5	15	2	PH1631
23	18	22.2	7	2	I48086
24	18	22.2	10	2	S43625
25	18	22.2	12	2	A61332
26	18	22.2	12	2	B58502
27	18	22.2	12	2	A61503
28	18	22.2	13	2	A33660
29	18	22.2	13	2	PT0331

30	18	22.2	14	2	PT0232	Ig heavy chain CRD
31	18	22.2	15	2	S32677	nitrogenase cofact
32	18	22.2	15	2	PA0097	starch phosphoryla
33	18	22.2	15	2	S29485	GTP-binding protei
34	18	22.2	15	2	S72432	epoxypropan isomer
35	17	21.0	8	2	I57018	gene Ctrr protein
36	17	21.0	9	2	PT0247	Ig heavy chain CRD
37	17	21.0	9	2	PL0139	carbon-monoxide de
38	17	21.0	10	2	B61512	variant surface gl
39	17	21.0	11	2	C53652	rh1r protein - pae
40	17	21.0	11	2	A29806	acidic proline-ric
41	17	21.0	11	2	S42449	anti protein - pha
42	17	21.0	12	2	S25485	transcription fact
43	17	21.0	12	2	PT0228	Ig heavy chain CDR
44	17	21.0	12	2	JU0356	cycloleucorin -
45	17	21.0	12	2	PN0170	alcohol dehydrogen

## ALIGNMENTS

RESULT 1  
PH1306  
Ig heavy chain DJ region (clone C96-100) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1306  
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1306  
A/Molecule type: DNA  
A/Residues: 1-14 <MAS>  
A/Cross-references: UNIPARC:UPI000017C253  
C/Keywords: heterotrimer; immunoglobulin

Query Match  
Best Local Similarity 100.0%; Score 28; DB 2; Length 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YTTTG 15  
Db 6 YTTTG 10

RESULT 2  
S71304  
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)  
C/Species: Aspergillus niger  
C/Date: 12-Feb-1998 #sequence\_revision 01-May-1998 #text\_change 09-Jul-2004  
C/Accession: S71304  
C/Fredort, I.; Tamaki, H.; Ishida, H.; Pec, P.; Lubova, L.; Tsuno, H.; Halata, M.; Asanc  
Eur. J. Biochem. 237, 255-265, 1996

A/Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc  
A/Reference number: S71303; MUID:96203933; PMID:8620882  
A/Accession: S71304

A/Molecule type: protein  
A/Residues: 1-11 <PRE>  
A/Cross-references: UNIPROT:Q7M504; UNIPARC:UPI000017B357  
C/Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquinine

Query Match  
Best Local Similarity 32.1%; Score 26; DB 2; Length 11;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTD 9  
Db 1 NDSPLAND 8

RESULT 3  
PS0249

porin - rice (strain Nihonbare) (fragment)  
C/Species: Oryza sativa (rice)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: PS0249  
R/Tsugita, A.  
submitted to JIPID, April 1993  
A/Reference number: PS0206  
A/Accession: PS0249  
A/Molecule type: protein  
A/Residues: 1-14 <TSU>  
A/Cross-references: UNIPROT:Q7M1U8; UNIPARC:UPI000017B118  
A/Experimental source: callus

Query Match 29.6%; Score 24; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 8 TDQYTTG 15  
DB 5 TDDHTANG 12

RESULT 4  
PH1305  
Ig heavy chain DJ region (clone C85-1B) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1305  
R/Maserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1305  
A/Molecule type: DNA  
A/Residues: 1-14 <MAS>  
A/Cross-references: UNIPARC:UPI000017C252  
C/Keywords: heterotrimer; immunoglobulin

Query Match 27.2%; Score 22; DB 2; Length 14;  
Best Local Similarity 62.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 6 IQTDQYTT 13  
DB 2 ILTGYYTT 9

RESULT 5  
PS0259  
39K protein 3225 - rice (strain Nihonbare) (fragment)  
C/Species: Oryza sativa (rice)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C/Accession: PS0259  
R/Tsugita, A.; Kamo, M.  
submitted to JIPID, April 1993  
A/Reference number: PS0209  
A/Accession: PS0259  
A/Molecule type: protein  
A/Residues: 1-11 <TSU>  
A/Cross-references: UNIPARC:UPI000017B102  
A/Experimental source: callus  
C/Comment: molecular weight 39K, pI 5.7.

Query Match 25.9%; Score 21; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 DSPIQTD 9  
DB 5 DGPIVAD 11

RESULT 6

H56046  
urinary tract stone matrix protein 10, 42K - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 09-Jul-2004  
C/Accession: H56046  
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.  
submitted to the Protein Sequence Database, February 1995  
A/Description: Isolation, characterization and sequence of stone proteins.  
A/Reference number: A56046  
A/Accession: H56046  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <BIN>  
A/Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NDSPIQTD 9  
DB 6 NDLAETD 13

RESULT 7  
S47376  
T-cell antigen receptor VJ junction beta chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C/Accession: S47376  
R/Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce  
A/Reference number: S47355  
A/Accession: S47376  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-13 <LEH>  
A/Cross-references: UNIPARC:UPI0000116687; EMBL:Z35702; NID:G527497; PIDN:CAA64771.1; PII  
C/Keywords: T-cell receptor

Query Match 25.3%; Score 20.5; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.9e+03;  
Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 4 SPIQTD-QY 11  
DB 4 SPRSTDYQY 12

RESULT 8  
S04875  
nifs protein - Bradyrhizobium japonicum (fragment)  
C/Species: Bradyrhizobium japonicum  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: S04875  
R/Beiling, S.  
submitted to the EMBL Data Library, December 1988  
A/Reference number: S04873  
A/Accession: S04875  
A/Molecule type: DNA  
A/Residues: 1-11 <EBE>  
A/Cross-references: UNIPROT:P37030; UNIPARC:UPI000016E719; EMBL:X13691; NID:G39544; PIDN  
A/Genetics: nifs  
A/Start codon: GTG

Query Match 24.7%; Score 20; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NDSPIQTD 9

Db 4 NRAPYLID 11

RESULT 9

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N:Alternate names: phosphofructokinase; phosphohexokinase

C:Species: Ascaris suum (pig roundworm)

C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #ext\_change 09-Jul-2004

C:Accession: A26120

R:Kulkarni, G.; Rao, G.S.V.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A:Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequen

A:Reference number: A26120; PMID:87083467; PMID:3025208

A:Accession: A26120

A:Molecule type: protein

A:Residues: 1-11 <KUL>

A:Cross-references: UNIPROT:Q7M4U2; UNIPARC:UPI000017B699

C:Keywords: glycolysis; phosphotransferase

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 11;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPROT 8

Db 4 RSDSIVPT 11

RESULT 10

S05002

corazonin - American cockroach

C:Species: Periplaneta americana (American cockroach)

C>Date: 07-Sep-1990 #sequence\_revision 09-Apr-1998 #ext\_change 09-Jul-2004

C:Accession: S05002

R:Veenastra, J.A.

FEBS Lett. 250, 231-234, 1989

A:Title: Isolation and structure of corazonin, a cardioactive peptide from the american

A:Reference number: S05002; PMID:8935572; PMID:2753132

A:Accession: S05002

A:Molecule type: protein

A:Residues: 1-11 <VE>

A:Cross-references: UNIPROT:P11496; UNIPARC:UPI0000127F28

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

P:1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 11;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QTDQYT 12

Db 1 QTFQYS 6

RESULT 11

PH0771

T-cell receptor beta chain (P55.1.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #ext\_change 05-Nov-1999

C:Accession: PH0771

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r

A:Reference number: PH0746; PMID:9207846; PMID:1836010

A:Accession: PH0771

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Cross-references: UNIPARC:UPI0000115FBE; EMBL:X60865; NID:953624; PIDD:CAA43255.1; PTD

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 12;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11

Db 3 SSFOYEQY 10

RESULT 12

PN0125

serine proteinase (EC 3.4.21.-) - Actinomyces sp. (fragment)

C:Species: Actinomyces sp.

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #ext\_change 09-Jul-2004

C:Accession: PN0125

R:Mosolova, O.V.; Rudenskaya, G.N.; Stepanov, V.M.; Khodova, O.M.; Tsaplina, I.A.

Biochimica 52, 414-422, 1987

A:Title: Glu, Asp-specific proteinase from Actinomyces.

A:Reference number: PN0125

A:Accession: PN0125

A:Molecule type: protein

A:Residues: 1-13 <MOS>

A:Cross-references: UNIPROT:Q7M107; UNIPARC:UPI000017AD24

A:Note: article in Russian with English abstract

C:Keywords: hydrolase; serine proteinase

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 13;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11

Db 1 SVIGTDVY 8

RESULT 13

PH1347

Ig heavy chain DJ region (clone C100-103A) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #ext\_change 07-May-1999

C:Accession: PH1347

R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; PMID:93094761; PMID:1460419

A:Accession: PH1347

A:Molecule type: DNA

A:Residues: 1-14 <MAS>

A:Cross-references: UNIPARC:UPI000017C21C

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 14;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 DQYTTG 15

Db 4 EDFLTG 10

RESULT 14

GM0012

leucosulfakinin-II - Madeira cockroach

N:Alternate names: LSK-II

C:Species: Leucophaea maderae (Madeira cockroach)

C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #ext\_change 09-Jul-2004

C:Accession: A26335

R:Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.

Biochem. Biophys. Res. Commun. 140, 357-364, 1986

A:Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to ch

A:Reference number: A26335; PMID:87048769; PMID:3778455

A:Accession: A26335

A;Molecule type: protein  
A;Residues: 1-10 <NAC>  
A;Cross-references: UNIPROT:P09039; UNIPARC:UPI000012B961  
C;Comment: This peptide was isolated from head extracts. It stimulates muscle contractio  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;5/Binding site: sulfate (Tyr) (covalent) #status experimental  
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 1; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QTDY 11  
|:|  
Db 1 QSDY 5

## RESULT 15

B60656  
leucosulfakinin II, non-sulfated - American cockroach  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C;Accession: B60656  
R;Veenstra, J. A.  
Neuropeptides 14, 145-149, 1989  
A;Title: Isolation and structure of two gastrin/CK-1-like neuropeptides from the American  
A;Reference number: A60656; MUID: 90137190; PMID: 2615921  
A;Accession: B60656  
A;Molecule type: protein  
A;Residues: 1-10 <VEE>  
A;Cross-references: UNIPROT:P09039; UNIPARC:UPI000012B961  
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QTDY 11  
|:|  
Db 1 QSDY 5

Search completed: December 12, 2005, 21:18:41  
Job time : 19 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:59:31 ; Search time 114 Seconds

(without alignments)  
92.833 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPICQDQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_crembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	26	32.1	11 2 Q7M504 ASPNG	Q7M504 aspergillus
2	24	29.6	13 2 Q804K2 FICPA	Q804K2 ficedula pa
3	24	29.6	14 2 Q7M1U8 ORYSA	Q7M1U8 oryza sativ
4	24	29.6	15 2 Q9S929 SOYBN	Q9S929 glycine max
5	23	28.4	13 1 PLMS LAMNA	P83009 lamna nasus
6	22	27.2	9 2 Q9TVF1 TRYCR	Q9TVF1 trypanosoma
7	22	27.2	14 2 Q7IGS6 9HYME	Q7IGS6 andrena n.
8	22	27.2	14 2 Q54394 STRLI	Q54394 streptomyces
9	22	27.2	15 1 UC19 MALIZ	P80625 zea mays (m
10	22	27.2	15 2 Q7IGV6 9HYME	Q7IGV6 andrena sim
11	22	27.2	15 2 Q7IH38 9HYME	Q7IH38 andrena aur
12	21	25.9	8 2 Q15893 HUMAN	Q15893 homo sapien
13	21	25.9	13 2 Q7M4P7 HUMAN	Q7M4P7 homo sapien
14	21	25.9	14 2 Q7Z2C2 CYPCA	Q7Z2C2 cyprinus ca
15	21	25.9	15 2 Q7IGT0 9HYME	Q7IGT0 andrena aff
16	20	24.7	8 2 Q7LIH2 YEAST	Q7LIH2 saccharomyc
17	20	24.7	10 1 ODP2 BOVIN	P11801 bos taurus
18	20	24.7	11 1 COR2 PERAM	P11966 periplaneta
19	20	24.7	11 2 Q7M4J2 ASCSU	Q7M4J2 ascaris suu
20	20	24.7	11 2 Q9TRR7 RABIT	Q9TRR7 oryctolagus
21	20	24.7	12 2 Q6SR12 CVHSA	Q6SR12 sars corona
22	20	24.7	12 2 Q6SR16 CVHSA	Q6SR16 sars corona
23	20	24.7	12 2 Q6SRJ0 CVHSA	Q6SRJ0 sars corona
24	20	24.7	12 2 Q6SRJ4 CVHSA	Q6SRJ4 sars corona
25	20	24.7	12 2 Q6SRJ8 CVHSA	Q6SRJ8 sars corona
26	20	24.7	12 2 Q6SRK2 CVHSA	Q6SRK2 sars corona
27	20	24.7	12 2 Q6SRK6 CVHSA	Q6SRK6 sars corona
28	20	24.7	12 2 Q6SRLO CVHSA	Q6SRLO sars corona
29	20	24.7	12 2 Q6SRL4 CVHSA	Q6SRL4 sars corona
30	20	24.7	12 2 Q6SRL8 CVHSA	Q6SRL8 sars corona
31	20	24.7	12 2 Q6SRM2 CVHSA	Q6SRM2 sars corona

32	20	24.7	12 2	Q6SRM6 CVHSA	Q6SRM6 sars corona
33	20	24.7	12 2	Q6SRN0 CVHSA	Q6SRN0 sars corona
34	20	24.7	12 2	Q6SRN4 CVHSA	Q6SRN4 sars corona
35	20	24.7	12 2	Q6SRN8 CVHSA	Q6SRN8 sars corona
36	20	24.7	12 2	Q6SRP2 CVHSA	Q6SRP2 sars corona
37	20	24.7	12 2	Q6SRP6 CVHSA	Q6SRP6 sars corona
38	20	24.7	12 2	Q6SRQ0 CVHSA	Q6SRQ0 sars corona
39	20	24.7	13 1	EP65 HUMAN	P54963 homo sapien
40	20	24.7	13 2	Q7M107 9ACTO	Q7M107 actinomyces
41	20	24.7	13 2	P90442 NPVSL	P90442 spodoptera
42	20	24.7	14 2	Q70L16 HUMAN	Q70L16 homo sapien
43	20	24.7	14 2	Q9P2X4 HUMAN	Q9P2X4 homo sapien
44	20	24.7	14 2	Q7IGI7 9HYME	Q7IGI7 macrotera t
45	20	24.7	14 2	Q7IGL2 9HYME	Q7IGL2 andrena fla

## ALIGNMENTS

## RESULT 1

Q7M504 ASPNG PRELIMINARY; PRT; 11 AA.  
AC Q7M504;  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
OS Aspergillus niger.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
ON NCBI\_TaxId=5061;  
RN [1]

PROTEIN SEQUENCE.  
RP Frebort I., Tamaki H., Ishida H., Pec P., Luhova L., Tsuno H.,  
RA Haila M., Asano Y., Kato Y., Matsushita K., Toyama H., Kumagai H.,  
RA Adachi O.;  
RT "Two distinct quinoprotein amine oxidases are induced by n-butylamine  
in the mycelia of Aspergillus niger AKU 3302: purification,  
RT characterization, cDNA cloning and sequencing.";  
RL Eur. J. Biochem. 237:255-265 (1996).  
DR PIR; S71304; S71304.  
DR GO; GO:0008131; F:amine oxidase activity; IEA.  
FT NON\_TER 1 11  
FT NON\_TER 1 11  
SQ SEQUENCE 11 AA; 1158 MM; 21BBBFDCA4472DC7 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## RESULT 2

Q804K2 FICPA PRELIMINARY; PRT; 13 AA.  
ID Q804K2;  
AC Q804K2;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Aldolase B (Fragment).  
GN Name=Aldob;  
OS Ficedula parva (Red-breasted flycatcher).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
ON NCBI\_TaxId=12611;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Saetre G.-P., Borge T., Lindroos K., Haavie J., Sheldon B.C.,  
RA Primer C.R., Svanen A.-C.;  
RT "Sex chromosome evolution and speciation in Ficedula flycatchers.";

```

RL  Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2003).
DR  EMBL; AY154343; AAO17275.1; -; Genomic_DNA.
FT  NON TER 1
FT  NON TER 13
SQ  SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 3 DSPIGTDQYTT 13
Db 1 DHDQRCQYVT 11

RESULT 3
O7MIU8 ORYSA
ID O7MIU8_ORYSA PRELIMINARY; PRT; 14 AA.
AC O7MIU8;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Porin (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatridae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP PROTEIN SEQUENCE.
RA Tsugita A.;
RL Submitted (APR-1993) to the PIR data bank.
DR PIR; PS0249; PS0249.
DR Gramene; O7MIU8; -.
FT NON TER 1
FT NON TER 14
SQ SEQUENCE 14 AA; 1490 MW; 83240AEOB1FA4EA CRC64;

Query Match 29.6%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 8 TDQYTTTG 15
Db 5 TDDHTANG 12

RESULT 4
O9S929 SOYBN
ID O9S929_SOYBN PRELIMINARY; PRT; 15 AA.
AC O9S929;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Pyroline-5-carboxylate reductase, PSOR (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=91378472; PubMed=1898034;
RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
RT "Pyroline-5-carboxylate reductase in soybean nodules:
RT isolation/partial primary structure/evidence for isozymes.";
RL Arch. Biochem. Biophys. 288:350-357(1991).
FT NON TER 15
SQ SEQUENCE 15 AA; 1715 MW; D9821F73F3DF524 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Oy 5 PIQTDQYTT 12
Db 5 PIPAESYTT 12

RESULT 5
PLMS_LAMNA
ID PLMS_LAMNA STANDARD; PRT; 13 AA.
AC P31009;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Phospholemman-like protein (PLMS) (Fragment).
OS Llama naeus (Purbeagle) (Squalus naeus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
OC Llama.
OX NCBI_TaxID=7849;
RN [1]
RP PROTEIN SEQUENCE.
RA TISSUE=Rectal gland;
RX MEDLINE=21514268; PubMed=11676495; DOI=10.1006/bhrc.2001.5826;
RA Schummers Stekhoven F.M.A.H., Plik G., Wendelaar Bonga S.E.;
RT "N-terminal sequences of small ion channels in rectal glands of
RT sharks: a biochemical hallmark for classification and phylogeny?";
RL Biochem. Biophys. Res. Commun. 288:670-675(2001).
CC -! FUNCTION: Induces a hyperpolarization-activated chloride current
CC when expressed in Xenopus oocytes. May have a functional role in
CC muscle contraction.
CC -! SUBCELLULAR LOCATION: Type I membrane protein. Mitochondrial
CC membrane.
CC -! PTM: Major plasma membrane substrate for camp-dependent protein
CC kinase (PK-A) and protein kinase C (PK-C) in several different
CC tissues. Phosphorylated in response to insulin and adrenergic
CC stimulation (By similarity)
CC -! SIMILARITY: Belongs to the FYXD family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC GO: GO:0005792; C:microsome; IDA.
DR InterPro; IPR000272; FYXD.
DR PROSITE; PS01310; FYXD: PARTIAL.
KW Chloride; Chloride channel; Direct protein sequencing;
KW Endoplasmic reticulum; Ion transport; Ionic channel; Microsome;
KW Phosphorylation; Transmembrane; Transport.
FT NON TER 13
SQ SEQUENCE 13 AA; 1542 MW; 081373C69724A444 CRC64;

Query Match 28.4%; Score 23; DB 1; Length 13;
Best Local Similarity 36.4%; Pred. No. 4.7e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 NDSPIGTDQYTT 12
Db 2 SDVPNDRFT 12

RESULT 6
O9TVF1 TRYCR
ID O9TVF1_TRYCR PRELIMINARY; PRT; 9 AA.
AC O9TVF1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Mucin-like protein (Fragment).
GN Name=EMUC-19c8;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;

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OC Schizotrypanum.
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Cl-Brenner;
RX MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
RA Di Nola J.M., D'Orso I., Aslund L., Sanchez D.O., Fraesch A.C.;
RT "The Trypanosoma cruzi mucin family is transcribed from hundreds of
RT genes having hypervariable regions.";
RU J. Biol. Chem. 273:10843-10850(1998).
DR EMBL AF036447; AAC14246.1; -; mRNA.
FT NON_TER
SQ SEQUENCE 9 AA; 896 MW; DBA31B1B85DD72D CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 9;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTTTG 15
DB 5 YTTTG 9

RESULT 7
Q7IGS6_9HYME PRELIMINARY; PRT; 14 AA.
ID Q7IGS6_9HYME PRELIMINARY; PRT; 14 AA.
AC Q7IGS6_9HYME PRELIMINARY; PRT; 14 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena n. sp. 'goth'.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205171;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Larkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL AF504376; AAQ07723.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 14 AA; 1692 MW; 79B3B922A4E7B5B CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 14;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPLOT 8
DB 6 NDSPLOT 12

RESULT 8
Q54394_STRLI PRELIMINARY; PRT; 14 AA.
ID Q54394_STRLI PRELIMINARY; PRT; 14 AA.
AC Q54394_STRLI PRELIMINARY; PRT; 14 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE S-adenosyl-L-homocysteine hydrolase (Fragment).
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TK21;
RA Romero N.M., Mellado R.P.;
RT "Activation of the actinorhodin biosynthetic pathway in Streptomyces

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RT lividans.";
RL FEMS Microbiol. Lett. 1217:79-84(1995).
DR EMBL X79814; CA56211.1; -; Genomic DNA.
DR GO; GO:0004013; F:adenosylhomocysteinase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006730; F:one-carbon compound metabolism; IEA.
DR InterPro; IPR00043; Ad_hcy_hydrolase.
DR Pfam; PF05221; AdoHcyase; 1.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 14 AA; 1725 MW; 1303D5023C485D2B CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 DSPLOT 11
DB 4 DSPLOT 12

RESULT 9
UC19_MAIZE STANDARD; PRT; 15 AA.
ID UC19_MAIZE STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 406)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP PROTEIN SEQUENCE.
RA Tousse P., Riccardi F., Morin C., Damerl C., Huet J.-C.,
RC Tissue=Coleoptile;
RA Pernellet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.6, its MW is: 18.4 kDa.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR Maize-2DPAGE; P80625; COLEOPTILE.
DR Gramese; P80625; -.
DR MaizeDB; 123951; -.
KW Direct protein sequencing.
FT NON_TER
FT NON_TER
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 1; Length 15;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 QYTTTG 15
DB 4 QYTTTG 9

RESULT 10
Q7IGV6_9HYME PRELIMINARY; PRT; 15 AA.
ID Q7IGV6_9HYME PRELIMINARY; PRT; 15 AA.
AC Q7IGV6_9HYME PRELIMINARY; PRT; 15 AA.

```

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DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena simulata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Iarkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504361; AACQ7693.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 15 AA; 1744 MW; 181B812922A4F3EE CRC64;

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 8.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQT 8
DB 6 NEIPIMT 12

RESULT 11
Q71H38_9HYME PRELIMINARY; PRT; 15 AA.
ID Q71H38_9HYME PRELIMINARY; PRT; 15 AA.
AC Q71H38;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena auripes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205215;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Iarkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504330; AACQ7611.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 15 AA; 1776 MW; 09EE90D922A4EE59 CRC64;

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 8.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQT 8
DB 6 NEIPIMT 12

RESULT 12
Q15893_HUMAN PRELIMINARY; PRT; 8 AA.
ID Q15893_HUMAN PRELIMINARY; PRT; 8 AA.
AC Q15893;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Homo sapiens (clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

```

```

OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh W.L., Chinnault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; -; mRNA.
FT NON TER
FT NON TER
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.2e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSPIQT 8
DB 1 SQNPIQT 7

RESULT 13
Q7M4P7_HUMAN PRELIMINARY; PRT; 13 AA.
ID Q7M4P7_HUMAN PRELIMINARY; PRT; 13 AA.
AC Q7M4P7;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Urinary tract stone matrix protein 10, 42K (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA Binette J.P., Binette M.B., Gawinowicz M.A., Kendrick N.;
RL Submitted (FEB-1995) to the PIR data bank.
DR PIR; H56046; H56046.
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1483 MW; 0A219099F5D32A4 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTD 9
DB 6 NDLAERTD 13

RESULT 14
Q7ZC2_CYPCA PRELIMINARY; PRT; 14 AA.
ID Q7ZC2_CYPCA PRELIMINARY; PRT; 14 AA.
AC Q7ZC2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Transcription factor Pit-1 (Fragment).
OS Cypripus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kausel G., Salazar M.F., Castro L.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AY273789; AAP33497.1; -; Genomic\_DNA.  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1557 MW; 893F88C975EA88B5 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 TDQYTT 13  
 ||:|  
 Db 9 TDCFTT 14

## RESULT 15

071GTO 9H9ME  
 ID 071GTO\_9H9ME PRELIMINARY; PRT; 15 AA.

AC 071GTO; 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit I.  
 OS Andrena aff. manifesta LIL-2002.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Andrenidae; Andreninae; Andrena.  
 OX NCBI\_TaxID=205242;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Larkin L.L., Neff J.L., Simpson B.B.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF504374; AA007719.1; -; Genomic\_DNA.  
 DR GO; GO:0005739; Mitochondrion; IEA.  
 KW Mitochondrion.  
 SQ SEQUENCE 15 AA; 1840 MW; 118E961922A39E59 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 30.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSPITQDQY 11  
 |:|:|:  
 Db 6 NEIPLMTMKF 15

Search completed: December 12, 2005, 21:17:21  
 Job time : 116 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:50 ; Search time 109.333 Seconds  
(without alignments)  
72.337 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDCQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 827869

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0610	Cat IGE e
2	87	89.7	18	ADRI0609	Dog IGE e
3	55	56.7	18	ADRI0612	Sheep IGE
4	37	38.1	18	ADCS6890	Peptide f
5	35	36.1	18	ADRI0611	Horse IGE
6	34	35.1	15	ADCS64569	Horse imm
7	33.5	33.5	15	ADJ38597	HSV-4 Gly
8	32.5	33.5	15	ADJ38596	HSV-4 Gly
9	32.5	33.5	15	ADW78189	Human met
10	32	33.0	9	AAU76520	Anti-Inte
11	32	33.0	9	AAE15818	Human mab
12	32	33.0	11	ADT40399	hSARS vir
13	32	33.0	11	ADT40399	hSARS vir
14	32	33.0	11	ADT40399	hSARS vir
15	32	33.0	15	AAI65747	Breast ca
16	32	33.0	15	ABU78631	Novel pro
17	32	33.0	15	ABU78631	Novel pro
18	32	33.0	15	ADN64911	HLA bindi
19	31	32.0	11	AAE02349	Caenorhab
20	31	32.0	12	AAE02349	Caenorhab
21	31	32.0	13	ADJ37003	Staphyloc
22	31	32.0	14	AAI31329	Staphyloc
23	31	32.0	15	ADN64927	HLA bindi
24	31	32.0	15	ADW77997	Human can

25	30	30.9	9	6	ABJ19961	AbJ19961 MHC bindi
26	30	30.9	9	7	ADD94584	Add94584 Human SIM
27	30	30.9	10	7	ADD94544	Add94544 Human SIM
28	30	30.9	11	9	AEI17405	Aei17405 Type II P
29	30	30.9	12	2	AAE49911	AAE49911 Glutamin
30	30	30.9	13	2	AAE49912	AAE49912 Glutamin
31	30	30.9	13	2	AAE49913	AAE49913 Glutamin
32	30	30.9	14	2	AAE49914	AAE49914 Glutamin
33	30	30.9	14	3	AAE49915	AAE49915 Human sec
34	30	30.9	14	3	AAE49916	AAE49916 Human sec
35	30	30.9	15	2	AAE49917	AAE49917 Murine sc
36	30	30.9	15	9	ADU70842	ADU70842 Human hep
37	30	30.9	16	2	AAE53562	AAE53562 Birch pol
38	30	30.9	16	8	ADG90450	ADG90450 RANTES re
39	30	30.9	17	2	AAE95159	AAE95159 bcl-x(L)/
40	30	30.9	18	9	ADV22975	ADV22975 HCV H77 i
41	29	29.9	9	2	AAW24775	AAW24775 Human imm
42	29	29.9	9	2	AAW80144	AAW80144 Light cha
43	29	29.9	9	2	AAW80142	AAW80142 Light cha
44	29	29.9	9	2	AAW40427	AAW40427 Amino aci
45	29	29.9	9	5	ABP62411	ABP62411 Human imm

## ALIGNMENTS

RESULT 1	ADRI0610	standard; peptide, 18 AA.
ADRI0610	ADRI0610	standard; peptide, 18 AA.
AC	ADRI0610	
XX		
XX		
DT	21-OCT-2004	(first entry)
XX		
DE	Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.	
XX		
KW	Antiaesthetic; Antiallergic; Immunosuppressive; IGF; dog; asthma;	
KW	anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;	
KW	cat.	
XX		
OS	Felis catus.	
XX		
PN	WO2004065936-A2.	
XX		
PD	05-AUG-2004.	
XX		
PF	15-JAN-2004; 2004WO-US003566.	
XX		
PR	16-JAN-2003; 2003US-0440472P.	
XX		
PA	(UNNC-) UNIV NORTH CAROLINA STATE.	
XX		
PI	Hammerberg B;	
XX		
DR	WPI; 2004-593545/57.	
XX		
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful	
PT	for testing an allergen reactivity of IGE sample, detecting mammalian IGE	
PT	or treating asthma or anaphylactic shock.	
XX		
XX	Example 6; Page 9; 14pp; English.	
CC	The present invention relates to a novel monoclonal antibody (I) that	
CC	specifically binds to a mammalian IGE epitope, where the epitope is	
CC	between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.	
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The	
CC	allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut	
CC	and corn allergens. The sample is a biological sample collected from a	
CC	dog, cat or horse. (I) is also useful for detecting mammalian IGE and for	
CC	treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal	
CC	antibodies recognise epitopes on canine IGE corresponding to amino acid	
CC	residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the	
CC	canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from	

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC cat IgE 3.76 recognition site.

XX  
 SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFPYTAPGKQ 18  
 |||||  
 Db 1 VDGGKATNIFPYTAPGKQ 18

RESULT 2

ID ADR10609 standard; peptide; 18 AA.

XX ADR10609;

XX 21-OCT-2004 (first entry)

XX Dog IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IgE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

XX MO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IgE epitope, useful  
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IgE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.

XX Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFPYTAPG 16  
 |||||  
 Db 1 VDGGKATNIFPYTAPG 16

RESULT 3

ID ADR10612 standard; peptide; 18 AA.

XX ADR10612;

XX 21-OCT-2004 (first entry)

XX Sheep IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IgE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

XX sheep.

XX Ovis aries.

XX MO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IgE epitope, useful  
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IgE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC sheep IgE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.063;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFPYTAP 15  
 |||||  
 Db 1 VDGGEDRNLFSTYAP 15

RESULT 4

ID ADC56890 standard; peptide; 15 AA.



```

XX AC ADC56890;
XX PI 18-DEC-2003 (first entry)
XX DT
XX DE Peptide fragment Seq ID7 related to human protein 36-41.
XX KW human; protein 36-41; arrhythmia; asthma; dementia.
XX OS Homo sapiens.
XX PN CN1382718-A.
XX PD 04-DEC-2002.
XX PF 26-APR-2001; 2001CN-00112751.
XX PR 26-APR-2001; 2001CN-00112751.
XX PA (BIOM-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2003-269480/27.
XX PT New human macroprotein-36-41, encoding polynucleotide, antagonist and
XX PT recombinant production, useful for treating dementia, arrhythmia, asthma
XX PT and digestive ulcers.
XX PS Example 6; SEQ ID NO 7; 33pp; Chinese.
XX CC This invention relates to a novel protein, human protein 36-41, and the
XX CC DNA sequence encoding it. The protein of the invention may be useful for
XX CC the treatment of diseases such as arrhythmia, asthma and dementia. The
XX CC present sequence is the amino acid sequence of a peptide fragment of
XX CC human protein 36-41 which was used in the exemplification of the
XX CC invention.
XX SQ Sequence 15 AA;

Query Match      38.1%; Score 37; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAP 15
   :|||:|:|:|
Db 1 MDGKMQPNSEFPWQSP 15

RESULT 5
ADRI0611
ID ADRI0611 standard; peptide; 18 AA.
XX
XX ADR10611;
XX
XX DT 21-OCT-2004 (first entry)
XX
XX DE Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX
XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX KW horse.
XX OS Equus caballus.
XX PN WO2004065936-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX

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PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX WPI; 2004-593545/57.
XX
XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful
XX PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX PT or treating asthma or anaphylactic shock.
XX
XX PS Example 6; Page 9; 14pp; English.
XX
XX CC The present invention relates to a novel monoclonal antibody (I) that
XX CC specifically binds to a mammalian IGE epitope, where the epitope is
XX CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX CC (I) is useful for testing an allergen reactivity of an IGE sample. The
XX CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX CC and corn allergens. The sample is a biological sample collected from a
XX CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX CC antibodies recognise epitopes on canine IGE corresponding to amino acid
XX CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX CC of IGE from cat and horse, but did not exhibit cross-reactivity with
XX CC either pig or human epsilon-chains of IGE. The present sequence is the
XX CC horse IGE 3.76 recognition site.
XX SQ Sequence 18 AA;

Query Match      36.1%; Score 35; DB 8; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPGKQ 18
   :|||:|:|:|
Db 1 IDGQKVDEQFPQHGVLKQ 18

RESULT 6
ADC64569
ID ADC64569 standard; peptide; 15 AA.
XX
XX ADC64569;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P5.
XX
XX KW Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX OS Equus caballus.
XX PN US2003087314-A1.
XX PD 08-MAY-2003.
XX PF 08-NOV-2001; 2001US-00052788.
XX PR 08-NOV-2001; 2001US-00052788.
XX PA (REGC ) UNIV CALIFORNIA.
XX Gershwin LJ, Pettigrew HD, Kalina WV;
XX WPI; 2003-765437/72.
XX
XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
XX PT polypeptide that induces production of antibodies which specifically bind
XX PT to equine immunoglobulin E.
XX PS Example 1; Page 8; 14pp; English.

```

XX The invention relates to an immunogenic composition comprising an  
CC isolated polypeptide having an amino acid sequence that is at least 80%  
CC identical to 6 (SI-86), 15 amino acid peptide sequences derived from  
CC equine immunoglobulin E (the composition induces production of an  
CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six  
CC polypeptides are not explicitly identified in the specification. Also  
CC included are a composition comprising an antibody that specifically binds  
CC to a polypeptide at least 80% identical to (SI)-(86), an antibody that  
CC specifically binds to equine IgE made by the process of immunising an  
CC animal with a polypeptide at least 80% identical to (SI)-(86), making an  
CC antibody that specifically binds to equine IgE (involving immunising an  
CC animal with a composition further comprising an isolated polypeptide (the  
CC (S6)), and collecting antiserum from the animal) and a kit for detection  
CC of equine IgE in a biological sample comprising the antibody and means  
CC for detecting specific binding of the antibody to equine IgE. The  
CC antibody is useful for detecting equine IgE protein in a biological  
CC sample (serum) which involves contacting the sample with the antibody,  
CC thus forming an antigen/antibody complex, and detecting the presence or  
CC absence of the antigen/antibody complex. The antibody and antigen are  
CC immobilised on a solid surface. The antibody is labelled such that the  
CC complex can be detected. The complex is detected using a second labelled  
CC antibody. The peptides are useful for generating antibodies specific for  
CC IgE which can serve as a diagnostic test for allergy. The present  
CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic  
CC peptide from the middle portion of the C2 region.  
XX  
SQ Sequence 15 AA;  
Query Match 35.1%; Score 34; DB 7; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 VDGKATNIEP 11  
| : | | | | |  
Db 2 IDGKVDGQFP 12  
| : | | | | |  
RESULT 7  
ADJ38597  
ID ADJ38597 standard; peptide; 15 AA.  
XX  
AC ADJ38597;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE HSV-4 Glycoprotein B late domain motif mutant peptide #1.  
XX  
XX Virucide; HSV infection; antiviral; late domain motif; mutcin; mutant.  
XX  
KM Human herpesvirus 4.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 6  
FT /note= "Wild-type residue replaced with Ala"  
XX  
PN WO2004009027-A2.  
XX  
PD 29-JAN-2004.  
XX  
PF 21-JUL-2003; 2003WO-US022828.  
XX  
PR 19-JUL-2002; 2002US-0397265P.  
PR 19-JUL-2002; 2002US-0397477P.  
PR 19-JUL-2002; 2002US-0397479P.  
PR 03-MAR-2003; 2003US-0451903P.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
XX Morham S, Zavitz K, Hobden A;  
XX

DR WPI; 2004-123282/12.  
XX  
XX Use of cells displaying herpes simplex virus (HSV) altered budding  
PT phenotype for the manufacture of a medicament for treating HSV infection.  
XX  
XX Example 13; Page 66; 74pp; English.  
XX  
XX The present invention relates to cells displaying herpes simplex virus  
CC (HSV) altered budding phenotype which are useful for the manufacture of a  
CC medicament for treating HSV infection. The medicament further comprises  
CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL  
CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and  
CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid  
CC encoding the polypeptide sufficient for virus-like particle assembly but  
CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.  
CC The genome is devoid of late domain motifs capable of effecting viral  
CC budding. The composition also comprises a compound capable of interfering  
CC with the protein-protein interaction between a host cell protein capable  
CC of binding a late domain motif and a HSV protein containing a late domain  
CC motif. The composition further comprises another HSV protein or its  
CC immunogenic fragment, and/or a nucleic acid encoding the other HSV  
CC protein or the immunogenic fragment. The present sequence is a mutant HSV  
CC peptide, derived from the wild-type peptide ADJ38596, used to illustrate  
CC the invention.  
XX  
SQ Sequence 15 AA;  
Query Match 34.5%; Score 33.5; DB 8; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
Qy 6 ATNIFYTAPGK 17  
| : | | | | |  
Db 1 ATTV-PATAPGX 11  
| : | | | | |  
RESULT 8  
ADJ38596  
ID ADJ38596 standard; peptide; 15 AA.  
XX  
AC ADJ38596;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE HSV-4 Glycoprotein B late domain motif wild-type peptide.  
XX  
XX Virucide; HSV infection; antiviral; late domain motif.  
XX  
KM Human herpesvirus 4.  
XX  
OS WO2004009027-A2.  
XX  
XX 29-JAN-2004.  
XX  
PF 21-JUL-2003; 2003WO-US022828.  
XX  
PR 19-JUL-2002; 2002US-0397265P.  
PR 19-JUL-2002; 2002US-0397477P.  
PR 19-JUL-2002; 2002US-0397479P.  
PR 03-MAR-2003; 2003US-0451903P.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
XX Morham S, Zavitz K, Hobden A;  
XX  
XX WPI; 2004-123282/12.  
XX  
XX Use of cells displaying herpes simplex virus (HSV) altered budding  
PT phenotype for the manufacture of a medicament for treating HSV infection.  
XX  
XX Example 13; Page 66; 74pp; English.  
XX  
XX The present invention relates to cells displaying herpes simplex virus  
CC

CC (HSV) altered budding phenotype which are useful for the manufacture of a  
 CC medicament for treating HSV infection. The medicament further comprises  
 CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL  
 CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and  
 CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid  
 CC encoding the polypeptide sufficient for virus-like particle assembly but  
 CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.  
 CC The genome is devoid of late domain motifs capable of effecting viral  
 CC budding. The composition also comprises a compound capable of interfering  
 CC with the protein-protein interaction between a host cell protein capable  
 CC of binding a late domain motif and a HSV protein containing a late domain  
 CC motif. The composition further comprises another HSV protein or its  
 CC immunogenic fragment, and/or a nucleic acid encoding the other HSV  
 CC protein or the immunogenic fragment. The present sequence is a wild-type  
 CC HSV peptide, from which mutant sequences (ADJ38597-ADJ38600) were  
 CC generated for use in the invention.

SQ Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 8; Length 15;

Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 ATNIPPYAPGK 17  
 |||:|||||  
 DB 1 ATTV-PPYAPGK 11

RESULT 9

ADM78189  
 ID ADM78189 standard; peptide; 15 AA.

AC ADM78189;

DT 07-APR-2005 (first entry)

DE Human metabolic therapy target peptide PACT.

XX DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;  
 XX vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;  
 XX antiallergic; immunosuppressive; antibacterial; antitumoric;  
 XX dermatological; antidiabetic; gastrointestinal-gen.; antitumor;  
 XX thrombolytic; neuroprotective; ophthalmological; antineumatic;  
 XX antipyretic; uteropathic; antipsoriatic; hepatotropic; muscular;  
 XX muscular-gen.; thymomimetic; antithyroid; gynecological; nephrotropic;  
 XX hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;  
 XX endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
 XX antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;  
 XX antinfertility; cancer; cardiovascular disease; inflammation;  
 XX metabolic disorder; neuropathy; sleep disorder.

OS Homo sapiens.

PN WO2005007090-A2.

PD 27-JAN-2005.

PF 02-JUL-2004; 2004WO-US021514.

PR 03-JUL-2003; 2003US-0484761P.

PA (HARD ) HARVARD COLLEGE.

PI Blenis J, Murphy LO;

XX WPI; 2005-112720/12.

PT Identification of compound for treating e.g. cancer by culturing cells  
 PT expressing target protein in the presence of growth factor, cytokine,  
 PT tumor promoter or oncogene and assessing binding after contacting with  
 PT the compound.

PS Claim 14; Page 64; 104pp; English.

XX The invention relates to a novel method for the identification of a  
 CC therapeutic compound. The method involves providing test cells that  
 CC express a target protein containing a DEF domain and MAP kinase;  
 CC culturing the cells in the presence of growth factor, cytokine, tumor  
 CC promoter or oncogene; contacting the cells with a candidate compound; and  
 CC assessing the binding of the MAP kinase to the DEF domain relative to the  
 CC binding in the absence of the candidate compound. The invention further  
 CC comprises a method for the identification of a therapeutic compound; a  
 CC method for treatment of cancer, which involves administering a compound  
 CC that inhibits the binding of a MAP kinase to the DEF domain of a target  
 CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos  
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds  
 CC have the following activities: cytosolic, cardiovascular-gen., cardiac,  
 CC vasoactive, hypotensive, antiarteriosclerotic, antiinflammatory,  
 CC antiallergic, immunosuppressive, antibacterial, antitumoric,  
 CC dermatological, antidiabetic, gastrointestinal-gen., antitumor,  
 CC thrombolytic, neuroprotective, ophthalmological, antineumatic,  
 CC antipyretic, uteropathic, antipsoriatic, hepatotropic, muscular  
 CC -gen., thymomimetic, antithyroid, gynecological, nephrotropic,  
 CC hepatotropic, virucide, anti-HIV, anabolic, hypertensive, anorectic,  
 CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,  
 CC antidepressant, antidiabetic, sedative, hypnotic, CNS-gen., and  
 CC antinfertility. The therapeutic compound may be used in the treatment  
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic  
 CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.  
 CC This sequence represents a metabolic therapy target peptide of the  
 CC invention.

SQ Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 9; Length 15;

Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 KATNIPPYAPG 16  
 |||:|||||  
 DB 1 KAT---PYTPFG 9

RESULT 10

AAU76520  
 ID AAU76520 standard; peptide; 9 AA.

AC AAU76520;

DT 05-JUN-2002 (first entry)

DE Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.

XX Human; antibody; anti-interleukin-12; CDR; light chain; circulatory;  
 XX complementarity determining region; neuroprotective; antipsoriatic;  
 XX immunostimulant; cytotoxic; anti-microbial; psoriasis; infection;  
 XX multiple sclerosis; immune disorder; cardiovascular; malignant disease;  
 XX neurological disorder.

OS Homo sapiens.

PN WO200212500-A2.

PD 14-FEB-2002.

PF 07-AUG-2001; 2001WO-US024720.

PR 07-AUG-2000; 2000US-023358P.

PR 29-SEP-2000; 2000US-0236827P.

PR 01-AUG-2001; 2001US-00920262.

PA (CENZ ) CENTOCOR INC.

XX Gilse-Komar J, Knight DM, Peritt D, Scallon B, Shealy D;  
 PI WPI; 2002-257482/30.

XX New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL  
PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as  
PT other for treating immune, infectious, malignant or neurological  
disorders.  
XX  
PS Claim 41, Page 93; 96pp; English.  
XX  
CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL  
CC -12) antibodies. The antibodies comprise at least one complementarity  
CC determining region (CDR) of a heavy or light chain, a heavy chain or  
CC light chain variable region, or a heavy chain or light chain constant  
CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or  
CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.  
CC The antibodies are also useful for treating immune, cardiovascular,  
CC infectious, malignant or neurological disorders or diseases. The present  
CC sequence represents the amino acid sequence of human anti-Interleukin-12  
CC (IL-12) antibody CDR3 light chain  
XX  
SQ Sequence 9 AA;  
Query Match 33.0%; Score 32; DB 5; Length 9;  
Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 8 NIPPYT 13  
||:||||  
Db 4 NIPPYT 9  
RESULT 11  
AAE15818  
ID AAE15818 standard; peptide; 9 AA.  
XX  
AC AAE15818;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human mAb 12B1 VK complementarity determining region (CDR) #3.  
XX  
XX Human: sialoadhesin factor-3; SAP-3; therapy; cancer; inflammation;  
KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;  
KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;  
KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;  
KW immunoglobulin; complementarity determining region; CDR; protozoacide;  
KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;  
KW fungicide; neuroprotective; light chain variable region; VK; mAb;  
KW monoclonal antibody.  
XX  
OS Homo sapiens.  
XX  
PN WO200190193-A1.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US016864.  
XX  
PR 24-MAY-2000; 2000US-00577930.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Abrahamson JA, Kikly KK;  
XX  
DR WPI; 2002-083094/11.  
XX  
PT Novel monoclonal antibody that binds to human sialoadhesin factor-3 for  
PT treating or preventing cancer, inflammation, autoimmunity, allergy,  
PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.  
PS Claim 13; Page 67; 69pp; English.  
XX  
CC The invention relates to monoclonal antibodies that bind to human

CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or  
CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central  
CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple  
CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections and  
CC for modulating an immune response in a mammal, where the immune response  
CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and  
CC therapeutic reagents, to subcharacterise cell populations during  
CC haematopoietic development, to treat anaemia, as a diagnostic marker to  
CC distinguish between different forms of cancer, to purge bone marrow ex  
CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo  
CC expansion (proliferation and/or differentiation) of haematopoietic  
CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell  
CC mobilisation into the periphery and as an vivo chemoprotective agent.  
CC Protein comprising immunoglobulin complementarity determining region  
CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure  
CC screening methods for detecting the effect of added compounds on the  
CC production of mRNA and polypeptide in cells. The present sequence is  
CC complementarity determining region of human monoclonal antibody (mAb)  
CC 12B1 light chain variable region (VK), which binds to SAF-3  
XX  
SQ Sequence 9 AA;  
Query Match 33.0%; Score 32; DB 5; Length 9;  
Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 8 NIPPYT 13  
||:||||  
Db 4 NIPPYT 9  
RESULT 12  
ADT40399  
ID ADT40399 standard; peptide; 11 AA.  
XX  
AC ADT40399;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE hSARS virus peptide, SEQ ID 1387.  
XX  
XX Viucide; Severe Acute Respiratory Syndrome; SARS; vaccine.  
KW  
KW SARS coronavirus.  
OS  
PN WO2004085650-A1.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-CN000246.  
XX  
PR 24-MAR-2003; 2003US-0457031P.  
PR 26-MAR-2003; 2003US-0457730P.  
PR 02-APR-2003; 2003US-045921P.  
PR 03-APR-2003; 2003US-0460357P.  
PR 08-APR-2003; 2003US-0461265P.  
PR 14-APR-2003; 2003US-0462805P.  
PR 23-APR-2003; 2003US-0464886P.  
PR 25-APR-2003; 2003US-0465738P.  
PR 14-MAY-2003; 2003US-0470935P.  
XX  
PA (UYHK-) UNIV HONG KONG.  
XX  
PI Chan K, Guan Y, Nicholas JM, Peiris JSM, Foon L, Yuen K,  
PI Leung FC;  
XX  
DR WPI; 2004-737326/72.  
XX  
PT New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of  
PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for  
PT diagnosing and treating SARS.  
PS Example; SEQ ID NO 1387; 200pp; English.  
XX

XX The present invention relates to novel human Severe Acute Respiratory  
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a  
CC hSARS virus having China Center for Type Culture Collection Deposit  
CC Accession No. CCTCC-V200303. The present invention also relates to novel  
CC nucleic acid molecules (1; ADT41483 or ADT41485) encoding a nucleocapsid-  
CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are  
CC methods for detecting the presence of a N- or S-gene of the hSARS virus  
CC or of the protein in a biological sample and identifying a subject  
CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein  
CC sequences are useful as vaccines for diagnosing or treating SARS. They  
CC are also useful in clinical and scientific research applications. The  
CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences  
CC of all three reading frames were deduced from the complementary strand.  
CC ADT40120 is the full-length protein encoded by the first reading frame of  
CC the complementary strand and ADT40121-ADT40601 are the peptides from the  
CC first reading frame protein. ADT40602 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT40603-  
CC ADT40976 are the peptides from the second reading frame protein. ADT40977  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT40978-ADT41482 are the peptides from the  
CC third reading frame protein.  
SQ Sequence 11 AA;  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 2.8e+02; Mismatches 4; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 3 GQKATNIPPYT 13  
||:|||||  
1 GQSQSNILPQT 11  
Db  
RESULT 13  
ADT379816  
ID ADT379816 standard; protein; 11 AA.  
AC ADAT379816;  
XX  
XX 30-DEC-2004 (first entry)  
XX  
DE SARS virus complementary DNA strand reading frame 1 protein #279.  
XX  
KM virucide; vaccine; detection; severe acute respiratory syndrome;  
KM real-time quantitative polymerase chain reaction; SARS.  
XX  
OS SARS coronavirus.  
XX  
XX MO2004085455-A1.  
XX  
XX 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-CN000247.  
XX  
XX 24-MAR-2003; 2003US-0457031P.  
PR 26-MAR-2003; 2003US-0457730P.  
PR 02-APR-2003; 2003US-0459931P.  
PR 03-APR-2003; 2003US-0460357P.  
PR 08-APR-2003; 2003US-0461265P.  
PR 14-APR-2003; 2003US-0462805P.  
PR 23-APR-2003; 2003US-0464886P.  
PR 05-MAY-2003; 2003US-0468139P.  
PR 16-MAY-2003; 2003US-0471200P.  
XX  
XX (UYHK-) UNIV HONG KONG.  
XX  
XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;  
XX WPI; 2004-737292/72.  
XX  
XX New isolated nucleic acid molecule useful for detecting, treating,  
PT ameliorating, or preventing the virus causing severe acute respiratory

PT syndrome in humans using a real-time quantitative polymerase chain  
PT reaction assay.  
XX  
XX Example; SEQ ID NO 1387; 183pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule consisting  
CC essentially of, and/or hybridizes under stringent conditions to a fully  
CC defined nucleotide sequence of 16-25 base pairs (bp; SEQ ID NO: 2471-  
CC 2476), or its complement. The methods and compositions of the present  
CC invention are useful for the detection of the virus causing Severe Acute  
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative  
CC polymerase chain reaction (PCR) assay. They can also be used in treating,  
CC ameliorating, managing or preventing SARS. This sequence corresponds to a  
CC partial SARS protein sequence from the complementary reading frame 1.  
XX  
SQ Sequence 11 AA;  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 2.8e+02; Mismatches 4; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 3 GQKATNIPPYT 13  
||:|||||  
1 GQSQSNILPQT 11  
Db  
RESULT 14  
ADT37929  
ID ADT37929 standard; peptide; 11 AA.  
XX  
XX ADT37929;  
XX  
XX 30-DEC-2004 (first entry)  
XX  
DE SARS virus peptide, SEQ ID 1387.  
XX  
XX Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.  
XX  
XX SARS coronavirus.  
XX  
XX MO2004085633-A1.  
XX  
XX 07-OCT-2004.  
XX  
XX 24-MAR-2004; 2004WO-CN000248.  
XX  
XX 24-MAR-2003; 2003US-0457031P.  
PR 26-MAR-2003; 2003US-0457730P.  
PR 02-APR-2003; 2003US-0459931P.  
PR 03-APR-2003; 2003US-0460357P.  
PR 08-APR-2003; 2003US-0461265P.  
PR 14-APR-2003; 2003US-0462805P.  
PR 23-APR-2003; 2003US-0464886P.  
XX  
XX (UYHK-) UNIV HONG KONG.  
XX  
XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;  
XX Leung FC;  
XX WPI; 2004-728736/71.  
XX  
XX New isolated human severe acute respiratory syndrome (hSARS) virus,  
PT useful as vaccine for diagnosing or treating SARS or in clinical and  
PT scientific research applications.  
XX  
XX Example; SEQ ID NO 1387; 176pp; English.  
XX  
XX The present invention relates to novel human Severe Acute Respiratory  
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a  
CC hSARS virus having China Center for Type Culture Collection Deposit  
CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein  
CC sequences are useful in clinical and scientific research applications. The

CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences  
CC of all three reading frames were deduced from the complementary strand.  
CC ADT37650 is the full-length protein encoded by the first reading frame of  
CC the complementary strand and ADT37651-ADT38131 are the peptides from the  
CC first reading frame protein. ADT38132 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT38133-  
CC ADT38506 are the peptides from the second reading frame protein. ADT38507  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT38508-ADT39012 are the peptides from the  
CC third reading frame protein.

XX Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKATNFPYT 13  
Db 1 GQSQSNILPOT 11

#### RESULT 15

AA65747 ID AAY65747 standard; peptide; 15 AA.

XX AAY65747;

DT 10-FEB-2000 (first entry)

DE Breast cancer susceptibility (BRCA 2) mutant peptide 31.

XX Human; frameshift mutant; T cell response; tumour; treatment; cancer;  
KW mutcin.

XX Homo sapiens.  
OS Synthetic.

XX MO9958552-A2.

XX 18-NOV-1999.

XX 03-MAY-1999; 99WO-NO000143.

XX 08-MAY-1998; 98NO-00002097.

XX (NH2D ) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Sæterdal I;

DR WPI; 2000-039064/03.

PT New peptides derived from genes with frameshift mutations, used to  
PT develop products for the treatment and prophylaxis of cancers.

PS Claim 13; Page 25; 166pp; English.

CC Peptides AAY65684-Y66142 are fragments of mutant proteins arising from a  
CC frameshift mutation in a gene from a cancer cell. The peptides are  
CC characterised in that they: (i) are at least 8 amino acids long and a  
CC fragment of a mutant protein arising from a frameshift mutation in a gene  
CC of a cancer cell; (ii) consist of at least one amino acid of the mutant  
CC part of a protein sequence encoded by the gene; (iii) comprise 0-10 amino  
CC acid from the carboxyl terminus of the normal part of the protein  
CC sequence preceding the amino terminus of the mutant sequence and may  
CC further extend to the carboxyl terminus of the mutant part of the protein  
CC as determined by a new stop codon generated by the frameshift mutation;  
CC and (iv) induce, either in their full lengths or after processing by an  
CC antigen presenting cell (APC), T cell responses. The genes that the  
CC peptides are derived from, are characterised as susceptible to frameshift  
CC mutation by having a mono nucleoside base repeat sequence of at least 5  
CC residues, or a di-nucleoside base repeat sequence of at least 4 di-  
CC nucleoside base units. The peptides are created by the addition or

CC deletion of 1 or 2 nucleoside base residues from the repeat sequence. The  
CC novel peptides can elicit T cell responses and toxicity against tumours  
CC and cancer cells carrying genes with frameshift mutations. The novel  
CC peptides and DNA sequences can be used for the preparation of a  
CC composition for the treatment or prophylaxis of cancer

XX Sequence 15 AA;

Query Match 33.0%; Score 32; DB 3; Length 15;  
Best Local Similarity 54.5%; Pred. No. 3.9e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGQKATNFP 11  
Db 4 VEDQKKTIVFP 14

Search completed: December 12, 2005, 21:52:03  
Job time : 110.333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:05:57 / Search time 27 Seconds  
(without alignments)  
55.117 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 208455

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:  
1: /cgn2\_6/prodata/1/1aa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/7 COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/8 COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/9 COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	33.0	9	2	US-09-920-262A-6
2	32	33.0	15	2	US-09-674-973A-64
3	31	33.0	11	2	US-09-307-265A-14
4	31	33.0	12	1	US-08-260-582-47
5	31	32.0	12	1	US-08-260-582-48
6	31	32.0	12	4	PCT-US95-05471-47
7	31	32.0	12	4	PCT-US95-05471-48
8	30	30.9	9	2	US-09-865-548A-126
9	30	30.9	17	1	US-08-333-565-22
10	30	30.9	17	1	US-08-661-479-22
11	29	29.9	9	2	US-09-042-353-366
12	29	29.9	9	2	US-08-758-417A-214
13	29	29.9	15	2	US-08-278-774-20
14	29	29.9	18	2	US-09-856-920-1
15	28	28.9	10	2	US-09-641-803-18
16	28	28.9	10	2	US-09-641-802-18
17	28	28.9	10	2	US-09-641-801-18
18	28	28.9	10	2	US-10-281-652-18
19	28	28.9	11	1	US-07-958-903A-10
20	28	28.9	11	1	US-08-462-018-10
21	28	28.9	11	1	US-08-823-245-10
22	28	28.9	11	2	US-07-963-329A-60
23	28	28.9	11	2	US-09-318-001-10
24	28	28.9	11	2	US-09-064-159-10
25	28	28.9	11	4	PCT-US92-09443A-60
26	28	28.9	15	1	US-08-080-073-26
27	28	28.9	16	2	US-10-044-708A-3

28	28	28.9	18	1	US-08-084-718-30	Sequence 30, Appl
29	28	28.9	18	1	US-08-443-976-30	Sequence 30, Appl
30	28	28.9	18	1	US-08-443-977-30	Sequence 30, Appl
31	27	27.8	11	2	US-09-809-517A-21	Sequence 21, Appl
32	27	27.8	18	1	US-08-421-702A-100	Sequence 100, App
33	27	27.8	18	1	US-08-303-052A-100	Sequence 100, App
34	27	27.8	18	1	US-08-421-696A-100	Sequence 100, App
35	27	27.8	18	1	US-08-421-697A-100	Sequence 100, App
36	27	27.8	18	1	US-08-421-698A-100	Sequence 100, App
37	27	27.8	18	1	US-08-421-699A-101	Sequence 101, App
38	27	27.8	18	1	US-09-017-205-48	Sequence 48, Appl
39	27	27.8	18	1	US-09-017-205-49	Sequence 49, Appl
40	26	26.8	5	2	US-09-788-006-9	Sequence 9, Appl
41	26	26.8	9	2	US-09-602-812A-12	Sequence 12, Appl
42	26	26.8	10	2	US-09-914-695-24	Sequence 24, Appl
43	26	26.8	12	1	US-08-096-762-208	Sequence 208, App
44	26	26.8	12	2	US-09-042-353-342	Sequence 322, App
45	26	26.8	12	2	US-08-758-417A-170	Sequence 170, App

## ALIGNMENTS

```

RESULT 1
US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patencin Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6

Query Match      33.0%; Score 32; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 NIPYPT 13
      |||
Db      4 NIPYPT 9

RESULT 2
US-09-674-973A-64
; Sequence 64, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hydr0 ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT

```

ORGANISM: Homo sapiens  
US-09-674-973A-64

Query Match  
Best Local Similarity 33.0%; Score 31; DB 2; Length 15;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDQKATNIFP 11  
Db 4 VEDQKTLVFP 14

RESULT 3  
US-09-307-265A-14  
Sequence 14, Application US/09307265A

PATENT INFORMATION:  
PATENT NO. 6225456  
APPLICANT: Gu, Trent  
APPLICANT: Orita, Satoshi  
TITLE OF INVENTION: RAS SUPPRESSOR SUR-5  
FILE REFERENCE: UTC-03732  
CURRENT APPLICATION NUMBER: US/09/307,265A  
CURRENT FILING DATE: 1999-05-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 14  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-307-265A-14

Query Match  
Best Local Similarity 32.0%; Score 31; DB 2; Length 11;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18  
Db 1 PYTSGKK 8

RESULT 4  
US-08-260-582-47

Sequence 47, Application US/08260582  
PATENT NO. 5635182  
GENERAL INFORMATION:  
APPLICANT: McCoy, John M.  
TITLE OF INVENTION: METHOD OF DETECTING LIGAND  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/260,582  
FILING DATE: 16-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiner, M. C.  
REGISTRATION NUMBER: 31,544  
REFERENCE/DOCKET NUMBER: GI 5236  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-260-582-47

Query Match  
Best Local Similarity 32.0%; Score 31; DB 1; Length 12;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18  
Db 4 PWLAPGEO 11

RESULT 5  
US-08-260-582-48

Sequence 48, Application US/08260582  
PATENT NO. 5635182  
GENERAL INFORMATION:  
APPLICANT: McCoy, John M.  
TITLE OF INVENTION: METHOD OF DETECTING LIGAND  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/260,582  
FILING DATE: 16-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiner, M. C.  
REGISTRATION NUMBER: 31,544  
REFERENCE/DOCKET NUMBER: GI 5236  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 876-1170  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-260-582-48

Query Match  
Best Local Similarity 32.0%; Score 31; DB 1; Length 12;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18  
Db 4 PWLAPGEO 11



RESULT 6  
PCT-US95-05471-47  
; Sequence 47, Application PC/TUS9505471  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS  
; NUMBER OF SEQUENCES: 76  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05471  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
PCT-US95-05471-47

Query Match  
Best Local Similarity 32.0%; Score 31; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPGKQ 18  
|: |||:|  
DB 4 PMLAPGEQ 11

RESULT 7  
PCT-US95-05471-48  
; Sequence 48, Application PC/TUS9505471  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS  
; NUMBER OF SEQUENCES: 76  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05471  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
PCT-US95-05471-48

Query Match  
Best Local Similarity 32.0%; Score 31; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPGKQ 18  
|: |||:|  
DB 4 PMLAPGEQ 11

RESULT 8  
US-09-865-548A-126  
; Sequence 126, Application US/09865548A  
; Patent No. 6867283

; GENERAL INFORMATION:  
; APPLICANT: Barnea, Eilon  
; APPLICANT: Beer, Ilan  
; APPLICANT: Ziv, Tamir  
; APPLICANT: Admon, Arie  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES  
; FILE REFERENCE: 01/22080  
; CURRENT APPLICATION NUMBER: US/09/865,548A  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR FILING DATE: 2001-05-16  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 126  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-865-548A-126

Query Match  
Best Local Similarity 30.9%; Score 30; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIPPY 12  
|||||  
DB 1 NIPPY 5

RESULT 9  
US-08-333-565-22  
; Sequence 22, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-333-565-22

Query Match  
Best Local Similarity 30.9%; Score 30; DB 1; Length 17;

Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16  
|||  
Db 3 PYLAPG 8

RESULT 10  
US-08-661-479-22

; Sequence 22, Application US/08661479

; Patent No. 5834209

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, Stanley J.

; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/661,479

; FILING DATE: 11-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/333,565

; FILING DATE: 31-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 15726A-000700

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-661-479-22

Query Match 30.9%; Score 30; DB 1; Length 17;

Best Local Similarity 83.3%; Pred. No. 2.3e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16  
|||  
Db 3 PYLAPG 8

RESULT 11  
US-09-042-353-366

; Sequence 366, Application US/09042353

; Patent No. 6255458

; GENERAL INFORMATION:

; APPLICANT: Lomborg, Nils

; APPLICANT: Kay, Robert M.

; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for

; NUMBER OF SEQUENCES: 421

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/042,353

; FILING DATE: 13-MAR-1998

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/810,279

; FILING DATE: 17-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/853,408

; FILING DATE: 18-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/904,068

; FILING DATE: 23-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/990,860

; FILING DATE: 16-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/053,131

; FILING DATE: 26-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/096,762

; FILING DATE: 22-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/155,301

; FILING DATE: 18-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/161,739

; FILING DATE: 03-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/165,699

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/209,741

; FILING DATE: 09-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/352,322

; FILING DATE: 07-DEC-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/544,404

; FILING DATE: 10-OCT-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/728,463

; FILING DATE: 10-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US96/16433

; FILING DATE: 10-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/758,417

; FILING DATE: 02-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/21803

; FILING DATE: 01-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 014643-009040US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 366:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-042-353-366

Query Match 29.9%; Score 29; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIPYPT 13  
| | | | |  
Db 4 NSFPYT 9

RESULT 12  
US-08-758-417A-214  
Sequence 214, Application US/08758417A  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-Dec-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 214:  
US-08-758-417A-214

Query Match 29.9%; Score 29; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIPYPT 13  
| | | | |  
Db 4 NSFPYT 9

RESULT 13  
US-08-278-774-20  
Sequence 20, Application US/08278774  
Patent No. 6653450  
GENERAL INFORMATION:  
APPLICANT: Berg, Richard A  
Tomam, David P  
APPLICANT: Wallace, Donald  
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COLLAGEN CORPORATION  
STREET: 2500 Faber Place  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,774  
FILING DATE: 22-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ralayko, Katchi L  
REGISTRATION NUMBER: 36,644  
REFERENCE/DOCKET NUMBER: 94-018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 354-4642  
TELEFAX: (415) 354-4752  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-278-774-20  
Query Match 29.9%; Score 29; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGOKATNIPY 12  
| | | | |  
Db 2 IGGERKGGAFY 13

RESULT 14  
US-09-856-920-1  
Sequence 1, Application US/09856920  
Patent No. 6740325  
GENERAL INFORMATION:  
APPLICANT: Yeda Research and Development Co.  
TITLE OF INVENTION: Peptide-based vaccine for influenza

; FILE REFERENCE: 9822 PCT  
; CURRENT APPLICATION NUMBER: US/09/856,920  
; CURRENT FILING DATE: 2002-02-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Influenza virus  
US-09-856-920-1

Query Match 29.9%; Score 29; DB 2; Length 18;  
Best Local Similarity 44.4%; Pred. NO. 3.6e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 TNIPPYTAP 15  
:|:|:|  
Db 5 SNCYPYDVP 13

RESULT 15  
US-09-641-803-18  
; Sequence 18, Application US/09641803  
; Patent No. 650798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: Peptide  
US-09-641-803-18

Query Match 28.9%; Score 28; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. NO. 2.8e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 IFPYTAP 15  
:|:|:|  
Db 1 VYPTGP 7

Search completed: December 12, 2005, 21:20:08  
Job time : 27 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:19 / Search time 95 Seconds  
(without alignments)  
79.168 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 356231

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10 Sequence 10, Appl
2	87	89.7	18	5	US-10-758-165-9 Sequence 9, Appl
3	55	56.7	18	5	US-10-758-165-12 Sequence 12, Appl
4	37	38.1	15	5	US-10-856-118-34 Sequence 34, Appl
5	35	36.1	18	5	US-10-758-165-11 Sequence 11, Appl
6	34	35.1	15	4	US-10-052-788-5 Sequence 5, Appl
7	32	33.0	9	3	US-09-920-262A-6 Sequence 6, Appl
8	32	33.0	9	5	US-10-912-994-6 Sequence 6, Appl
9	32	33.0	9	5	US-10-975-883-6 Sequence 6, Appl
10	32	33.0	9	5	US-10-975-740A-6 Sequence 6, Appl
11	32	33.0	9	5	US-10-975-708-6 Sequence 6, Appl
12	32	33.0	11	5	US-10-808-187-1387 Sequence 1387, Ap
13	32	33.0	11	5	US-10-807-807-1387 Sequence 1387, Ap
14	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
15	32	33.0	15	4	US-10-107-532-6124 Sequence 6124, Ap
16	32	33.0	15	5	US-10-776-224-64 Sequence 64, Appl
17	31	32.0	13	4	US-10-300-694A-64 Sequence 64, Appl
18	31	32.0	14	3	US-09-929-751A-16 Sequence 16, Appl
19	30	30.9	9	3	US-09-865-548A-126 Sequence 126, App
20	30	30.9	9	5	US-10-705-459-126 Sequence 126, App
21	29	29.9	14	5	US-10-804-772-27 Sequence 27, Appl
22	29	29.9	9	5	US-10-482-630-40 Sequence 40, Appl
23	29	29.9	12	3	US-09-813-653-26 Sequence 26, Appl
24	29	29.9	14	5	US-10-865-478-786 Sequence 786, Appl
25	29	29.9	15	5	US-10-720-831-20 Sequence 20, Appl
26	29	29.9	17	4	US-10-306-631-76 Sequence 76, Appl
27	29	29.9	18	4	US-10-654-200-28 Sequence 28, Appl

28	29	29.9	18	4	US-10-654-200-29 Sequence 29, Appl
29	29	29.9	18	5	US-10-846-548A-1 Sequence 1, Appl
30	28	28.9	9	4	US-10-160-506-34 Sequence 34, Appl
31	28	28.9	9	4	US-10-449-379-34 Sequence 34, Appl
32	28	28.9	9	4	US-10-688-015-34 Sequence 34, Appl
33	28	28.9	9	4	US-10-160-505-34 Sequence 34, Appl
34	28	28.9	9	5	US-10-482-284A-186 Sequence 186, App
35	28	28.9	10	4	US-10-281-652-18 Sequence 18, Appl
36	28	28.9	10	5	US-10-691-157-18 Sequence 18, Appl
37	28	28.9	10	5	US-10-691-330-18 Sequence 18, Appl
38	28	28.9	14	3	US-09-880-748-2653 Sequence 2653, Ap
39	28	28.9	14	4	US-10-293-418-2653 Sequence 2653, Ap
40	28	28.9	14	4	US-10-742-379-44 Sequence 44, Appl
41	28	28.9	16	3	US-09-736-959A-29 Sequence 29, Appl
42	28	28.9	16	4	US-10-044-708A-3 Sequence 3, Appl
43	28	28.9	16	4	US-10-225-567A-1478 Sequence 1478, Ap
44	28	28.9	17	4	US-10-239-313A-30 Sequence 30, Appl
45	28	28.9	18	5	US-10-758-165-13 Sequence 13, Appl

## ALIGNMENTS

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RESULT 1
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match      100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDQKATNIFPYTAPGKQ 18
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Db      1 VDQKATNIFPYTAPGKQ 18

RESULT 2
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match      89.7%; Score 87; DB 5; Length 18;
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Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGKATNIPFYTAPG 16  
Db 1 VDGKATNIPFYTAPG 16

RESULT 3  
US-10-758-165-12  
; Sequence 12, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-12

Query Match 56.7%; Score 55; DB 5; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.055;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGKATNIPFYTAP 15  
Db 1 VDGKEDRNLFSYTAP 15

RESULT 4  
US-10-856-118-34  
; Sequence 34, Application US/10856118  
; Publication No. US20050025747A1  
; GENERAL INFORMATION:  
; APPLICANT: Laidlaw, Stephen  
; APPLICANT: Skinner, Mike  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Anderson, Richard  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: 3742.1000-000  
; CURRENT APPLICATION NUMBER: US/10/856,118  
; CURRENT FILING DATE: 2004-05-27  
; PRIOR APPLICATION NUMBER: PCT/GB02/005411  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: GB0128733.3  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 60/334,649  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking sequence  
US-10-856-118-34

Query Match 38.1%; Score 37; DB 5; Length 15;  
Best Local Similarity 55.6%; Pred. No. 45;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 TNIPFYTAP 15  
Db 7 TNIPFYTAP 15

Db 2 TNIPFYDVP 10

RESULT 5  
US-10-758-165-11  
; Sequence 11, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Equus caballus  
US-10-758-165-11

Query Match 36.1%; Score 35; DB 5; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.2e+02;  
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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Db 1 IDGKVDGQFQHGIVKQ 18

RESULT 6  
US-10-052-788-5  
; Sequence 5, Application US/10052788  
; Publication No. US20030087314A1  
; GENERAL INFORMATION:  
; APPLICANT: Getchwin, Laurel J.  
; APPLICANT: Pettigrew, Howard David  
; APPLICANT: Kalina, Warren V.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for  
; FILE REFERENCE: 023070-121000US  
; CURRENT APPLICATION NUMBER: US/10/052,788  
; CURRENT FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide  
; OTHER INFORMATION: P5, middle portion of C2 of equine IgE epsilon  
; OTHER INFORMATION: heavy chain  
US-10-052-788-5

Query Match 35.1%; Score 34; DB 4; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGKATNIPP 11  
Db 2 IDGKVDGQF 12

RESULT 7  
US-09-920-262A-6  
; Sequence 6, Application US/09920262A  
; Publication No. US20030124123A1  
; GENERAL INFORMATION:  
; APPLICANT: Shealy, David

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/ APPLICANT: Knight, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Peritt, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CEN0248
/ CURRENT APPLICATION NUMBER: US/09/920,262A
/ CURRENT FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-920-262A-6
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Query Match          33.0%; Score 32; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      8 NIEPYT 13
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        4 NIEPYT 9
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QY      8 NIEPYT 13
        ||:||||
        4 NIEPYT 9
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RESULT 8
US-10-912-994-6
/ Sequence 6, Application US/10912994
/ Publication No. US20050002937A1
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RESULT 10
US-10-975-740A-6
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/ GENERAL INFORMATION:
/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Knight, David
/ APPLICANT: Peritt, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Shealy, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CEN0248DIV1
/ CURRENT APPLICATION NUMBER: US/10/912,994
/ CURRENT FILING DATE: 2004-08-06
/ PRIOR APPLICATION NUMBER: US 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: US 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: US 09/920,262
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-912-994-6
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/ Sequence 6, Application US/10975740A
/ Publication No. US20050196838A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Knight, David
/ APPLICANT: Peritt, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Shealy, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
/ FILE REFERENCE: CEN0248DIV03
/ CURRENT APPLICATION NUMBER: US/10/975,740A
/ CURRENT FILING DATE: 2004-01-28
/ PRIOR APPLICATION NUMBER: US 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: US 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: US 09/920,262
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-975-740A-6
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/ APPLICANT: Peritt, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Shealy, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
/ FILE REFERENCE: CEN0248DIV04
/ CURRENT APPLICATION NUMBER: US/10/975,883
/ CURRENT FILING DATE: 2004-10-28
/ PRIOR APPLICATION NUMBER: US 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: US 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: US 09/920,262
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-975-883-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      8 NIEPYT 13
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        4 NIEPYT 9
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QY      8 NIEPYT 13
        ||:||||
        4 NIEPYT 9
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RESULT 9
US-10-975-883-6
/ Sequence 6, Application US/10975883
/ Publication No. US20050112127A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Knight, David
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RESULT 11
US-10-975-708-6
/ Sequence 6, Application US/10975708
/ Publication No. US20050214293A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilles-Komar, Jill
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; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: CEN0248DI02
; CURRENT APPLICATION NUMBER: US/10/975,708
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-708-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      4 NIPYPT 9
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RESULT 12
US-10-808-187-1387
; Sequence 1387, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1387
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Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Db      1 GOSQSNTLPQT 11
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RESULT 13
US-10-807-807-1387
; Sequence 1387, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1387
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Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      3 GOKATNIPYPT 13
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Db      1 GOSQSNTLPQT 11
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RESULT 14
US-10-107-532-5915
; Sequence 5915, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afari, Daniel E.H.
```



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; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Archur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: 51158-200064.00
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US/10/107,532
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5915
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-5915
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Query Match          33.0%; Score 32; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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Qy      5 KATNIPYTPGK 17
      ||||:|
Db      3 KATNLAPADPNK 15
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RESULT 15
US-10-107-532-6124
; Sequence 6124, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Faxis, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Archur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: 51158-200064.00
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US/10/107,532
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6124
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-6124
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Query Match          33.0%; Score 32; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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```
Qy      5 KATNIPYTPGK 17
      ||||:|
Db      3 KATNLAPADPNK 15
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Search completed: December 12, 2005, 21:29:23  
Job time : 95 secs

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GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: December 12, 2005, 21:17:33 ; Search time 3 Seconds  
(without alignments)  
33.507 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDGQKATNIPFYTAFGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 9754

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New: \*  
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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep: \*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep: \*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep: \*  
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7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep: \*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.9	14	7	US-11-054-515-2653	Sequence 2653, Ap
2	27.8	14	7	US-11-054-515-2682	Sequence 2682, Ap
3	26.8	13	6	US-10-511-559-1085	Sequence 1085, Ap
4	25.8	9	7	US-11-009-939-10	Sequence 10, Appl
5	25.8	9	7	US-11-009-939-40	Sequence 40, Appl
6	25.8	18	6	US-10-828-033-36	Sequence 36, Appl
7	24.7	8	6	US-10-999-866-57	Sequence 57, Appl
8	24.7	13	6	US-10-977-334-8	Sequence 8, Appl
9	24.7	16	6	US-10-507-275-17	Sequence 17, Appl
10	24.7	17	7	US-11-082-381-3	Sequence 3, Appl
11	23.7	9	6	US-10-952-535A-28	Sequence 28, Appl
12	23.7	9	6	US-10-952-535A-43	Sequence 43, Appl
13	23.7	9	7	US-11-010-748A-334	Sequence 334, Appl
14	23.7	9	7	US-11-010-748A-346	Sequence 346, Appl
15	23.7	9	7	US-11-158-848-41	Sequence 41, Appl
16	23.7	9	7	US-11-178-639-3	Sequence 3, Appl
17	23.7	9	7	US-11-137-671-4	Sequence 19, Appl
18	23.7	10	6	US-10-933-025-19	Sequence 16, Appl
19	23.7	10	7	US-11-093-274-16	Sequence 3, Appl
20	23.7	10	7	US-11-137-671-3	Sequence 2, Appl
21	23.7	11	6	US-11-137-671-2	Sequence 82, Appl
22	23.7	11	6	US-10-632-150-82	Sequence 9, Appl
23	23.7	12	6	US-10-507-662-9	Sequence 33, Appl
24	23.7	12	6	US-10-952-535A-33	Sequence 82, Appl
25	23.7	12	7	US-11-073-457-82	

26	23.7	12	7	US-11-137-671-1	Sequence 1, Appl
27	23.7	13	6	US-10-511-559-719	Sequence 719, Appl
28	23.7	13	7	US-11-089-551A-8	Sequence 8, Appl
29	23.7	14	7	US-11-054-515-2374	Sequence 2374, Ap
30	23.7	14	7	US-11-054-515-2474	Sequence 2474, Ap
31	23.7	14	7	US-11-054-515-2654	Sequence 2654, Ap
32	23.7	14	7	US-11-054-515-2656	Sequence 2656, Ap
33	23.7	14	7	US-11-054-515-2657	Sequence 2657, Ap
34	23.7	14	7	US-11-054-515-2658	Sequence 2658, Ap
35	23.7	14	7	US-11-054-515-2670	Sequence 2670, Ap
36	23.7	14	7	US-11-054-515-2673	Sequence 2673, Ap
37	23.7	14	7	US-11-054-515-2676	Sequence 2676, Ap
38	23.7	14	7	US-11-054-515-2679	Sequence 2679, Ap
39	23.7	14	7	US-11-054-515-2710	Sequence 2710, Ap
40	23.7	14	7	US-11-054-515-2719	Sequence 2719, Ap
41	23.7	15	6	US-10-952-535A-32	Sequence 32, Appl
42	22.5	14	7	US-11-054-515-2361	Sequence 2361, Ap
43	22.5	14	7	US-11-054-515-2385	Sequence 2385, Ap
44	22.5	14	7	US-11-054-515-2608	Sequence 2608, Ap
45	22.5	14	7	US-11-054-515-2617	Sequence 2617, Ap

## ALIGNMENTS

RESULT 1  
US-11-054-515-2653  
; Sequence 2653, Application US/11054515  
; Publication No. US20050255532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23p3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; PRIOR FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2653  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-2653  
Query Match 28.9%; Score 28; DB 7; Length 14;  
Best Local Similarity 57.1%; Pred. No. 20;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 9 IFPYTAP 15  
:|||:  
Db 6 LFYINP 12  
RESULT 2

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US-11-054-515-2682
; Sequence 2682, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2682
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2682

Query Match          27.8%; Score 27; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      9 FPPYT 13
       :|||
Db      6 LFPYT 10

RESULT 3
US-10-511-559-1085
; Sequence 1085, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Tim
; APPLICANT: JONES, Tim
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1085
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1085
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Query Match          26.8%; Score 26; DB 6; Length 13;
Best Local Similarity 45.5%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      7 TNFFPYAPGK 17
       :|:|:|
Db      1 TNMFATWSPSK 11

RESULT 4
US-11-009-939-10
; Sequence 10, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-10

Query Match          25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 FPPYT 13
       :|||
Db      6 FPYT 9

RESULT 5
US-11-009-939-40
; Sequence 40, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-40

Query Match          25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      8 NIPPYT 13
       |||:|
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Db 4 NTFPWT 9

RESULT 6  
US-10-828-033-36  
; Sequence 36, Application US/10828033  
; Publication No. US20050250206A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul B. Fisher and Ruqunian Shen  
; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND IMMUNOLOGICAL REAGENTS  
; TITLE OF INVENTION: SPECIFIC FOR CELL  
; FILE REFERENCE: SURFACE-EXPRESSED MOLECULES AND TRANSFORMATION-ASSOCIATED GENES  
; CURRENT FILING DATE: 2004-04-20  
; PRIOR FILING DATE: 2004-04-20  
; PRIOR APPLICATION NUMBER: US/08/875,553  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Human  
US-10-828-033-36

Query Match 25.8%; Score 25; DB 6; Length 18;  
Best Local Similarity 55.6%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GQKATNIFP 11  
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10 GQEAVFYFP 18

Db 10 GQEAVFYFP 18

RESULT 7  
US-10-999-866-57  
; Sequence 57, Application US/10999866  
; Publication No. US2005026004A1  
; GENERAL INFORMATION:  
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND  
; FILE REFERENCE: CENS042NP  
; CURRENT APPLICATION NUMBER: US/10/999,866  
; CURRENT FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: 60/527,794  
; PRIOR FILING DATE: 2003-12-08  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 57  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: LC CDR3  
US-10-999-866-57

Query Match 24.7%; Score 24; DB 6; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 NIFPPT 13  
|||:  
3 NTLFPT 8

Db 3 NTLFPT 8

RESULT 8  
US-10-977-334-8  
; Sequence 8, Application US/10977334  
; Publication No. US20050244904A1  
; GENERAL INFORMATION:  
; APPLICANT: NG, LEONG

; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION  
; FILE REFERENCE: ISA-016.01  
; CURRENT APPLICATION NUMBER: US/10/977,334  
; CURRENT FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: 60/542,647  
; PRIOR FILING DATE: 2004-02-06  
; PRIOR APPLICATION NUMBER: GB 0325279.8  
; PRIOR FILING DATE: 2003-10-29  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 8  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-977-334-8

Query Match 24.7%; Score 24; DB 6; Length 13;  
Best Local Similarity 57.1%; Pred. No. 89;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 PYTAPGK 17  
|||:  
1 PQTAPSR 7

Db 1 PQTAPSR 7

RESULT 9  
US-10-507-275-17  
; Sequence 17, Application US/10507275  
; Publication No. US20050250166A1  
; GENERAL INFORMATION:  
; APPLICANT: Masai, Hisao  
; APPLICANT: Tamai, Katsuyuki  
; APPLICANT: Medical and Biological Laboratories Co., Ltd.  
; APPLICANT: Japan Science and Technology Agency  
; TITLE OF INVENTION: Ginkgo Biomedical Research Institute Co., Ltd.  
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,  
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods  
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK  
; TITLE OF INVENTION: Kinase Inhibitory Ability  
; FILE REFERENCE: 082368-001100US  
; CURRENT APPLICATION NUMBER: US/10/507,275  
; CURRENT FILING DATE: 2004-09-09  
; PRIOR APPLICATION NUMBER: JP 2002-067702  
; PRIOR FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: WO PCT/JP03/02918  
; PRIOR FILING DATE: 2003-03-12  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: an artificially  
US-10-507-275-17

Query Match 24.7%; Score 24; DB 6; Length 16;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 IFPYTAP 15  
|||:  
1 MTFIDVP 7

Db 1 MTFIDVP 7

RESULT 10  
US-11-082-381-3  
; Sequence 3, Application US/11082381  
; Publication No. US20050244434A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, David I.  
; TITLE OF INVENTION: Tat-based Tolerogen Compositions and Method of Making and Using

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; TITLE OF INVENTION: Same
; FILE REFERENCE: 51311-00001
; CURRENT APPLICATION NUMBER: US/11/082,381
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: 60/553733
; PRIOR FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 60/649021
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: 10/456865
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 09/636057
; PRIOR FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-082-381-3
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Query Match      24.7%; Score 24; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY      11 PYTAGSQ 18
      :|||
Db      8 PMKHPSQ 15
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```
RESULT 11
US-10-952-535A-28
; Sequence 28, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-28
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Query Match      23.7%; Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY      10 FPYTPAP 15
      :|||
Db      1 YPYDVP 6
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RESULT 12
US-10-952-535A-43
; Sequence 43, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Leeseit, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
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; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-43
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Query Match      23.7%; Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      10 FPYTPAP 15
      :|||
Db      1 YPYDVP 6
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RESULT 13
US-11-010-748A-334
; Sequence 334, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOHL, Heidrun
; APPLICANT: SCHARW, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 334
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328
US-11-010-748A-334
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Query Match      23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY      5 KATNIPFY 12
      :|||
Db      1 KIQEIPFP 8
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RESULT 14
US-11-010-748A-346
; Sequence 346, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOHL, Heidrun
; APPLICANT: SCHARW, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
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; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 346  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328  
US-11-010-748A-346

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 KATNIPFY 12  
| | | | |  
Db 1 KIQEIFPF 8

RESULT 15  
US-11-158-848-41  
; Sequence 41, Application US/1158848  
; Publication No. US20050249703A1  
; GENERAL INFORMATION:  
; APPLICANT: Anne Dam Jensen  
; TITLE OF INVENTION: Interferon gamma polypeptide variants  
; FILE REFERENCE: 23us410 - INFG variants  
; CURRENT APPLICATION NUMBER: US/11/158,848  
; CURRENT FILING DATE: 2005-06-22  
; PRIOR APPLICATION NUMBER: US/10/116,273  
; PRIOR FILING DATE: 2002-04-04  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 41  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Tag  
US-11-158-848-41

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 PPYTAP 15  
: | | | |  
Db 1 YPYDVP 6

Search completed: December 12, 2005, 21:20:42  
Job time : 3 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 12, 2005, 21:18:48 / Search time 10.6667 Seconds  
(without alignments)  
162.366 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDGKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	27.8	17	2 H49048	T-cell receptor be
2	27	27.8	18	2 A59137	protein p11 - gold
3	26	26.8	18	2 A61577	24k serine protein
4	24	24.7	14	2 B58502	36K kidney stone p
5	24	24.7	17	2 S18534	hypothetical prote
6	23	23.7	12	2 P00786	NADH2 dehydrogenas
7	23	23.7	15	2 B45115	peptidylprolyl iso
8	23	23.7	18	2 S20322	gluten - wheat
9	22	22.7	13	2 PNO170	alcohol dehydrogen
10	22	22.7	12	2 S01904	H+-transporting tw
11	22	22.7	15	2 PA0056	protein QF200002 -
12	22	22.7	15	2 PA0087	cytochrome c2 - fu
13	22	22.7	15	2 PA0099	phenotypic variact
14	22	22.7	16	2 A28144	ribosomal protein
15	22	22.7	17	2 C84063	hypothetical prote
16	22	22.7	18	2 C56046	urinary tract ston
17	21	21.6	10	2 S71948	matrix metalloprot
18	21	21.6	10	2 A39745	endo-glucosylceram
19	21	21.6	11	2 A34135	DNA-binding protei
20	21	21.6	12	2 A53524	ubiquinol-cytochro
21	21	21.6	14	2 PLO142	carbon-monoxide de
22	21	21.6	15	2 S59495	formate dehydrogen
23	21	21.6	15	2 B61457	alpha-glucosidase
24	21	21.6	16	2 E53284	T-cell receptor be
25	21	21.6	16	2 S18292	30K allergen - rye
26	21	21.6	17	2 S50901	chlorophyll a/b-bi
27	21	21.6	18	2 S57518	T cell receptor be
28	21	21.6	18	2 S70612	alpha-macroglobulin
29	20.5	21.1	18	2 A28027	protein p2 - curle

30	20	20.6	9	2 S59902	glutathione transf
31	20	20.6	9	2 D48186	Arpase R1 subunit
32	20	20.6	9	2 S10784	enamelin i - bovin
33	20	20.6	13	2 B58533	CD61 homolog - cha
34	20	20.6	14	2 S22236	lipoxigenase (EC 1
35	20	20.6	14	2 S19803	ubiquitin - potato
36	20	20.6	14	2 PA0109	porin por 1B - Ara
37	20	20.6	14	2 G44957	photosystem II oxy
38	20	20.6	14	2 PH1306	Ig heavy chain DJ
39	20	20.6	14	2 PA0305	porin por1 - Arabi
40	20	20.6	14	2 S12904	protein kinase (EC
41	20	20.6	15	2 PA0097	starch phosphoryla
42	20	20.6	15	2 S71300	ICU3 protein - Par
43	20	20.6	15	2 PS0455	superoxide dismuta
44	20	20.6	15	2 PA0063	ubiquitin - fungus
45	20	20.6	15	2 A49177	22k protein p1, mi

## ALIGNMENTS

RESULT 1  
H49048  
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C:Accession: H49048  
R:Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.  
Eur. J. Immunol. 22, 2413-2418, 1992  
A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile  
A:Reference number: A49048; MUID:92387250; PMID:1387614  
A:Accession: H49048  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-17 <SIO>  
A:Cross-references: UNIPARC:UPI0000176DF0  
A:Experimental source: patient SS, IL-2R+ synovial T-cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:113270)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 27.8%; Score 27; DB 2; Length 17;  
Best Local Similarity 62.5%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATNIFPYT 13  
DB 8 AWTFFPYT 15

RESULT 2  
A59137  
protein p11 - golden needle mushroom (fragment)  
C:Species: Flammulina velutipes (golden needle mushroom)  
C:Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: A59137  
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
Submitted to the Protein Sequence Database, November 1999  
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A:Reference number: A59137  
A:Accession: A59137  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <SAK>  
A:Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

Query Match 27.8%; Score 27; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15  
DB 2 PYTSP 6

RESULT 3  
A61577  
24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)  
C:Species: Streptomyces fradiae  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: A61577  
R:Sinha, U.; Wolz, S.A.; Lad, P.J.  
Int. J. Biochem. 23, 979-984, 1991  
A:Title: Two new extracellular serine proteases from Streptomyces fradiae.  
A:Reference number: A61577; MUID:92155439; PMID:1786859  
A:Accession: A61577  
A:Molecule type: protein  
A:Residues: 1-18 <SIN>  
A:Cross-references: UNIPROT:Q7M19; UNIPARC:UPI000017AE13  
C:Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 26.8%; Score 26; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 VDGGKATNIPY 12  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 VGGTRAAQEPFW 13

RESULT 4  
B58502  
36k kidney stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C:Accession: B58502  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: B58502  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <BIN>  
A:Cross-references: UNIPARC:UPI000017A8D0  
A:Experimental source: human kidney stone containing Ca ox.monoh dihyd, 1% struvite, CaH  
A>Note: tentative identification of 8-Tyr and 9-Thr

Query Match 24.7%; Score 24; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 NIPPYT 13  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 NLFGYT 9

RESULT 5  
S18534  
hypothetical protein 7 (eryg 3' region) - Saccharopolyspora erythraea (fragment)  
C:Species: Saccharopolyspora erythraea  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 07-Apr-1994  
C:Accession: S18534  
R:Haydock, S.F.; Dowson, J.A.; Dillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.  
Mol. Gen. Genet. 230, 120-128, 1991  
A:Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in  
methylintraferases.  
A:Reference number: S18530; MUID:92079886; PMID:1840640  
A:Accession: S18534  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-17 <HAY>  
A:Cross-references: UNIPARC:UPI000017AD81; EMBL:X60379  
A>Note: the authors translated the codon CTG for residue 12 as Gly

Query Match 24.7%; Score 24; DB 2; Length 17;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 IFPYTAPG 16  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 IFPAVAG 8

RESULT 6  
P00786  
NADH2 dehydrogenase (EC 1.6.99.3) 26K chain - fava bean mitochondrion (fragment)  
N:Alternate names: complex I 26K chain; NADH-ubiquinone reductase 26K chain  
C:Species: mitochondrion Vicia faba (fava bean)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: P00786  
R:lesterme, S.; Boutry, M.  
Plant Physiol. 102, 435-443, 1993  
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH2  
A:Reference number: P00775; MUID:94151437; PMID:8108509  
A:Accession: P00786  
A:Molecule type: protein  
A:Residues: 1-12 <LET>  
A:Cross-references: UNIPROT:Q7M2G3; UNIPARC:UPI000017CDA8  
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th  
ranging from 5K to 75K.  
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by  
C:Genetics:  
A:Genome: mitochondrion  
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 23.7%; Score 23; DB 2; Length 12;  
Best Local Similarity 53.8%; Pred. No. 1.2e+03;  
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

OY 6 ATNI-PPYTARG 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 ATGVPIPY-APGE 12

RESULT 7  
B45115  
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)  
N:Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: B45115  
R:Wiederecht, G.; Hung, S.; Chan, H.K.; Marxy, A.; Martin, M.; Calaycay, J.; Boulton, D  
J. Biol. Chem. 267, 21753-21760, 1992  
A:Title: Characterization of high molecular weight FK-506 binding activities reveals a nc  
A:Reference number: A45115; MUID:93016131; PMID:1383226  
A:Accession: B45115  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <WIE>  
A:Cross-references: UNIPROT:Q9UDK1; UNIPARC:UPI0000035473  
A:Experimental source: JURKAT cells  
A>Note: sequence extracted from NCBI backbone (NCBIP:116748)  
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 23.7%; Score 23; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 6 ATNIFPYTAP 15  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 ATESIAVILAP 10

RESULT 8  
S20322  
gluten - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S20322  
R:Fukudome, S.; Yoshikawa, M.  
FEBS Lett. 296, 107-111, 1992  
A>Title: Opioid peptides derived from wheat gluten: their isolation and characterization  
A:Reference number: S20322; MUID:92111773; PMID:1309704  
A:Accession: S20322  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <PDK>  
A:Cross-references: UNIPROT:Q7MIG0; UNIPARC:UPI000017B139

Query Match 23.7%; Score 23; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIPY 12  
DB 1 GYPTGYPPY 10

RESULT 9  
PN0170  
alcohol dehydrogenase (EC 1.1.1.1) - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 05-Aug-1994 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: PN0170  
R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.  
submitted to JRPID, May 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A:Reference number: PN0160  
A:Accession: PN0170  
A:Molecule type: protein  
A:Residues: 1-12 <PDK>  
A:Cross-references: UNIPROT:Q7MA29; UNIPARC:UPI000017B3F6  
A:Experimental source: strain M-1-1  
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 22.7%; Score 22; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPGK 17  
DB 6 YTVGK 11

RESULT 10  
S01904  
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloro  
C:Species: chloroplast Arabidopsis thaliana (mouse-ear cress)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: S01904  
R:Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.T.N.  
Nucleic Acids Res. 16, 10372, 1988  
A>Title: Nucleotide sequence of chloroplast CFI-ATPase epsilon-subunit and elongator rRN  
A:Reference number: S01903; MUID:89057486; PMID:2904134  
A:Accession: S01904  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-13 <CHE>  
A:Cross-references: UNIPROT:P19366; UNIPARC:UPI00001ED348; EMBL:X12889; NID:g11332; PIDN  
C:Genetics:  
A:Gene: atpB  
A:Genome: chloroplast  
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 22.7%; Score 22; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KATNI 9  
DB 1 KATNI 5

RESULT 11  
PA0056  
protein QP200002 - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0056  
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JRPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A:Reference number: PA0051  
A:Accession: PA0056  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
A:Cross-references: UNIPARC:UPI000017B408

Query Match 22.7%; Score 22; DB 2; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATNIF 10  
DB 11 ATNIF 15

RESULT 12  
PA0087  
cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: PA0087  
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JRPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A:Reference number: PA0051  
A:Accession: PA0087  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
A:Cross-references: UNIPROT:Q7MA27; UNIPARC:UPI000017B3F8  
C:Keywords: electron transfer; heme; photosynthesis

Query Match 22.7%; Score 22; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 2.2e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGKATNIF 10  
DB 4 DIKGANLP 12

RESULT 13  
PA0099  
phenolic variation protein - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: PA0099  
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JRPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
A:Reference number: PA0051  
A:Accession: PA0099  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
A:Cross-references: UNIPROT:Q7MA17; UNIPARC:UPI000017B405

Query Match 22.7%; Score 22; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 2.2e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPTAPG 16  
DB 7 FKYSASG 13

## RESULT 14

A28144  
ribosomal protein S27a - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 09-Jul-2004  
C:Accession: A28144  
R:Redman, K.L.; Rechsteiner, M.  
J. Biol. Chem. 263, 4926-4931, 1988  
A:Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic P  
A:Reference number: A28144; MUID:88169619; PMID:2832412  
A:Accession: A28144  
A:Molecule type: protein  
A:Residues: 1-16 <RED>  
A:Cross-references: UNIPROT:O97577; UNIPARC:UPI0000177161  
C:Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;  
C:Keywords: protein biosynthesis

Query Match 22.7%; Score 22; DB 2; Length 16;  
Best local similarity 66.7%; Pred. No. 2.4e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 12 YTPRK 17  
| | | | |  
Db 9 YTPRK 14

## RESULT 15

C84063  
hypothetical protein BH3107 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: C84063  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: C84063  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-17 <STO>  
A:Cross-references: UNIPROT:Q9K7Q4; UNIPARC:UPI00000C4168; GB:AP001518; GB:BA000004; NIT  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH3307

Query Match 22.7%; Score 22; DB 2; Length 17;  
Best local similarity 57.1%; Pred. No. 2.6e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 DGQRATN 8  
| : | | |  
Db 10 DNKKQTN 16

Search completed: December 12, 2005, 21:24:32  
Job time : 11.6667 secs



RX PubMed=15019625; DOI=10.1016/j.jmpev.2003.08.002;  
RA Paton A., Spingade D.A., Sude S., Otiemo D., Gray R., Harley M.M.,  
RA Willis F., Simons M.S.J., Powell M.P., Savolainen V.,  
RT "Phylogeny and evolution of basilis and allies (Ociemeae, Labiatae)  
RT based on three plastid DNA regions."  
RL Mol. Phylogenet. Evol. 31:277-299(2004).  
DR EMBL; AJ505368; CAD5489.1; -; Genomic DNA.  
KW Ribosomal protein.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 789 MW; 86786772D1BA4772 CRC64;  
  
Query Match 33.0%; Score 32; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 PYTAPG 16  
DB 2 PYTVPG 7  
  
RESULT 3  
ID Q9TWA4\_LUCCU PRELIMINARY; PRT; 18 AA.  
AC Q9TWA4;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE 25 kDa chymotrypsin-like enzyme (Fragment).  
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Lucilia.  
OX NCBI\_TaxID=7375;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=95219141; PubMed=7704304;  
RA Caeu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Ridding G.A.,  
RA Tellam R.L.;  
RT "Excretory/secretory chymotrypsin from *Lucilia cuprina*: purification,  
RT enzymatic specificity and amino acid sequence deduced from mRNA."  
RL Insect Mol. Biol. 3:201-211(1994).  
SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126B11 CRC64;  
  
Query Match 29.4%; Score 28.5; DB 2; Length 18;  
Best Local Similarity 58.3%; Pred. No. 1.8e+03;  
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
  
QY 2 DGQKAT-NIPFY 12  
DB 3 NGQKATVQGFY 14  
  
RESULT 4  
ID Q8LIY7\_PLEBO PRELIMINARY; PRT; 16 AA.  
AC Q8LIY7;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Plectonema boryanum.  
OS Plectonema boryanum.  
OC Bacteria; Cyanobacteria; Oscillatoriales; Leptolyngbya.  
OX NCBI\_TaxID=1184;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=UTEX 485;  
RX MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;  
RA Williams K.P.;  
RT "Descent of a split RNA."  
RL Nucleic Acids Res. 30:2025-2030(2002).  
DR EMBL; AY082652; AAM03311.1; -; Genomic DNA.

FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1640 MW; 60FE5985B9B00982 CRC64;  
  
Query Match 28.4%; Score 27.5; DB 2; Length 16;  
Best Local Similarity 53.8%; Pred. No. 2.3e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
  
QY 6 ATNIPY---TAP 15  
DB 1 ANNIVPARKTAP 13  
  
RESULT 5  
ID Q7M4W6\_FLAVE PRELIMINARY; PRT; 18 AA.  
AC Q7M4W6;  
DT 01-MAR-2004 (TReMBLrel. 26, Created)  
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Protein P11 (Fragment).  
OS Flammulina velutipes.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Agaricales; Tricholomataceae; Flammulina.  
OX NCBI\_TaxID=38945;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA Sakamoto Y., Ando A., Tamai Y., Miura K.;  
RL Submitted (NOV-1999) to the PIR data bank.  
DR PIR; A59137; A59137.  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 1956 MW; FB0434B0AF005AEC CRC64;  
  
Query Match 27.8%; Score 27; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 3.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 PYTAP 15  
DB 2 PYTSP 6  
  
RESULT 6  
ID Q7S007\_NEUCR PRELIMINARY; PRT; 15 AA.  
AC Q7S007;  
DT 01-MAR-2004 (TReMBLrel. 26, Created)  
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Predicted protein.  
GN Name=NCU09752.1;  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=OR74A;  
RA Gajaffe D., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,  
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endlitz M.,  
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
RA Selltreinckoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,  
RA Kohe G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,  
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnere S.,  
RA Kamai M., Kamyselis M., Mauceli E., Bielke C., Rudd S., Frisman D.,  
RA Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,  
RA Desouza C.C., Glase L., Orbach M.J., Berglund J., Voelker R.,  
RA Varden O., Piamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebohe D.J., Freitag M.,  
RA Paulsen I., Sachs M.S., Lander E.S., Nubbaum C., Birren B.,  
RT "The genome sequence of the filamentous fungus *Neurospora crassa*."

RL Nature 0:0-0(2003).  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: AABX01000580; EAA28619.1; -; Genomic DNA.  
SQ SEQUENCE 15 AA; 1832 MW; 012D0180A8C7089D CRC64;

Query Match 26.8%; Score 26; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.9e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIFPPT 13  
|:|:|:  
DB 2 NVFEY 7

RESULT 7  
Q7M198 STRFR PRELIMINARY; PRT; 18 AA.  
ID Q7M198;  
AC Q7M198;  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).  
OS Streptomyces fradiae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxId=1906;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;  
RA Sinha U., Wolz S.A., Lad P.J.;  
RL Int. J. Biochem. 23:979-984(1991).  
DR PIR. A61577; A61577.  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 26.8%; Score 26; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 4.7e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIFPY 12  
|:|:|:|:  
DB 2 VQGTAAAEFPW 13

RESULT 8  
Q9UR63 EMENI PRELIMINARY; PRT; 15 AA.  
ID Q9UR63;  
AC Q9UR63;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight  
DE isoform (EC 3.2.1.26) (Fragment).  
OS Emericella nidulans (Aspergillus nidulans).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxId=162425;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;  
RA Chen U.S., Saxton J., Hemming F.W., Peberdy J.F.;  
RT "Purification and partial characterization of the high and low  
RT molecular weight form (S- and F-form) of invertase secreted by  
RT Aspergillus nidulans.";  
RL Biochim. Biophys. Acta 1296:207-218 (1996).  
DR GO, GO:0004564; F-beta-fructofuranosidase activity; IEA.  
SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match 25.8%; Score 25; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 5.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAP 15  
|:|:|:  
DB 10 PYTEP 14

RESULT 9  
Q714T5 9CRYP PRELIMINARY; PRT; 14 AA.  
ID Q714T5;  
AC Q714T5;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE tmRNA proteolysis tag (Fragment).  
GN Name=tmRNA;  
OS Rhodomonas salina.  
OC Chloviplast.  
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.  
OX NCBI\_TaxId=52970;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CCMP1319;  
RX PubMed=14681369; DOI=10.1093/nar/9kh102;  
RA Guenau de Nova P., Williams K.P.;  
RT "The tmRNA website: reductive evolution of tmRNA in plastids and other  
RT endosymbionts.";  
RL Nucleic Acids Res. 32:D104-D108 (2004).  
DR EMBL: AF550355; AAQ12671.1; -; Genomic\_DNA.  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1528 MW; D95F9B3698210B9 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 7.9e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATNIFPY 13  
|:|:|:  
DB 1 ANNIVPFS 8

RESULT 10  
Q7TPH9 PHOSU PRELIMINARY; PRT; 16 AA.  
ID Q7TPH9;  
AC Q7TPH9;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Per2 protein (Fragment).  
GN Name=Per2;  
OS Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Cricetinae; Phodopus.  
OX NCBI\_TaxId=10044;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Soua V., Semikhodskii A.G., Loudon A.S.I.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY316536; AAP87362.1; -; mRNA.  
FT NON\_TER 1  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1831 MW; 845C849E44AE531 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 9.2e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 PYTAPGQ 18  
|:|:|:  
DB 6 PUTSPKE 13

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RESULT 11
Q65YZ6 HORSE PRELIMINARY; PRT; 17 AA.
ID Q65YZ6 HORSE PRELIMINARY; PRT; 17 AA.
AC Q65YZ6;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Asparagine-linked glycosylation 8 homolog (Fragment).
GN Name=ALG8;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN NUCLEOTIDE SEQUENCE.
RA Hasegawa T., Sato F., Tozaki T., Hirota K.;
RT "Fine mapping of equine chromosomes corresponding to HSA11."
RU Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB167785; BAD44704.1; -; Genomic_DNA.
FT NON TER 1 1
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1907 MW; 24AB4757508FF8FC CRC64;

Query Match 24.7%; Score 24; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 9.8e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

OY 8 NIFP--YTAP 15
DB 6 SLPLPLFTAP 15

RESULT 12
Q9ZIB1 CLODI PRELIMINARY; PRT; 10 AA.
ID Q9ZIB1 CLODI PRELIMINARY; PRT; 10 AA.
AC Q9ZIB1;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Toxin B (Fragment).
GN Name=ToxB;
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=8864;
RA Dodson A.P., Borriello S.P.;
RU Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035716; AAD02038.1; -; Genomic_DNA.
FT NON TER 1 1
FT NON TER 10 AA; 1120 MW; 913DA042C736DDC1 CRC64;

SQ SEQUENCE 10 AA; 1120 MW; 913DA042C736DDC1 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PYTA 14
DB 1 PYTA 4

RESULT 13
Q7MG3 VICFA PRELIMINARY; PRT; 12 AA.
ID Q7MG3 VICFA PRELIMINARY; PRT; 12 AA.
AC Q7MG3;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE NADH2 dehydrogenase (EC 1.6.99.3) 26k chain (Fragment).
OS Vicia faba (Broad Bean).
OX NCBI_TaxID=4097;
RN NUCLEOTIDE SEQUENCE.

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Vicia.
OX NCBI_TaxID=3906;
RN NUCLEOTIDE SEQUENCE.
RA MEDLINE=94151437; PubMed=8108509; DOI=10.1104/pp.102.2.435;
RA Letenne S., Boutry M.;
RT "Purification and preliminary characterization of mitochondrial
RT complex I (NADH:ubiquinone reductase) from broad bean (Vicia faba
RT L.)".
RL Plant Physiol. 102:435-443(1993).
DR PIR; P00786; P00786.
DR GO; GO:0003954; F:NADH dehydrogenase activity; IEA.
FT NON TER 1 1
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1171 MW; 29C1BC39CE476047 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 1e+04;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

OY 6 ATNI-FPYTAPK 17
DB 1 ATGVPIPY-APGE 12

RESULT 14
P78359 HUMAN PRELIMINARY; PRT; 14 AA.
ID P78359 HUMAN PRELIMINARY; PRT; 14 AA.
AC P78359;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NF-kappa-B transcription factor p65 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Umbilical vein;
RA Remacle J.E., Brys R., Pye S., Nelles L., Huylebroeck D.;
RU Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88316; AAB48487.1; -; mRNA.
FT NON TER 14 14
FT NON TER 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 IFPYTAP 15
DB 8 IFPOSQP 14

RESULT 15
P82435 TOBAC PRELIMINARY; PRT; 14 AA.
ID P82435 TOBAC PRELIMINARY; PRT; 14 AA.
AC P82435;
DT 01-JUN-2000 (TREMBlrel. 14, Created)
DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 29 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN NUCLEOTIDE SEQUENCE.

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RC STRAIN=CV. PETIT HAVANA;  
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Siabas A.R.,  
Wojtaszek P., Bolwell G.P.;  
RT "Proteomic study of secondary cell wall proteins from transformed  
RT tobacco culture.";  
RL Planta 0:0-0(2000).  
CC -1- SUBCELLULAR LOCATION: CELL WALL.  
DR GO:0005618; C:cell wall; IEA.  
KW Cell wall.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1645 MW; CA0D490EF7F851B2 CRC64;  
Query Match 23.7%; Score 23; DB 2; Length 14;  
Best Local Similarity 30.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 4 QKATNIFPYT 13  
:|:|:|:  
Db 4 RKTVDVFTEFT 13

Search completed: December 12, 2005, 21:23:54  
Job time : 61.6667 secs

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CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
CC either pig or human epsilon-chains of IGE. The present sequence is the  
CC cat IGE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGGKATNIPPYTAPGKQ 18  
1 VDGGKATNIPPYTAPGKQ 18

RESULT 2  
ADG73237  
ID ADG73237 standard; protein; 431 AA.

XX ADG73237;

XX 11-MAR-2004 (first entry)

XX Cat immunoglobulin E (IGE) constant region.

XX antiallergic; IGE-modulator; vaccine; feline; IGF; immunoglobulin E;  
KW immune response; IGE-mediated response; allergy; cat; constant region.

XX Felis catus.

XX US2003216565-A1.

XX 20-NOV-2003.

XX 07-APR-2003; 2003US-00409772.

XX 07-JAN-1999; 99US-0115033P.

XX 07-JAN-2000; 2000US-00479614.

XX (MCCA/) MCCALL C.

XX (WEBB/) WEBBER E.

XX Mccall C, Weber E;

XX WPI: 2004-010802/01.

XX N-PSDB; ADG73236.

XX New isolated nucleic acid molecule encoding a portion of a feline IGE  
PT heavy chain protein, useful for treating and/or eliciting feline immune  
XX responses for IGE-mediated responses, such as allergies.

XX Claim 12; SEQ ID NO 14; 44pp; English.

XX The invention describes an isolated nucleic acid molecule (1) encoding a  
CC portion of a feline IGE heavy chain protein. The methods and compositions  
CC of the present invention are useful for eliciting feline immune responses  
CC for and/or treating IGE-mediated responses, such as allergies. This is  
CC the amino acid sequence of a cat immunoglobulin E (IGE) constant region.

XX Sequence 431 AA;

Query Match 100.0%; Score 97; DB 8; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGGKATNIPPYTAPGKQ 18  
151 VDGGKATNIPPYTAPGKQ 168

RESULT 3

ABP96580  
ID ABP96580 standard; protein; 496 AA.

XX ABP96580;

XX 28-MAY-2003 (first entry)

XX Cat IGE heavy chain amino acid sequence SEQ ID NO:25.

XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
KW immune response; major histocompatibility complex; MHC; immunogenic;  
KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
KW dermatological; antiinflammatory; IGE-mediated condition; food allergy;  
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
KW urticaria hives.

XX Felis catus.

XX WO2003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026586.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI: 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
PT against IGE, by identifying peptide eliciting CTL response to IGE  
PT peptides naturally presented by major histocompatibility complex class I  
PT protein.

XX Example 7; Page 145-147; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides  
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
CC E (IGE), comprising providing a test peptide (T) suspected of being able  
CC to bind to major histocompatibility complex (MHC) class I molecule, and  
CC evaluating (T) for ability to elicit in a mammal a CTL response to  
CC naturally processed and presented IGE peptides, where a peptide that  
CC induces such a response is identified. Also described are compositions:  
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
CC elicit in a mammal a CTL response to naturally processed and presented  
CC IGE peptides, C1-3 have antiallergic, antiasthmatic, immunosuppressive,  
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
CC and can be used as inducers of a CTL response against IGE, and in  
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
CC IGE-mediated atopic hypersensitivity condition. IGE-mediated non-atopic  
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
CC useful for treating atopic hypersensitivity conditions (such as allergic  
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
CC hives). The present sequence represents an IGE heavy chain amino acid  
CC sequence, which is given in an example from the present invention

XX Sequence 496 AA;

Query Match 100.0%; Score 97; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGGKATNIPPYTAPGKQ 18  
|||||

Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 4  
ABU09338  
ID ABU09338 standard; protein; 496 AA.  
XX  
AC ABU09338;  
XX  
DT 27-JUN-2003 (first entry)  
XX  
DE Feline IGE epsilon heavy chain #2.  
XX  
KW Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
KW antibody technology; antiallergic; antiparasitic; cytostatic.  
XX  
OS Felis catus.  
XX  
PN US2003013183-A1.  
XX  
PD 16-JAN-2003.  
XX  
PE 07-JAN-2000; 2000US-00479614.  
XX  
PF 07-JAN-1999; 99US-0115033P.  
XX  
PR 07-JAN-1999; 99US-0115033P.  
XX  
PA (MCCA/) MCCALL C.  
XX (WEBER/) WEBER E.  
XX  
PI Mccall C, Weber E;  
XX  
DR MPI: 2003-391997/37.  
XX N-PSDB; ABX95715.  
XX  
PT New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or  
PT light chain protein, useful for treating feline IGE-mediated responses  
PT e.g. allergies, parasitic infections or neoplasia.  
XX  
PS Claim 1; Page 37-39; 45pp; English.  
XX  
CC The present invention relates to the isolation of feline immunoglobulin E  
CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the  
CC polynucleotide sequences encoding them. The sequences of the invention  
CC are useful for treating feline IGE-mediated immune responses (e.g.  
CC allergies, parasitic infections or neoplasia), in vaccine technology,  
CC small molecule/antibody technology, molecular biology, and various  
CC immunological techniques related to feline IGE and its functions. The  
CC present sequence represents feline IGE epsilon heavy chain #2  
XX  
SQ Sequence 496 AA;

Query Match 100.0%; Score 97; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18  
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 5  
ABU09336  
ID ABU09336 standard; protein; 496 AA.  
XX  
AC ABU09336;  
XX  
DT 27-JUN-2003 (first entry)  
XX  
DE Feline IGE epsilon heavy chain #1.  
XX  
KW Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;

KW antibody technology; antiallergic; antiparasitic; cytostatic.  
XX  
OS Felis catus.  
XX  
FH Key  
XX  
FT Region  
FT Location/Qualifiers  
66..496  
/note="This sequence is given as SEQ ID No:14 and is  
specifically claimed in Claim 12"  
FT 284..309  
/note="This sequence is given as SEQ ID No:11 and is  
specifically claimed in Claim 9"  
FT 288..305  
/note="This sequence is given as SEQ ID No:8 and is  
specifically claimed in Claim 10"  
FT 291..302  
/note="This sequence is given as SEQ ID No:5 and is  
specifically claimed in Claim 11"  
XX  
FT Region  
XX  
PN US2003013183-A1.  
XX  
PD 16-JAN-2003.  
XX  
PE 07-JAN-2000; 2000US-00479614.  
XX  
PF 07-JAN-1999; 99US-0115033P.  
XX  
PR 07-JAN-1999; 99US-0115033P.  
XX  
PA (MCCA/) MCCALL C.  
XX (WEBER/) WEBER E.  
XX  
PI Mccall C, Weber E;  
XX  
DR MPI: 2003-391997/37.  
XX N-PSDB; ABX95715.  
XX  
PT New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or  
PT light chain protein, useful for treating feline IGE-mediated responses  
PT e.g. allergies, parasitic infections or neoplasia.  
XX  
PS Claim 1; Page 24-25; 45pp; English.  
XX  
CC The present invention relates to the isolation of feline immunoglobulin E  
CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the  
CC polynucleotide sequences encoding them. The sequences of the invention  
CC are useful for treating feline IGE-mediated immune responses (e.g.  
CC allergies, parasitic infections or neoplasia), in vaccine technology,  
CC small molecule/antibody technology, molecular biology, and various  
CC immunological techniques related to feline IGE and its functions. The  
CC present sequence represents feline IGE epsilon heavy chain #1  
XX  
SQ Sequence 496 AA;

Query Match 100.0%; Score 97; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18  
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 6  
ADG73251  
ID ADG73251 standard; protein; 496 AA.  
XX  
AC ADG73251;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Cat partial immunoglobulin E (IGE) heavy chain #2.  
XX  
KW antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;  
KW immune response; IGE-mediated response; allergy; cat; heavy chain.

```

OS   Felis catus.
XX   US2003216565-A1.
XX   20-NOV-2003.
XX
PF   07-APR-2003; 2003US-00409772.
XX
PR   07-JAN-1999; 99US-0115033P.
XX   07-JAN-2000; 2000US-00479614.
XX
PA   (MCCA/) MCCALL C.
XX   (WEBE/) WEBER E.
XX
PI   Mccall C, Weber E;
XX
DR   WPI; 2004-010802/01.
XX   N-PsDB; ADG73250.
XX
PT   New isolated nucleic acid molecule encoding a portion of a feline IGE
PR   heavy chain protein, useful for treating and/or eliciting feline immune
PS   responses for IGE-mediated responses, such as allergies.
XX
PS   Claim 8; SEQ ID NO 29; 44pp; English.
XX
CC   The invention describes an isolated nucleic acid molecule (I) encoding a
CC   portion of a feline IGE heavy chain protein. The methods and compositions
CC   of the present invention are useful for eliciting feline immune responses
CC   for and/or treating IGE-mediated responses, such as allergies. This is
CC   the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
CC   chain.
XX
SQ   Sequence 496 AA;

Query Match          100.0%; Score 97; DB 8; Length 496;
Beet Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY       1 VDGQKATNIFPYTAPGKQ 18
         |||||
Db        216 VDGQKATNIFPYTAPGKQ 233

RESULT 7
ADG73225
ID      ADG73225 standard; protein; 496 AA.
XX
AC      ADG73225;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Cat partial immunoglobulin E (IGE) heavy chain #1.
XX
KW      antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
KM      immune response; IGE-mediated response; allergy; cat; heavy chain.
OS
OS      Felis catus.
XX
PN      US2003216565-A1.
XX
PD      20-NOV-2003.
XX
PF      07-APR-2003; 2003US-00409772.
XX
PR      07-JAN-1999; 99US-0115033P.
PR      07-JAN-2000; 2000US-00479614.
XX
PA      (MCCA/) MCCALL C.
PA      (WEBE/) WEBER E.
XX
PI      Mccall C, Weber E;
XX
DR      WPI; 2004-010802/01.

```

```
DR N-PSDB; ADG73224.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IGE
PT heavy chain protein, useful for treating and/or eliciting feline immune
PT responses for IGE-mediated responses, such as allergies.
XX
XX Claim 8; SEQ ID NO 2; 44pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
CC portion of a feline IGE heavy chain protein. The methods and compositions
CC of the present invention are useful for eliciting feline immune responses
CC for and/or treating IGE-mediated responses, such as allergies. This is
CC the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
CC chain.
XX
SQ Sequence 496 AA;
OY Query Match 100.0%; Score 97; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Dy 1 VDGGKATNIFPYTAGKKQ 18
|||
216 VDGKATNIFPYTAGKKQ 233
RESULT 8
ADRI0609
ID ADRI0609 standard; peptide; 18 AA.
XX
XX ADRI0609;
XX
XX DT 21-OCT-2004 (first entry)
XX
DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
XX
XX Antiaethmatic; Antiallergic; Immunosuppressive; IGF; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX
OS Canis familiaris.
XX
WM WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX
DR WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
```

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.

XX Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNFFPYTAG 16  
 |||||  
 DB 1 VDGQKATNFFPYTAG 16

RESULT 9  
 AAY79995  
 ID AAY79995 standard; protein; 312 AA.

XX AAY79995;  
 XX 15-MAY-2000 (first entry)

DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

PS Example 1; Page 66-68; 155pp; English.

CC The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IGE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IGE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IGE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX Sequence 312 AA;

Query Match 89.7%; Score 87; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VDGQKATNFFPYTAG 16  
 |||||  
 DB 48 VDGQKATNFFPYTAG 63

RESULT 10  
 AAW23067  
 ID AAW23067 standard; protein; 417 AA.

XX AAW23067;

XX 30-JUN-2005 (revised)

XX 16-JUN-2005 (revised)

XX 19-FEB-1998 (first entry)

DE Canine IGE heavy chain constant region (exon 1-4 product).  
 KW IGE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEX LAB INC.

XX Mermer B, Harrie RA, Steffing AB;

XX WPI; 1997-425031/39.

XX N-PSDB; AAT79278.

PT Isolated canine IGE heavy chain constant region DNA - useful to develop  
 PT products for treatment of canine allergies and for immunomodulation in  
 PT dogs.

XX Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IGE  
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat Type I immediate hypersensitivity, and for immunomodulation





Query Match	79.4%	Score 77	DB 6	Length 577
Best Local Similarity	77.8%	Pred. No. 0.00047		
Matches 14, Conservative	2	Mismatches	2	Indels 0
Gaps	0			
QY	1	VDGQKATNIFPYTAPGKQ	18	

```

Db      295 VDSGQKAENLPFYTAAPPKR 312
||||| : ||||| :
RESULT 14
AAB06204
ID      AAB06204 standard; protein: 343 AA.
XX
AC      AAB06204;
XX
DT      22-NOV-2000 (first entry)
XX
DE      Platyus IGE heavy chain constant regions 2, 3 and 4.
XX
KW      Platyus; immunoglobulin E; IGE; vaccination; infection; allergy; asthma;
XX      eczema; immunogenic peptide.
XX      Ornithorhynchus anatinus.
OS
FH      Key Location/Qualifiers
FT      Misc-difference 1..343
FT      /label= OTHER
FT      /note= "Xaa=unknown"
XX
PM      WO200025722-A2.
XX
PD      11-MAY-2000.
XX
PF      21-OCT-1999; 99WO-SE001896.
XX
PR      02-NOV-1998; 98US-0106652P.
PR      22-SEP-1999; 99US-00401636.
XX
PA      (RESI-) RESISTENTIA PHARM AB.
XX
PI      Hellman LT;
XX
DR      WPI; 2000-365342/31.
XX
PT      Immunogenic polypeptides useful for preventing the harmful effects of
PR      immunoglobulin E in mammals.
XX
PS      Disclosure; Fig 2; 50pp; English.
XX
CC      The present sequence is an immunogenic peptide consisting of the heavy
CC      chain constant regions 2, 3 and 4 of the platypus IGE. It was used to
CC      construct a number of immunogenic peptides which consisted of regions of
CC      IGE from different mammals, which appear to cause a stronger polyclonal
CC      anti-self IGE response than peptides consisting of the same regions from
CC      one mammal. Immunogenic peptides, particularly those consisting of
CC      different heavy chain constant regions, can be used for vaccination in
CC      humans, against bacterial and viral infections and allergies, such as
CC      asthma, fur, pollen and food allergies and eczema
XX
SQ      Sequence 343 AA;
OY      1 VDSGQKATNIPFYTAAPGKQ 18
      ||||| : ||||| :
      61 VDSGQKAENLPFYTAAPPKR 78
Query Match 74.2%; Score 72; DB 3; Length 343;
Best Local Similarity 72.2%; Pred. No. 0.0019;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 15
ADF90022
ID      ADF90022 standard; protein: 337 AA.
XX
AC      ADF90022;
XX
DT      26-FEB-2004 (first entry)
XX

```

```

DE Opossum-rat chimeric IGE polypeptide.
XX
XX IGE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;
KW antiaesthetic; dermatological.
XX
XX Chimeric.
OS Didelphis virginiana.
OS Rattus sp.
XX
XX WO2003096966-A2.
XX
XX 27-NOV-2003.
XX
XX 15-MAY-2003; 2003WO-IB002503.
XX
XX 21-MAY-2002; 2002US-0382552P.
XX
XX (RESISTENTIA PHARM AB.
XX
XX Lundgren M, Fuentes A, Magnusson A;
XX
XX WPI; 2004-042496/04.
XX
XX N-PSDB; ADF90020, ADF90021.
XX
XX New host cell comprising a nucleic acid vector comprising a
XX cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
XX SV40 late polyadenylation sequence, useful in producing a chimeric IGE
XX polypeptide.
XX
XX PS Claim 3; SEQ ID NO 3; 23pp; English.
XX
XX The present sequence is the protein sequence of an opossum CH2-rat CH3-
XX opossum CH4 (ORO) chimeric IGE polypeptide. A vector comprising a nucleic
XX acid encoding ORO can be used for recombinant production of this chimeric
XX IGE in host, e.g. CHO, cells. The invention provides methods and
XX materials related to expressing chimeric IGE proteins. Nucleic acid
XX vectors, host cells, and methods for producing chimeric IGE polypeptides
XX are provided. When administered to a mammal, the chimeric polypeptides
XX can reduce the IGE antibody effects of IGE-related diseases such as
XX asthma, allergies and eczema.
XX
XX SQ Sequence 337 AA;

Query Match 61.9%; Score 60; DB 8; Length 337;
Best Local Similarity 61.1%; Pred. No. 0.19;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDSQKATNIPPTARGKQ 18
   |||||:|:|||||:|
Db 56 VDSQEAENLFPYTRPKR 73

```

Search completed: December 12, 2005, 20:30:30  
 Job time : 98.6034 secs

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 24.5172 Seconds  
(without alignments)  
60.699 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDGOKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/7\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/ECTUS\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	431	2	US-09-479-614-14
2	97	100.0	496	2	US-09-479-614-2
3	97	100.0	496	2	US-09-479-614-29
4	87	89.7	108	2	US-09-701-623C-35
5	87	89.7	312	2	US-09-701-623C-2
6	87	89.7	426	1	US-08-336-583-2
7	87	89.7	426	4	PCT-US95-13795-2
8	77	79.4	343	2	US-09-401-636-7
9	60	61.9	341	2	US-09-401-636-3
10	60	61.9	341	2	US-09-401-636-4
11	60	61.9	341	2	US-09-401-636-6
12	60	61.9	341	2	US-09-401-636-9
13	60	61.9	341	2	US-09-401-636-11
14	60	61.9	342	2	US-09-401-636-8
15	60	61.9	342	2	US-09-401-636-5
16	60	61.9	345	2	US-09-401-636-10
17	42	43.3	449	2	US-09-252-991A-28547
18	42	43.3	985	2	US-09-593-777-6
19	42	43.3	985	2	US-09-593-777-66
20	42	43.3	985	4	PCT-US96-03916-6
21	42	43.3	985	4	PCT-US96-03916-66
22	41	42.3	135	2	US-09-252-991A-30004
23	41	42.3	232	2	US-09-489-039A-8106
24	40	41.2	497	2	US-10-077-699C-5
25	40	41.2	63	2	US-09-612-402B-29
26	40	41.2	63	2	US-09-542-520-29
27	40	41.2	242	2	US-09-286-690-8

28	40	41.2	391	2	US-09-721-870-38	Sequence 38, Appl
29	40	41.2	503	2	US-09-147-009-11	Sequence 11, Appl
30	40	41.2	505	2	US-09-612-402B-17	Sequence 17, Appl
31	40	41.2	505	2	US-09-542-520-17	Sequence 17, Appl
32	40	41.2	659	2	US-09-248-796A-24809	Sequence 24809, A
33	40	41.2	670	2	US-10-197-220-169	Sequence 169, Appl
34	40	41.2	829	2	US-10-055-364-46	Sequence 46, Appl
35	40	41.2	854	2	US-09-350-841A-1589	Sequence 1589, Ap
36	40	41.2	856	2	US-08-486-099-103	Sequence 103, App
37	40	41.2	856	2	US-08-484-223B-103	Sequence 103, App
38	40	41.2	856	2	US-08-919-597-103	Sequence 103, App
39	40	41.2	856	2	US-08-475-668A-103	Sequence 103, App
40	40	41.2	856	2	US-08-485-551A-103	Sequence 103, App
41	40	41.2	856	2	US-08-471-913A-103	Sequence 103, App
42	40	41.2	856	2	US-08-485-264A-103	Sequence 103, App
43	40	41.2	856	2	US-08-474-349A-103	Sequence 103, App
44	40	41.2	856	2	US-08-470-896-103	Sequence 103, App
45	40	41.2	856	2	US-08-485-546A-103	Sequence 103, App

## ALIGNMENTS

```
RESULT 1
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER APPLICATION NUMBER: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match      100.0%; Score 97; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIFPYTAPGKQ 18
Db      151 VDGOKATNIFPYTAPGKQ 168

RESULT 2
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER APPLICATION NUMBER: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
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Query Match 100.0%; Score 97; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 9.6e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTPGKQ 18  
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Db 216 VDGKATNIPFYTPGKQ 233

RESULT 3  
US-09-479-614-29  
; Sequence 29, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-29

Query Match 100.0%; Score 97; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 9.6e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTPGKQ 18  
|||  
Db 216 VDGKATNIPFYTPGKQ 233

RESULT 4  
US-09-281-760E-35  
; Sequence 35, Application US/09281760E  
; Patent No. 6734287  
; GENERAL INFORMATION:  
; APPLICANT: Lawton, Robert  
; APPLICANT: Mermet, Brion  
; APPLICANT: Francoeur, Greg  
; TITLE OF INVENTION: Specific Binding Protein for Treating  
; FILE REFERENCE: 01-1275A  
; CURRENT APPLICATION NUMBER: US/09/281,760E  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: 09/058,331  
; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (81)..(81)  
; OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,  
; OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (82)..(82)  
; OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (136)..(136)

OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (413)..(414)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (451)..(451)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (460)..(462)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (500)..(500)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (530)..(530)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (568)..(568)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (847)..(849)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (853)..(853)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1382)..(1382)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1832)..(1832)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
US-09-281-760E-35

Query Match 89.7%; Score 87; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTPG 16  
|||  
Db 47 VDGKATNIPFYTPG 62

RESULT 5  
US-09-701-623C-2  
; Sequence 2, Application US/09701623C  
; Patent No. 6811782  
; GENERAL INFORMATION:  
; APPLICANT: Wang Ph.D., Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; FILE REFERENCE: 11514153US1  
; CURRENT APPLICATION NUMBER: US/09/701,623C  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Dog

QY 1 VDGKATNIFPYAPGKQ 18  
||||| |:||||| :  
||||| |:||||| :

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Db          61 VDGQKATNIPPYTAPRK 78

RESULT 9
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match          61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY          1 VDGQKATNIPPYTAPRK 18
||||:|:|||||:
Db          62 VDGQEAENLFPYTTRPKR 79

RESULT 10
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match          61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY          1 VDGQKATNIPPYTAPRK 18
||||:|:|||||:
Db          62 VDGQEAENLFPYTTRPKR 79

RESULT 11
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
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; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

Query Match          61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY          1 VDGQKATNIPPYTAPRK 18
||||:|:|||||:
Db          62 VDGQEAENLFPYTTRPKR 79

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match          61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY          1 VDGQKATNIPPYTAPRK 18
||||:|:|||||:
Db          62 VDGQEAENLFPYTTRPKR 79

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-11

Query Match 61.9%; Score 60; DB 2; Length 341;  
Best Local Similarity 61.1%; Pred. No. 0.072;  
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTPAGKQ 18  
||||:|||||:  
DB 62 VDGQEAENLFPYTRPKR 79

RESULT 14  
US-09-401-636-5

; Sequence 5, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401,636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-5

Query Match 61.9%; Score 60; DB 2; Length 342;  
Best Local Similarity 61.1%; Pred. No. 0.072;  
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTPAGKQ 18  
||||:|||||:  
DB 62 VDGQEAENLFPYTRPKR 79

RESULT 15

US-09-401-636-8  
; Sequence 8, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401,636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-8

Query Match 61.9%; Score 60; DB 2; Length 342;  
Best Local Similarity 61.1%; Pred. No. 0.072;  
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTPAGKQ 18  
||||:|||||:  
DB 62 VDGQEAENLFPYTRPKR 79

Search completed: December 12, 2005, 19:37:06  
Job time : 25.5172 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 80.3793 Seconds  
(without alignments)  
93.568 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDGQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10
2	97	100.0	431	3	US-09-479-614-14
3	97	100.0	431	4	US-10-409-772-14
4	97	100.0	496	3	US-09-479-614-2
5	97	100.0	496	3	US-09-479-614-29
6	97	100.0	496	4	US-10-214-524-25
7	97	100.0	496	4	US-10-409-772-2
8	97	100.0	496	4	US-10-409-772-29
9	87	89.7	18	5	US-10-758-165-9
10	87	89.7	426	4	US-10-214-524-28
11	77	79.4	343	3	US-09-401-636-7
12	77	79.4	343	4	US-10-176-664-7
13	77	79.4	343	4	US-10-673-594-7
14	77	79.4	577	4	US-10-214-524-29
15	60	61.9	337	4	US-10-438-794-3
16	60	61.9	337	4	US-10-453-915-3
17	60	61.9	338	4	US-10-438-794-6
18	60	61.9	338	4	US-10-453-915-6
19	60	61.9	341	3	US-09-401-636-3
20	60	61.9	341	3	US-09-401-636-6
21	60	61.9	341	3	US-09-401-636-9
22	60	61.9	341	3	US-09-401-636-11
23	60	61.9	341	3	US-09-401-636-14
24	60	61.9	341	4	US-10-176-664-3
25	60	61.9	341	4	US-10-176-664-4
26	60	61.9	341	4	US-10-176-664-6
27	60	61.9	341	4	US-10-176-664-9

28	60	61.9	341	4	US-10-176-664-11	Sequence 11, Appl
29	60	61.9	341	4	US-10-673-594-3	Sequence 3, Appl
30	60	61.9	341	4	US-10-673-594-4	Sequence 4, Appl
31	60	61.9	341	4	US-10-673-594-6	Sequence 6, Appl
32	60	61.9	341	4	US-10-673-594-9	Sequence 9, Appl
33	60	61.9	341	4	US-10-673-594-11	Sequence 11, Appl
34	60	61.9	342	3	US-09-401-636-5	Sequence 5, Appl
35	60	61.9	342	3	US-09-401-636-8	Sequence 8, Appl
36	60	61.9	342	4	US-10-176-664-5	Sequence 5, Appl
37	60	61.9	342	4	US-10-176-664-8	Sequence 8, Appl
38	60	61.9	342	4	US-10-673-594-5	Sequence 5, Appl
39	60	61.9	342	4	US-10-673-594-8	Sequence 8, Appl
40	60	61.9	345	3	US-09-401-636-10	Sequence 10, Appl
41	60	61.9	345	4	US-10-176-664-10	Sequence 10, Appl
42	60	61.9	345	4	US-10-673-594-10	Sequence 10, Appl
43	60	61.9	347	4	US-10-438-794-14	Sequence 14, Appl
44	60	61.9	347	4	US-10-453-915-14	Sequence 14, Appl
45	60	61.9	353	4	US-10-453-915-21	Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-10-758-165-10  
; Sequence 10, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 10  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-10

Query Match 100.0%; Score 97; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.6e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPGKQ 18  
|||||  
Db 1 VDGQKATNIFPYTAPGKQ 18

RESULT 2  
US-09-479-614-14  
; Sequence 14, Application US/09479614  
; Publication No. US20030013183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-14

Query Match 100.0%; Score 97; DB 3; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTAPGKQ 18  
|||||  
Db 151 VDGOKATNIPFYTAPGKQ 168

RESULT 3  
US-10-409-772-14  
; Sequence 14, Application US/10409772  
; Publication No. US20030216565A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/10/409,772  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/479,614  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-409-772-14

Query Match 100.0%; Score 97; DB 4; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTAPGKQ 18  
|||||  
Db 151 VDGOKATNIPFYTAPGKQ 168

RESULT 4  
US-09-479-614-2  
; Sequence 2, Application US/09479614  
; Publication No. US20030013183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-2

Query Match 100.0%; Score 97; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTAPGKQ 18  
|||||  
Db 216 VDGOKATNIPFYTAPGKQ 233

RESULT 5  
US-09-479-614-29  
; Sequence 29, Application US/09479614  
; Publication No. US20030013183A1

; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-29

Query Match 100.0%; Score 97; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTAPGKQ 18  
|||||  
Db 216 VDGOKATNIPFYTAPGKQ 233

RESULT 6  
US-10-214-524-25  
; Sequence 25, Application US/10214524  
; Publication No. US20030073142A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Swei-Shen Alex  
; APPLICANT: Yang, Yong-Min  
; APPLICANT: Barankiewicz, Theresa J.  
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
; FILE REFERENCE: ICE-00101.P.1.1  
; CURRENT APPLICATION NUMBER: US/10/214,524  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/312,120  
; PRIOR FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Cat (Felis catus)  
US-10-214-524-25

Query Match 100.0%; Score 97; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTAPGKQ 18  
|||||  
Db 216 VDGOKATNIPFYTAPGKQ 233

RESULT 7  
US-10-409-772-2  
; Sequence 2, Application US/10409772  
; Publication No. US20030216565A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/10/409,772  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/479,614  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-2

Query Match 100.0%; Score 97; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18  
|||||  
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 8  
US-10-409-772-29  
Sequence 29, Application US/10409772  
Publication No. US20030216565A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/10/409,772  
CURRENT FILING DATE: 2003-04-07  
PRIOR APPLICATION NUMBER: US/09/479,614  
PRIOR FILING DATE: 2000-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-29

Query Match 100.0%; Score 97; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18  
|||||  
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 9  
US-10-758-165-9  
Sequence 9, Application US/10758165  
Publication No. US20050196816A1  
GENERAL INFORMATION:  
APPLICANT: Hammetberg, Bruce  
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
FILE REFERENCE: 5051-661  
CURRENT APPLICATION NUMBER: US/10/758,165  
CURRENT FILING DATE: 2004-01-16  
PRIOR APPLICATION NUMBER: US 60/440,472  
PRIOR FILING DATE: 2003-01-16  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 9  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-758-165-9

Query Match 89.7%; Score 87; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPG 16  
|||||  
Db 1 VDGOKATNIFPYTAPG 16

RESULT 10  
US-10-214-524-28  
Sequence 28, Application US/10214524  
Publication No. US20030073142A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Swei-Shen Alex  
APPLICANT: Yang, Yong-Min  
APPLICANT: Barankiewicz, Theresa J.  
APPLICANT: Chen, Zhong  
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
FILE REFERENCE: IGE-00101.P.1.1  
CURRENT APPLICATION NUMBER: US/10/214,524  
CURRENT FILING DATE: 2002-08-08  
PRIOR APPLICATION NUMBER: 60/312,120  
PRIOR FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 28  
LENGTH: 426  
TYPE: PRT  
ORGANISM: Dog (Canis familiaris)  
US-10-214-524-28

Query Match 89.7%; Score 87; DB 4; Length 426;  
Best Local Similarity 100.0%; Pred. No. 8.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPG 16  
|||||  
Db 146 VDGOKATNIFPYTAPG 161

RESULT 11  
US-09-401-636-7  
Sequence 7, Application US/09401636  
Patent No. US20010038843A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/006001  
CURRENT APPLICATION NUMBER: US/09/401,636  
CURRENT FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 343  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-7

Query Match 79.4%; Score 77; DB 3; Length 343;  
Best Local Similarity 77.8%; Pred. No. 0.00031;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18  
|||||  
Db 61 VDGOKATNIFPYTAPGKX 78

RESULT 12  
US-10-176-664-7  
Sequence 7, Application US/10176664  
Publication No. US20030031663A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/006001  
CURRENT APPLICATION NUMBER: US/10/176,664

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; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match          79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00031;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
        |||||:|||||:|
        61 VDGQKAENLFPYTAPPKR 78

RESULT 13
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match          79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00031;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
        |||||:|||||:|
        61 VDGQKAENLFPYTAPPKR 78

RESULT 14
US-10-214-524-29
; Sequence 29, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: 1GE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Duckbilled platypus (Ornithorhynchus anatinus)
US-10-214-524-29

Query Match          79.4%; Score 77; DB 4; Length 577;
Best Local Similarity 77.8%; Pred. No. 0.00054;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
        |||||:|||||:|
        295 VDGQKAENLFPYTAPPKR 312

RESULT 15
US-10-438-794-3
; Sequence 3, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric 1GE Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated ORO
US-10-438-794-3

Query Match          61.9%; Score 60; DB 4; Length 337;
Best Local Similarity 61.1%; Pred. No. 0.02;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
        |||||:|||||:|
        56 VDGQKAENLFPYTTPPKR 73

Search completed: December 12, 2005, 20:19:25
Job time : 80.3793 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.94828 Seconds  
(without alignments)  
34.094 Million cell updates/sec

Title: US-10-758-165a-10

Perfect score: 97

Sequence: 1 VDQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
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2: /cgn2\_6/prodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/1/pubppaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	89.7	312	6	US-10-723-207-2
2	44	45.4	102	6	US-10-821-234-1457
3	43	44.3	254	6	US-10-485-517-188
4	41	42.3	497	6	US-10-763-712A-24
5	40	41.2	430	6	US-10-763-712A-91
6	40	42.3	497	6	US-10-467-657-2346
7	39	40.2	121	6	US-10-793-626-2524
8	38	39.2	241	6	US-10-485-517-189
9	37	38.1	345	6	US-10-793-626-3168
10	36	37.1	532	7	US-10-793-626-3168
11	36	37.1	588	7	US-11-184-380-5
12	36	37.1	724	7	US-11-184-380-5
13	36	37.1	805	7	US-10-518-599-4
14	35.5	36.6	1045	7	US-11-113-424-54
15	35.5	36.6	1094	6	US-10-821-234-1097
16	35.5	36.6	2376	7	US-11-096-051-4
17	35.5	36.6	2715	7	US-11-096-051-2
18	35.5	36.6	2715	7	US-11-113-424-51
19	35.5	36.6	2721	7	US-11-096-051-10
20	35.5	36.6	2725	7	US-11-096-051-8
21	35	36.1	288	6	US-10-467-657-1682
22	35	36.1	433	6	US-10-131-826A-6
23	35	36.1	605	6	US-10-821-234-1207
24	35	36.1	636	6	US-10-763-712A-29
25	35	36.1	636	6	US-10-763-712A-93

26	35	36.1	805	6	US-10-518-599-24	Sequence 24, Appl
27	35	36.1	826	6	US-10-793-626-1066	Sequence 1066, Ap
28	35	36.1	853	6	US-10-821-234-1110	Sequence 1110, Ap
29	35	36.1	1006	6	US-10-467-657-8400	Sequence 8400, Ap
30	35	36.1	2335	6	US-10-821-234-1610	Sequence 1610, Ap
31	34	35.1	72	6	US-10-986-501-118	Sequence 118, App
32	34	35.1	232	6	US-10-510-386-116	Sequence 116, App
33	34	35.1	233	6	US-10-467-657-5470	Sequence 5470, Ap
34	34	35.1	409	6	US-10-793-626-2002	Sequence 2002, Ap
35	34	35.1	409	6	US-10-793-626-2306	Sequence 2306, Ap
36	34	35.1	410	6	US-10-858-730-233	Sequence 233, App
37	34	35.1	424	6	US-10-485-517-405	Sequence 405, App
38	34	35.1	485	6	US-10-467-657-4512	Sequence 4512, Ap
39	34	35.1	1892	7	US-11-075-185-6	Sequence 5, Appl
40	34	35.1	3655	7	US-11-075-185-5	Sequence 5, Appl
41	33.5	34.5	2011	7	US-11-080-991-56	Sequence 56, Appl
42	33	34.0	139	6	US-10-467-657-55292	Sequence 5292, Ap
43	33	34.0	154	6	US-10-467-657-2034	Sequence 2034, Ap
44	33	34.0	481	6	US-10-467-657-4396	Sequence 4396, Ap
45	33	34.0	530	6	US-10-131-826A-130	Sequence 130, App

## ALIGNMENTS

RESULT 1  
US-10-723-207-2  
Sequence 2, Application US/10723207  
Publication No. US20050250934A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Yi  
TITLE OF INVENTION: Walfield, Alan M.  
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
FILE REFERENCE: 1151-4153US2  
CURRENT FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: US/10/723,207  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/701,623  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US99/13959  
PRIOR FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: 09/100,287  
PRIOR FILING DATE: 1998-06-20  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Dog  
FEATURE:  
OTHER INFORMATION: CH2CHN of dog Ige  
PUBLICATION INFORMATION:  
AUTHORS: Patel,  
JOURNAL: Immunogenetics  
VOLUME: 41  
PAGES: 282-286  
DATE: 1995  
US-10-723-207-2

Query Match 89.7%; Score 87; DB 6; Length 312;  
Best Local Similarity 100.0%; Pred. No. 5.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDQKATNIFPYTAPG 16  
|||||  
Db 48 VDQKATNIFPYTAPG 63

RESULT 2  
US-10-821-234-1457  
Sequence 1457, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:

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; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: DE_SEQ_genes Version 1.0
; SEQ ID NO 1457
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1457

Query Match      45.4%; Score 44; DB 6; Length 102;
Best Local Similarity 43.8%; Pred. No. 0.32;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 DGKATNIFPYTPGK 17
Db      14 DGEAPDVAVFAPGE 29

RESULT 3
US-10-485-517-188
; Sequence 188, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: BioSynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; PRIOR FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-188

Query Match      44.3%; Score 43; DB 6; Length 254;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 KATNIFPYT 13
Db      58 KOTNIFPYT 66

RESULT 4
US-10-763-712A-24
; Sequence 24, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
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; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-763-712A-24

Query Match      42.3%; Score 41; DB 6; Length 497;
Best Local Similarity 50.0%; Pred. No. 5.9;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 VDQKATNIFPYTPGKQ 18
Db      324 MDGKETNITWVPAPGSK 341

RESULT 5
US-10-763-712A-91
; Sequence 91, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 497
; TYPE: PRT
; ORGANISM: C. reinhardtii
US-10-763-712A-91

Query Match      42.3%; Score 41; DB 6; Length 497;
Best Local Similarity 50.0%; Pred. No. 5.9;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 VDQKATNIFPYTPGKQ 18
Db      324 MDGKETNITWVPAPGSK 341

RESULT 6
US-10-467-657-2346
; Sequence 2346, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
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;; PRIOR FILING DATE: 2001-02-12  
;; NUMBER OF SEQ ID NOS: 9218  
;; SOFTWARE: SeqMan9, version 1.04  
;; SEQ ID NO 2346  
;; LENGTH: 430  
;; TYPE: PRT  
;; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2346

Query Match 41.2%; Score 40; DB 6; Length 430;  
Best Local Similarity 46.7%; Pred. No. 7.4;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDGKATNIFPYTAP 15  
Db 127 LDGQDITKLAPYDRP 141

RESULT 7  
US-10-793-626-2524  
;; Sequence 2524, Application US/10793626  
;; Publication No. US20050255478A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KIMMERLY, WILLIAM JOHN  
;; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
;; FILE REFERENCE: PU3480US  
;; CURRENT APPLICATION NUMBER: US/10/793,626  
;; CURRENT FILING DATE: 2004-03-04  
;; PRIOR APPLICATION NUMBER: 60/164,258  
;; PRIOR FILING DATE: 1999-11-09  
;; NUMBER OF SEQ ID NOS: 4472  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 2524  
;; LENGTH: 121  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-2524

Query Match 40.2%; Score 39; DB 6; Length 121;  
Best Local Similarity 57.1%; Pred. No. 2.8;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GOKATNIFPYTAPG 16  
Db 44 GKATNIERYTSQG 57

RESULT 8  
US-10-485-517-189  
;; Sequence 189, Application US/10485517  
;; Publication No. US20050256299A1  
;; GENERAL INFORMATION:  
;; APPLICANT: University of Sheffield  
;; APPLICANT: Biosynex Incorporated  
;; APPLICANT: Foster, Simon  
;; TITLE OF INVENTION: Antigenic Polypeptides  
;; FILE REFERENCE: P100623WO  
;; CURRENT APPLICATION NUMBER: US/10/485,517  
;; CURRENT FILING DATE: 2004-02-02  
;; PRIOR APPLICATION NUMBER: GB 0118825.9  
;; PRIOR FILING DATE: 2001-08-02  
;; PRIOR APPLICATION NUMBER: GB 0200349.9  
;; PRIOR FILING DATE: 2002-01-09  
;; NUMBER OF SEQ ID NOS: 424  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 189  
;; LENGTH: 241  
;; TYPE: PRT  
;; ORGANISM: Staphylococcus aureus

US-10-485-517-189

Query Match 39.2%; Score 38; DB 6; Length 241;  
Best Local Similarity 87.5%; Pred. No. 8.7;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KATNIFPY 12  
Db 46 KOTNIFPY 53

RESULT 9  
US-10-793-626-3168  
;; Sequence 3168, Application US/10793626  
;; Publication No. US20050255478A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KIMMERLY, WILLIAM JOHN  
;; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
;; FILE REFERENCE: PU3480US  
;; CURRENT APPLICATION NUMBER: US/10/793,626  
;; CURRENT FILING DATE: 2004-03-04  
;; PRIOR APPLICATION NUMBER: 60/164,258  
;; PRIOR FILING DATE: 1999-11-09  
;; NUMBER OF SEQ ID NOS: 4472  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 3168  
;; LENGTH: 345  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-3168

Query Match 38.1%; Score 37; DB 6; Length 345;  
Best Local Similarity 63.6%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGKATNIFP 11  
Db 223 LDGKRAANIFP 233

RESULT 10  
US-11-184-380-6  
;; Sequence 6, Application US/11184380  
;; Publication No. US20050255089A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Chlorini, John  
;; APPLICANT: Kotin, Robert M.  
;; TITLE OF INVENTION: RAYS NUCLEIC ACIDS  
;; FILE REFERENCE: 14014.032303  
;; CURRENT APPLICATION NUMBER: US/11/184,380  
;; CURRENT FILING DATE: 2005-07-19  
;; PRIOR APPLICATION NUMBER: PCT/US99/11958  
;; PRIOR FILING DATE: 1999-05-28  
;; PRIOR APPLICATION NUMBER: 60/087,029  
;; PRIOR FILING DATE: 1998-05-28  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 532  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence; Note =  
US-11-184-380-6

Query Match 37.1%; Score 36; DB 7; Length 532;  
Best Local Similarity 46.7%; Pred. No. 45;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTAP 15  
Db 63 VDGSNANAYFGYSTP 77

RESULT 11  
US-11-184-380-5  
; Sequence 5, Application US/11184380  
; Publication No. US20050255089A1  
; GENERAL INFORMATION:  
; APPLICANT: Kiorini, John  
; APPLICANT: Kiorini, Robert M.  
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS  
; FILE REFERENCE: 14014.0323U3  
; CURRENT APPLICATION NUMBER: US/11/184,380  
; PRIOR FILING DATE: 2005-07-19  
; PRIOR APPLICATION NUMBER: PCT/US99/11958  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087,029  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; Note =  
US-11-184-380-5  
OTHER INFORMATION: synthetic construct

Query Match 37.1%; Score 36; DB 7; Length 588;  
Best Local Similarity 46.7%; Pred. No. 50;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTAP 15  
Db 119 VDGSNANAYFGYSTP 133

RESULT 12  
US-11-184-380-4  
; Sequence 4, Application US/11184380  
; Publication No. US20050255089A1  
; GENERAL INFORMATION:  
; APPLICANT: Kiorini, John  
; APPLICANT: Kiorini, Robert M.  
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS  
; FILE REFERENCE: 14014.0323U3  
; CURRENT APPLICATION NUMBER: US/11/184,380  
; PRIOR FILING DATE: 2005-07-19  
; PRIOR APPLICATION NUMBER: PCT/US99/11958  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087,029  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 724  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; Note =  
US-11-184-380-4  
OTHER INFORMATION: synthetic construct

Query Match 37.1%; Score 36; DB 7; Length 724;  
Best Local Similarity 46.7%; Pred. No. 63;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTAP 15  
Db 255 VDGSNANAYFGYSTP 269

RESULT 13  
US-10-518-599-4  
; Sequence 4, Application US/10518599  
; Publication No. US20050251873A1  
; GENERAL INFORMATION:  
; APPLICANT: PENNINGER, JOSEPH M.  
; APPLICANT: CRACKOWER, MICHAEL A.  
; TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND  
; TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION  
; FILE REFERENCE: SONN.064US  
; CURRENT APPLICATION NUMBER: US/10/518,599  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: PCT/CA03/00882  
; PRIOR FILING DATE: 2003-06-19  
; PRIOR APPLICATION NUMBER: US 60/389,709  
; PRIOR FILING DATE: 2002-06-19  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 805  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-518-599-4

Query Match 37.1%; Score 36; DB 6; Length 805;  
Best Local Similarity 43.8%; Pred. No. 70;  
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GOKATNIPFYTPGKQ 18  
Db 272 GREFTNLYPLTVPPAQ 287

RESULT 14  
US-11-113-424-54  
; Sequence 54, Application US/11113424  
; Publication No. US20050260713A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangolli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/11/113,424  
; PRIOR FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 1045  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-113-424-54

Query Match 36.6%; Score 35.5; DB 7; Length 1045;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;



Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;  
Oy 2 DG---QKATNPPYTAPG 16  
|||:|||||:  
Db 540 DGFRLRGRTETREYSSKG 557

RESULT 15  
US-10-821-234-1097  
; Sequence 1097; Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Grain, Birgit  
; APPLICANT: Andarmat, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes Version 1.0  
; SEQ ID NO 1097  
; LENGTH: 1094  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1097

Query Match 36.6%; Score 35.5; DB 6; Length 1094;  
Best Local Similarity 44.4%; Pred. No. 1.2e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

Oy 2 DG---QKATNPPYTAPG 16  
|||:|||||:  
Db 589 DGFRLRGRTETREYSSKG 606

Search completed: December 12, 2005, 20:19:49  
Job time : 2.94828 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 15.2069 Seconds  
(without alignments)  
113.889 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97

Sequence: 1 VDGQKATNIPPYTAPGKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2	T16880
2	43	44.3	633	2	S62057
3	43	44.3	658	2	AH0110
4	42	43.3	381	2	AD2436
5	42	43.3	643	1	S15623
6	42	43.3	683	2	B71325
7	42	43.3	1032	2	S74487
8	42	43.3	1686	2	A87692
9	41	42.3	544	2	T17798
10	41	42.3	544	2	D88449
11	41	42.3	623	2	T22177
12	41	42.3	713	2	J80230
13	41	42.3	2298	2	T49648
14	40.5	41.8	363	2	C82607
15	40.5	41.8	1371	2	D82606
16	40	41.2	101	2	G69203
17	40	41.2	109	2	F89886
18	40	41.2	179	2	D90167
19	40	41.2	227	2	C75582
20	40	41.2	240	2	C89967
21	40	41.2	242	1	LXBS
22	40	41.2	258	2	AF0306
23	40	41.2	327	2	S40753
24	40	41.2	374	2	G81926
25	40	41.2	391	2	T33714
26	40	41.2	419	2	C81179
27	40	41.2	454	2	AH2821
28	40	41.2	470	2	H97599
29	40	41.2	506	2	T07942

30	40	41.2	645	2	T16078	hypothetical prote
31	40	41.2	812	2	T07745	phosphatidylinosit
32	40	41.2	814	2	T07761	phosphatidylinosit
33	40	41.2	831	2	T05265	coat protein gamma
34	40	41.2	857	1	O0BE1L	glycoprotein B - h
35	40	41.2	915	2	T12526	hypothetical prote
36	40	41.2	1013	2	G71460	hypothetical prote
37	40	41.2	1064	2	T40751	probable outer mem
38	40	41.2	1203	2	T28895	isoenzyme1-trna syn
39	40	41.2	1069	2	T70656	hypothetical prote
40	40	41.2	3076	2	A87058	fatty acid synthas
41	39	40.2	157	2	A69637	transcription elon
42	39	40.2	213	2	C64041	hypothetical prote
43	39	40.2	308	2	H95965	hypothetical prote
44	39	40.2	308	2	F95416	hypothetical prote
45	39	40.2	374	2	G86267	T6d4.7 protein - A

## ALIGNMENTS

RESULT 1  
T16880  
Hypothetical protein T14G12.4 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 05-Oct-2004  
C:Accession: T16880  
R:Wilcox, L.  
Submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid T14G12.  
A:Reference number: Z18596  
A:Accession: T16880  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-270 <M1>  
A:Cross-References: UNIPROT:Q22510; UNIPARC:UPI0000075025; EMBL:U41268; NID:G1086843; PI  
C:Genetics:  
A:Gene: CBSP:T14G12.4  
A:Introns: 37/1; 72/3; 164/1  
F:93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;  
Best Local Similarity 57.1%; Pred. No. 1.8;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKATNIPPYTAPG 16  
DB 205 GAANAALPPYFSPG 218

RESULT 2  
S62057  
Proline-rich protein LAS17 - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: protein Q4724; protein YOR181w  
C:Species: *Saccharomyces cerevisiae*  
C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: S62057; S67073  
R:Toh-e, A.  
Submitted to the EMBL Data Library, December 1995  
A:Description: Yeast mutants sensitive to local anesthetics.  
A:Reference number: S62057  
A:Accession: S62057  
A:Molecule type: DNA  
A:Residues: 1-633 <TOH>  
A:Cross-References: UNIPROT:Q12446; UNIPARC:UPI000003CA29; EMBL:D78487; NID:G1101756; PI  
R:Hughes, B.; Pohl, T.M.  
Submitted to the Protein Sequence Database, July 1996  
A:Reference number: S66685  
A:Accession: S67073  
A:Molecule type: DNA  
A:Residues: 1-633 <HUG>  
A:Cross-References: UNIPARC:UPI000003CA29; EMBL:Z75089; NID:G1420436; PID:e252060; PID:G1  
A:Experimental source: strain S288C



A:Residues: 1-1032 <KAN>  
A:Cross-references: UNIPROT:P72637; UNIPARC:UPI0000139F6B; EMBL:D90899; GB:AB001339; NID  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Genetics:  
A:Start codon: GTG

Query Match 43.3%; Score 42; DB 2; Length 1032;  
Best Local Similarity 35.3%; Pred. No. 87;  
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
QY 1 VDGQKATNIFPYTAPGK 17  
Db 732 IDAYTNSNYPYSDGE 748

RESULT 8  
A87692  
Conserved hypothetical protein CC3571 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: A87692  
R:Nierman, W.C.; Feldlym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laud, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Klot  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete genome sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: A87692  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1686 <STO>  
A:Cross-references: UNIPROT:Q9A2U0; UNIPARC:UPI00000C7B14; GB:AE005673; NID:G1342511; F  
C:Genetics:  
A:Gene: CC3571

Query Match 43.3%; Score 42; DB 2; Length 1686;  
Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GOKATNIFPYTA 14  
Db 286 GOKATVFPPLGA 297

RESULT 9

T17798  
hypothetical protein A301L - Chlorella virus PBCV-1  
C:Species: Chlorella virus PBCV-1  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T17798  
R:Graves, M.V.; Van Etten, J.L.  
submitted to the EMBL Data Library, May 1999  
A:Reference number: Z18806  
A:Accession: T17798  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-241 <GRA>  
A:Cross-references: UNIPROT:Q84617; UNIPARC:UPI00000F4B38; EMBL:U42580; NID:G4028896; PI  
A:Experimental source: specific host Chlorella strain NC64A  
C:Genetics:  
A>Note: A301L  
C:Superfamily: Chlorella virus PBCV-1 hypothetical protein A301L

Query Match 42.3%; Score 41; DB 2; Length 241;  
Best Local Similarity 75.0%; Pred. No. 26;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIFPYTAP 15  
Db 182 NVFPYITGP 189

RESULT 10

D88449  
protein P54D8.3 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: D88449  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A>Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.ganger.ac.uk/Projects/C\_ele  
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: D88449  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-544 <STO>  
A:Cross-references: UNIPROT:Q20780; UNIPARC:UPI0000174F99; GB:chr\_III; PIDN:AAA20615.1;  
C:Genetics:  
A:Gene: P54D8.3  
A:Map position: 3  
C:Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 42.3%; Score 41; DB 2; Length 544;  
Best Local Similarity 44.4%; Pred. No. 63;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPGKQ 18  
Db 369 VDGQVETILKTIYAGKK 406

RESULT 11

T22177  
hypothetical protein F44F1.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22177  
R:Dobson, R.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19527  
A:Accession: T22177  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-623 <WIL>  
A:Cross-references: UNIPROT:Q02260; UNIPARC:UPI000017B9C4; EMBL:Z81083; PIDN:CAB03101.1;  
A:Experimental source: clone F44F1  
C:Genetics:  
A:Gene: CESP:F44F1.3  
A:Map position: 1  
A:introns: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3

Query Match 42.3%; Score 41; DB 2; Length 623;  
Best Local Similarity 55.0%; Pred. No. 74;  
Matches 11; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 1 VDGQKATNIFPYTAPG 16  
Db 152 VDGQKATNIFPYTIDG 171

RESULT 12

JE0230  
NADPH-cytochrome P450 oxidoreductase (BC 1.-.-.-) - common tobacco  
C:Species: Nicotiana glauca (common tobacco)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
C:Accession: JE0230  
R:Yamada, T.; Imahishi, H.; Oka, A.; Ohkawa, H.  
Biosci. Biotechnol. Biochem. 62, 1403-1411, 1998  
A:Title: Molecular cloning and expression in Saccharomyces cerevisiae of tobacco NADPH-c  
A:Reference number: JE0230; MUID:98386693; PMID:9720224  
A:Accession: JE0230  
A:Molecule type: mRNA  
A:Residues: 1-713 <YAM>  
A:Cross-references: UNIPROT:Q7M275; UNIPARC:UPI0000175049

C:Superfamily: NADPH-ferrithemoprotein reductase; flavodoxin homology; NADPH-ferrithemoprid  
C:Keywords: Flavoprotein; oxidoreductase  
F:107-712/Domain: NADPH-ferrithemoprotein reductase homology <FEH>  
F:109-257/Domain: flavodoxin homology <FLX>

Query Match 42.3%; Score 41; DB 2; Length 713;  
Best Local Similarity 57.1%; Pred. No. 85;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQGKATNIPFYTA 14  
Db 265 LDGDDATRATPYTA 278

## RESULT 13

T49648 hypochlorite protein B8B20.20 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C/Accession: T49648

R/Schulte, U.; Aign, V.; Hehnel, J.; Brandt, P.; Fairmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A/Accession: T49648

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2298 <SCH>

A/Cross-references: UNIPROT:Q96U00; UNIPARC:UPI00001784BA; EMBL:AL355933; GSPDB:GN00116;

C:Genetics:

A:Gene: NCSP:B8B20.20

A/Map position: 6

A/Intons: 426/3

Query Match 42.3%; Score 41; DB 2; Length 2298;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QKATNIPFYTAGK 17  
Db 1694 ERVTQVLPPQPK 1707

## RESULT 14

C82607

DNA primase XF2025 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C/Accession: C82607

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; MUID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: C82607

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-363 <SIM>

A/Cross-references: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28BE; GB:AE004021; GB:AE003849; NID

A:Experimental source: strain 9a5c

R/Simpson, A.U.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation  
C:Genetics:  
A:Gene: XF2025

Query Match 41.8%; Score 40.5; DB 2; Length 363;  
Best Local Similarity 55.6%; Pred. No. 49;  
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQGKATNIPFYTAGK 18  
Db 264 VDQ---TAFPIFAPGEO 298

## RESULT 15

D82606

DNA primase XF2061 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C/Accession: D82606

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; MUID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: D82606

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1371 <SIM>

A/Cross-references: UNIPROT:Q9PBS8; UNIPARC:UPI00000C290E; GB:AE004022; GB:AE003849; NID

A:Experimental source: strain 9a5c

R/Simpson, A.U.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A/Contents: annotation

C:Genetics:

A:Gene: XF2061

Query Match 41.8%; Score 40.5; DB 2; Length 1371;  
Best Local Similarity 55.6%; Pred. No. 2.2e+02;  
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQGKATNIPFYTAGK 18  
Db 1292 VDQ---TAFPIFAPGEO 1306

Search completed: December 12, 2005, 20:42:51

job time : 16.2069 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 97.7586 Seconds  
(without alignments)  
129.907 Million cell updates/sec

Title: US-10-758-165a-10  
Perfect score: 97  
Sequence: 1 VDQKATNIFPYTAPKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_crembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	52.6	382	Q7PSV1_FUSNV	Q7PSV1 fusobacteri
2	51	52.6	382	Q8R6B3_FUSNN	Q8R6B3 fusobacteri
3	48	49.5	168	Q95QAG_CAEEL	Q95QAG caenorhabdi
4	48	49.5	270	Q22510_CAEEL	Q22510 caenorhabdi
5	47	48.5	1054	Q608X6_METCA	Q608X6 methylcocci
6	47	48.5	1538	Q94H26_ORYSA	Q94H26 oryza sativ
7	46	47.4	408	Q565U8_9BACT	Q565U8 uncultured
8	45	46.4	279	Q619H6_CABBR	Q619H6 caenorhabdi
9	45	46.4	445	ALN_STRCO	Q91XUS streptomyce
10	45	46.4	811	Q41FN3_GIBZE	Q41FN3 gibberella
11	44	45.4	102	GAGC1_HUMAN	Q60829 homo sapien
12	44	45.4	102	Q61B11_HUMAN	Q61B11 homo sapien
13	44	45.4	340	Q9AYAO_ORYSA	Q9AYAO oryza sativ
14	44	45.4	525	Q6A1L1_DESPS	Q6A1L1 desulfocale
15	44	45.4	589	Q53Q04_ORYSA	Q53Q04 oryza sativ
16	44	45.4	760	Q6UDM4_ORYSA	Q6UDM4 oryza sativ
17	44	45.4	875	Q7FA19_ORYSA	Q7FA19 oryza sativ
18	44	45.4	884	Q53JX1_ORYSA	Q53JX1 oryza sativ
19	44	45.4	1037	Q55IS1_CRYNE	Q55IS1 cyptococcu
20	44	45.4	1037	Q5KXC8_CRYNE	Q5KXC8 cyptococcu
21	44	45.4	1336	Q7PAL2_ORYSA	Q7PAL2 oryza sativ
22	44	45.4	1685	Q7XSP1_ORYSA	Q7XSP1 oryza sativ
23	43	44.3	1338	Q5FK37_LACAC	Q5FK37 lactobacilli
24	43	44.3	52	Q7WYM4_BACSH	Q7WYM4 bacillus sp
25	43	44.3	104	Q5TSY2_ANOGA	Q5TSY2 anopheles g
26	43	44.3	120	Q52EG8_MAGGR	Q52EG8 magnaporthe
27	43	44.3	166	Q6GCH5_STYAS	Q6GCH5 staphylococ
28	43	44.3	166	Q8NTE3_STYAW	Q8NTE3 staphylococ
29	43	44.3	240	Q9KH50_STYAW	Q9KH50 staphylococ
30	43	44.3	240	Q6G8C2_STYAS	Q6G8C2 staphylococ
31	43	44.3	240	Q8NVX6_STYAW	Q8NVX6 staphylococ

32	43	44.3	240	Q5HEW1_STYAC	Q5HEW1 staphylococ
33	43	44.3	343	QUBA_BORBU	Q51053 borrelia bu
34	43	44.3	346	Q662Z1_BORGA	Q662Z1 borrelia ga
35	43	44.3	400	Q8G6D4_CORST	Q8G6D4 corynebacte
36	43	44.3	633	LAS17_YEAST	Q12446 saccharomyc
37	43	44.3	641	Q8CKM1_YERPE	Q8CKM1 yersinia pe
38	43	44.3	658	Q8ZHU0_YERPE	Q8ZHU0 yersinia pe
39	43	44.3	1175	Q7XG40_ORYSA	Q7XG40 oryza sativ
40	43	44.3	1175	Q94124_ORYSA	Q94124 oryza sativ
41	43	44.3	1207	Q4P6A9_USYMA	Q4P6A9 usyllago ma
42	43	44.3	1271	Q7XW55_ORYSA	Q7XW55 oryza sativ
43	43	44.3	1335	Q9LA54_9CAUD	Q9LA54 bacterioph
44	43	44.3	1335	Q9LA58_9CAUD	Q9LA58 prophage p-
45	42.5	43.8	480	Q82A46_STYAW	Q82A46 streptomyce

## ALIGNMENTS

```

RESULT 1
ID Q7PSV1_FUSNV PRELIMINARY; PRT; 382 AA.
AC Q7PSV1;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).
GN Name=FNV1343;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_Taxid=209882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49256;
RA Karpatsch V., Ivanova N., Anderson I., Reznik G., Bhattacharya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyrpides N.;
RU Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBU; AABF0100055; EAA24105.1; -; Genomic_DNA.
DR GO; GO:0016829; F.1-lyase activity; IEA.
DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
KW Lyase.
SQ SEQUENCE 382 AA; 43893 MW; 441C73816E1C761E CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 6.9;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKATNIFPYTAP 15
   :|:|:|:|:|:|
Db 28 EGGKAVGIRPYTAP 41

RESULT 2
ID Q8R6B3_FUSNN PRELIMINARY; PRT; 382 AA.
AC Q8R6B3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).
GN OrderedAccession=FNO208;
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_Taxid=76856;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RC STRAIN=ATCC 25586;
RX MEDLINE=2186394; PubMed=11889109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kaparatel V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grecklin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Forststein M., Kyriplides N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018 (2002).
DR EMBL: AE009951; AA194414.1; -, Genomic_DNA.
DR InterPro: IPR010327; HGD-D.
DR Pfam: PF06050; HGD-D; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 6.9;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGKATNIPYTPAP 15
Db 28 BGKXAVGIFPYAP 41

RESULT 3
095QA9 CAEEL PRELIMINARY; PRT; 168 AA.
ID 095QA9 CAEEL PRELIMINARY; PRT; 168 AA.
AC 095QA9;
DT 01-DEC-2001 (TREMBlrel. 19; Created)
DT 01-DEC-2001 (TREMBlrel. 19; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Forkhead transcription factor family protein 2, isoform b.
GN Name=Fkh-2; ORFNames=TI4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL: U41268; AA102521.1; -, Genomic_DNA.
DR HSSP: Q99958; 1D5V.
DR SMR: Q95QA9; 2-68.
DR WormBase: WBGene0001434; Fkh-2.
DR WormPep: TI4G12.4b; CE29342.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR011766; TF_Fork_head.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head; 1.
DR PRINTS: PR00053; FORKHEAD.
DR PRODOM: PD000425; TF_Fork_head; 1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4E6968572 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 3 GQKATNIPYTPAPG 16
Db 103 GAAANLFPYSPFG 116

RESULT 4
022510 CAEEL PRELIMINARY; PRT; 270 AA.
ID 022510 CAEEL PRELIMINARY; PRT; 270 AA.
AC 022510;
DT 01-NOV-1996 (TREMBlrel. 01; Created)
DT 01-NOV-1996 (TREMBlrel. 01; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Forkhead transcription factor family protein 2, isoform a.
GN Name=Fkh-2; ORFNames=TI4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
CC -1- INTERACTION:
CC 021648; R02F2.5; NDEXP=1; IntAct=EBI-327741, EBI-314179;
CC 09XW88; Y75B8A.1; NDEXP=1; IntAct=EBI-327741, EBI-316766;
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL: U41268; AA82436.1; -, Genomic_DNA.
DR PIR: T16880; T16880.
DR HSSP: Q99958; 1D5V.
DR SMR: Q22510; 93-170.
DR IntAct: Q22510; -.
DR EMBL: TI4G12.4; Caenorhabditis elegans.
DR WormBase: WBGene0001434; Fkh-2.
DR WormPep: TI4G12.4a; CE04965.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR011766; TF_Fork_head.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head; 1.
DR PRINTS: PR00053; FORKHEAD.
DR PRODOM: PD000425; TF_Fork_head; 1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 270 AA; 30491 MW; 7C49116B5EC76175 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPYTPAPG 16
Db 205 GAAANLFPYSPFG 218

RESULT 5
Q608X6 METCA PRELIMINARY; PRT; 1054 AA.
ID Q608X6 METCA PRELIMINARY; PRT; 1054 AA.
AC Q608X6;
DT 25-OCT-2004 (TREMBlrel. 28; Created)
DT 25-OCT-2004 (TREMBlrel. 28; Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28; Last annotation update)
DE Hydrophobe/amphiphile Efflux-1 (HAE1) family protein.

```



GN OrderedLocustNames=MCA1360;  
 OS Methylococcus capsulatus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;  
 OC Methylococcaceae; Methylococcus.  
 OK NCBI\_TaxId=414;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Bach / NCIMB 11132;  
 RX PubMed=15383640; DOI=10.1371/journal.pbio.0020303;  
 RA Ward N.L., Larsen O., Sakwa J., Brubach L., Khouri H.M., Durkin A.S.,  
 RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,  
 RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,  
 RA Rayvel J., Tettein H., Ren Q., Read T.D., Deboy R.T., Sehnadri R.,  
 RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,  
 RA Grindberg S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S.,  
 RA Uterbeck T.R., Feldblyum T.V., Frazer C.M., Lilienhaug J.R.,  
 RA Eiden J.A.;  
 RT "Genomic insights into methanotrophy: the complete genome sequence of  
 RT Methylococcus capsulatus (Bach)."  
 RL Plos Biol. 2:1616-1628(2004).  
 DR EMBL: AE017282; AAU92574.1; -; Genomic\_DNA.  
 DR TIGR: MCA1360; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0005215; P:transporter activity; IEA.  
 DR GO: GO:0006810; P:transport; IEA.  
 DR InterPro: IPR001036; ACRflavin\_res.  
 DR InterPro: IPR004764; HAE1.  
 DR Pfam: PF00873; ACR\_tran; 1.  
 DR PRINTS: PR00702; ACRIFLAVINP.  
 DR TIGRFAMs: TIGR00915; 2A0602; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 1054 AA; 115004 MW; BB032CB91B3BD1A8 CRC64;  
 QY Query Match 48.5%; Score 47; DB 2; Length 1054;  
 Best Local Similarity 56.2%; Pred. No. 97;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 DB 1 VDGOKATNIFPYTAPG 16  
 294 VNGHKSTQIVYTLPG 309  
 RESULT 6  
 Q94H26 ORYSA  
 ID Q94H26\_ORYSA PRELIMINARY; PRT; 1538 AA.  
 AC Q94H26;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative gag-pol polyprotein.  
 GN Name=OSUN8077G22.13;  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OK NCBI\_TaxId=4530;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,  
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Teitlin T.,  
 RA Riggs F., Heiso J., Ziemann V., Blunt S., Pal G., Vanaken S.E.,  
 RA Uterbeck T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,  
 RA White O., Frazer C.M.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC Buell R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC084831; AA52152.1; -; Genomic\_DNA.  
 DR Gramene: Q94H26; -;  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0004523; F:ribonuclease H activity; IEA.  
 DR GO: GO:0003723; F:RNA binding; IEA.

DR GO: GO:000364; F:RNA-directed DNA polymerase activity; IEA.  
 DR GO: GO:0006310; F:DNA recombination; IEA.  
 DR GO: GO:0006278; P:DNA-dependent DNA replication; IEA.  
 DR InterPro: IPR001562; Retrotrans\_gag.  
 DR InterPro: IPR002156; RNaseH.  
 DR InterPro: IPR001584; Rve.  
 DR Pfam: PF03732; Retrotrans\_gag; 1.  
 DR Pfam: PF00075; RNaseH; 1.  
 DR Pfam: PF00665; rve; 1.  
 DR PROSITE: PS50879; RNase\_H; 1.  
 KW Polyprotein.  
 SQ SEQUENCE 1538 AA; 174627 MW; 5E7A521B398BC776 CRC64;  
 QY Query Match 48.5%; Score 47; DB 2; Length 1538;  
 Best Local Similarity 61.5%; Pred. No. 1,5e+02;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 DB 1 VDGOKATNIFPYT 13  
 740 VDGRAAVNLMPT 752  
 RESULT 7  
 ID Q565U8\_9BACT PRELIMINARY; PRT; 408 AA.  
 AC Q565U8;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE 3-oxoacyl-CoA thiolase.  
 GN ORFNames=fc62;  
 OS uncultured bacterium.  
 OC Bacteria; environmental samples.  
 OK NCBI\_TaxId=77133;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kube M., Beck A., Meyerlietks A., Amann R., Reinhardt R., Rabus R.;  
 RT "A catabolic gene cluster for anaerobic benzoate degradation in  
 RT methanotrophic microbial Black Sea mats."  
 RL Syst. Appl. Microbiol. 28:287-294(2005).  
 DR EMBL: CR931837; CAI78864.1; -; Genomic\_DNA.  
 SQ SEQUENCE 408 AA; 43368 MW; F9BEC546FA32193 CRC64;  
 QY Query Match 47.4%; Score 46; DB 2; Length 408;  
 Best Local Similarity 38.9%; Pred. No. 52;  
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 DB 1 VDGOKATNIFPYTAPGQ 18  
 45 IDASIGANVYQFTAPGQ 62  
 RESULT 8  
 Q619H6 CAEBR  
 ID Q619H6\_CAEBR PRELIMINARY; PRT; 279 AA.  
 AC Q619H6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein CBG14280.  
 GN Name=CBG14280;  
 OS Caenorhabditis briggsae.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Felodermatidae; Caenorhabditis.  
 OK NCBI\_TaxId=6238;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC The C. briggsae Sequencing Consortium;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 CC -i- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL: CAC01000068; CAE68479.1; -; Genomic\_DNA.  
 DR SMR: Q619H6; 101-178.  
 DR GO: GO:0005634; C:nucleus; IEA.

```

DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001766; TP Fork head.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head_1.
DR PRINTS: PR00053; FORKHEAD.
DR ProDom: PD000425; TP_Fork_head_1.
DR SMART: SM00339; FH_1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS0039; FORK_HEAD_3; 1.
DR DNA-binding, Hypothetical protein; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 279 AA; 31322 MW; 0C926B95AD122D9B CRC64;

Query Match 46.4%; Score 45; DB 2; Length 279;
Best Local Similarity 57.1%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIFPYTAPG 16
Db 213 GAAANLFPYFPG 226

RESULT 9
ALN_STRCO STANDARD; PRT; 445 AA.
AC O9RKU5;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable allantoinase (EC 3.5.2.5).
GN Ouredlocusnames=SCO6247; ORENAMES=SCAH10.12, STAH10.12;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bertley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- CAPTAYTIC ACTIVITY: (S)-allantoin + H(2)O = allantate.
CC -1- COPFACTOR: Zinc (By similarity).
CC -1- PATHWAY: Degradation of allantoin (purine catabolism); first step.
CC -1- SIMILARITY: Belongs to the DHOase family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AL939126; CAB60166.1; -, Genomic_DNA.
DR HSSP: P81006; 1GKR.
DR InterPro: IPR00680; Amidohydro_1.
DR InterPro: IPR005847; DHOase.
DR Pfam: PF01979; Amidohydro_1; 1.
DR ProDom: PD000518; DHOase; 1.
KW Complete proteome; Hydrolase; Hypothetical protein; Metal-binding;
KW Purine metabolism; Zinc.
FT METAL 63 Zinc (Potential).

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FT METAL 65 Zinc (Potential).
SQ SEQUENCE 445 AA; 47492 MW; 75955C5F98632570 CRC64;

Query Match 46.4%; Score 45; DB 1; Length 445;
Best Local Similarity 53.3%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDQKATNIFPYTAP 15
Db 26 VTGKRTAVPYDAP 40

RESULT 10
Q4IFN3_GIBZE PRELIMINARY; PRT; 811 AA.
ID Q4IFN3_GIBZE
AC Q4IFN3;
DT 13-SEP-2005 (TREMURel. 31, Last sequence update)
DT 13-SEP-2005 (TREMURel. 31, Last annotation update)
DE Hypothetical protein.
GN ORENAMES=FG03975.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.B., Camarata J., Chang Y.,
RA Choepel Y., Collamore A., Cook A., Cooke P., Corman B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gierre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamel M., Kamet A., Karatae A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunhkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramesamy U., Raymond C., Rette R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAC01000168; EAA73443.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 811 AA; 84248 MW; C2C5A4A02E10DA79 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 811;
Best Local Similarity 58.8%; Pred. No. 1.6e+02;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 DGQKATNIFPYTAPGK 18
Db 676 DDDKRTATGCTAPGK 692

RESULT 11
GAGC1_HUMAN STANDARD; PRT; 102 AA.
ID GAGC1_HUMAN
AC 060825;
DT 16-OCT-2001 (Rel. 40, Created)

```



DR Gramene; Q9AYA0; -.  
 DR GO; GO:0003723; F:RNA binding; IEA.  
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.  
 DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.  
 KM Polypeptin.  
 SQ SEQUENCE 340 AA; 37731 MW; 88DE72BBA5A44C9E CRC64;

Query Match 45.4%; Score 44; DB 2; Length 340;  
 Best Local Similarity 61.5%; Pred. No. 94;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 VDGOKATNIPYPT 13  
 DB 128 VDGGAAYVNLMPYT 140

RESULT 14  
 06ALL1 DESPS  
 ID 06ALL1 DESPS PRELIMINARY; PRT; 525 AA.  
 AC 06ALL1;  
 DT 25-OCT-2004 (TRENBLrel. 28, Created)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
 DE Related to Mtr restriction system protein.  
 GN OrderedLocustNames=DP2035;  
 OS Desulfotalea psychrophila.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;  
 OC Desulfobulbaceae; Desulfotalea.  
 OX NCBI\_TaxID=84980;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=LSV54 / DSM 12343;  
 RA PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;  
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,  
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,  
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,  
 RA Klenk H.-P.;  
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium  
 RT from permanently cold Arctic sediments";  
 RL Environ. Microbiol. 6:887-902(2004).  
 DR EMBL; CRS52870; CAG36764.1; -; Genomic DNA.  
 DR InterPro; IPR007560; Mtr\_cat.  
 DR Pfam; PF04471; Mtr\_cat; I.  
 KM Complete proteome.  
 SQ SEQUENCE 525 AA; 58444 MW; 22D0BB93FD105099 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 525;  
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 TNIFPYTAPG 16  
 DB 106 TNLFPIYKPG 115

RESULT 15  
 Q53Q04 ORYSA PRELIMINARY; PRT; 589 AA.  
 ID Q53Q04 ORYSA PRELIMINARY;  
 AC Q53Q04;  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Retrotransposon protein, putative, unclassified.  
 GN ORFNames=LOC\_Os11g19590;  
 OS Oryza sativa (Japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriatloideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=35947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,  
 RA Zhu W., Hamilton J., Jones K., Talton L., Feldblyum T., Tsirlin T.,

RA Bera J., Kim M., Jin S., Fadrosh D., Vuong H., Overton II L.,  
 RA Reardon M., Weaver B., Johni S., Lewis M., Uteirack T., Van Aken S.,  
 RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Iobst S.,  
 RA de Vazelles A., White O., Salzberg S., Fraser C.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RA Buell R.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC120306; AAX94889.1; -; Genomic DNA.  
 SQ SEQUENCE 589 AA; 67737 MW; 21931C5BD43DB7 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 589;  
 Best Local Similarity 61.5%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 VDGOKATNIPYPT 13  
 DB 333 VDGGAAYVNLMPYT 345

Search completed: December 12, 2005, 20:41:11  
 Job time : 98.7586 secs



CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC horse IGE 3.76 recognition site.

XX Sequence 18 AA;

SQ Query Match 100.0%; Score 96; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDGPPQGLVKQ 18  
 |||||  
 Db 1 IDGQKVDGPPQGLVKQ 18

#### RESULT 2

ADc64569  
 ID ADC64569 standard; peptide; 15 AA.

XX ADc64569;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P5.

XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

OS Equus caballus.

PN US2003087314-A1.

PD 08-MAY-2003.

PF 08-NOV-2001; 2001US-00052788.

PR 08-NOV-2001; 2001US-00052788.

PA (REGC ) UNIV CALIFORNIA.

PI Gershwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

PT Immunogenic composition comprising an isolated equine immunoglobulin E  
 PT polypeptide that induces production of antibodies which specifically bind  
 PT to equine immunoglobulin E.

PS Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (Ig) E), the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that  
 CC specifically binds to equine IGE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an  
 CC antibody that specifically binds to equine IGE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-  
 CC (S6)), and collecting antiserum from the animal) and a kit for detection  
 CC of equine IGE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IGE. The  
 CC antibody is useful for detecting equine IGE protein in a biological  
 CC sample (serum) which involves contacting the sample with the antibody,  
 CC thus forming an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the  
 CC complex can be detected. The complex is detected using a second labelled

CC antibody. The peptides are useful for generating antibodies specific for  
 CC IGE which can serve as a diagnostic test for allergy. The present  
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic  
 CC peptide from the middle portion of the C2 region.

XX Sequence 15 AA;

SQ Query Match 81.2%; Score 78; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGQKVDGPPQGLV 14  
 |||||  
 Db 2 IDGQKVDGPPQGLV 15

#### RESULT 3

ABP46438  
 ID ABP46438 standard; peptide; 14 AA.

XX ABP46438;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scfv VH CDR3 SEQ ID 2449.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.

PS Claim 2; Page 2992; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX  
SQ Sequence 14 AA;  
Query Match 37.5%; Score 36; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 FPQHGL 15  
Db 7 FPQHGL 12  
RESULT 4  
ADG97265  
ID ADG97265 standard; peptide; 14 AA.  
XX  
AC ADG97265;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE scFv VHCDR3 peptide that immunospecifically binds Blys SegID 2449.  
XX  
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;  
KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;  
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.  
XX  
OS Unidentified.  
XX  
PN WO2003055979-A2.  
XX  
PD 10-JUL-2003.  
XX  
PF 14-NOV-2002; 2002WO-US036496.  
XX  
PR 16-NOV-2001; 2001US-0331469P.  
PR 19-DEC-2001; 2001US-0340817P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
XX  
DR WPI; 2003-505530/47.  
XX  
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
PT (Blys). Useful for detecting and treating diseases or disorders e.g.  
PT rheumatoid arthritis, asthma and leukemia.  
XX  
PS Example 1; SEQ ID NO 2449; 394pp; English.  
XX  
CC This invention relates to novel antibodies that immunospecifically bind  
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to  
CC chromosome 13q34 and encodes a protein that is a member of the tumour  
CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
CC proliferation and differentiation. Specifically, it refers to single  
CC chain antibody molecules (scFvs) derived, preferably, from the variable  
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
CC fragment thereof, of either human, murine, rat or monkey Blys. The  
CC present invention refers to the use of such antibodies in various methods  
CC for the detection, diagnosis and prognosis of diseases related to the  
CC aberrant expression or inappropriate function of Blys or its receptor. As  
CC such, these compositions are useful for identifying immune disorders  
CC including myasthenia gravis and multiple sclerosis, inflammatory  
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
CC as AIDS and proliferative disorders including leukemia, carcinoma and  
CC lymphoma. Accordingly, they can be described as exhibiting various  
CC activities such as antirheumatic, antiarthritic, neuroprotective,  
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
CC peptide sequence is a single chain antibody variable heavy CDR3 peptide

CC that immunospecifically binds Blys of the invention.  
XX  
SQ Sequence 14 AA;  
Query Match 37.5%; Score 36; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 FPQHGL 15  
Db 7 FPQHGL 12  
RESULT 5  
ADR10610  
ID ADR10610 standard; peptide; 18 AA.  
XX  
AC ADR10610;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Cat Ige epitope recognised by monoclonal antibody 3.76, SEQ ID 10.  
XX  
KW Antiasthmatic; Antiallergic; Immunosuppressive; Ige; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW cat.  
XX  
OS Fells catus.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
DR WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian Ige epitope, useful  
PT for testing an allergen reactivity of Ige sample, detecting mammalian Ige  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian Ige epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige.  
CC (I) is useful for testing an allergen reactivity of an Ige sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian Ige and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine Ige corresponding to amino acid  
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
CC canine Ige epsilon-chain. Recognition of epsilon-chains from Ige from  
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
CC of Ige from cat and horse, but did not exhibit cross-reactivity with  
CC either pig or human epsilon-chains of Ige. The present sequence is the  
CC cat Ige 3.76 recognition site.  
XX  
SQ Sequence 18 AA;  
Query Match 36.5%; Score 35; DB 8; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.9e+02;  
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;  
QY 1 IDGKVDQFPQHGLVKQ 18

Db 1 VDSGKATNIFPYTAPGKQ 18

|||||

RESULT 6  
AAR50232  
ID AAR50232 standard; protein; 15 AA.

XX AAR50232;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 09-OCT-1994 (first entry)

XX Sequence of NH2 terminal fragment of Group A streptococcal surface

XX protein M3.

KM B subunit; labile toxin; M protein; fusion protein; antigen;

XX Group A streptococci; rheumatic fever; pharyngitis; ss.

XX Streptococcus sp.

XX MO9406465-A1.

XX 31-MAR-1994.

XX 15-SEP-1993; 93WO-US008704.

XX 16-SEP-1992; 92US-00945860.

XX (UYTE-) UNIV TENNESSEE RES CORP.

XX Dale JB;

XX WPI; 1994-118162/14.

XX New recombinant hybrid streptococcal M protein antigen(s) - which elicit

XX opsonic antibodies without eliciting cross-reactive antibodies to

XX mammalian heart tissue.

XX Disclosure; Page 11; 45pp; English.

XX The surface M protein of Group A streptococci is the major virulence

XX factor and protective antigen of these organisms. However, there are a

XX tremendous number of M protein serotypes. The invention provides a

XX recombinant M protein antigens comprising a gene encoding a carrier

XX protein and an NH2 or COOH terminal M protein fragment carrying one or

XX more epitopes. AAR50232 is a suitable NH2-terminal fragment of M3 protein

XX for constructing antigens which elicit opsonic antibodies in an immunised

XX animal when linked or fused to an appropriate carrier. (Updated on 25-

XX MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS

XX field.)

XX Sequence 15 AA;

XX Query Match 35.4%; Score 34; DB 2; Length 15;

XX Best Local Similarity 41.7%; Pred. No. 2.3e+02;

XX Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX 2 DQKVDQFPQOH 13

XX 1 DARSVNGEFPRH 12

XX Human; 121P2A3; cytosolic; immunostimulant; vaccine; SSH;

KM humoral immune response; cellular immune response;

XX suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002MO-US011359.

XX 10-APR-2001; 2001US-0282739P.

XX 25-APR-2001; 2001US-0286630P.

XX 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX Claim 13; Page 270; 362pp; English.

XX The invention relates to a novel composition comprising a substance that

XX modulates the status of a protein, 121P2A3. The composition of the

XX invention has cytostatic and immunostimulant activity, and is useful as a

XX vaccine. The 121P2A3 proteins and polynucleotides are useful for

XX eliciting humoral or cellular immune response. The polynucleotides are

XX useful for characterizing cytogenetic abnormalities of this chromosomal

XX locus, as tools that can be used to delineate cytogenetic abnormalities

XX in the chromosomal region that encodes 121P2A3 that may contribute to

XX malignant phenotype, and in assessing the status of 121P2A3 gene products

XX in normal versus cancerous tissues. The proteins are useful for

XX generating and characterizing domain-specific antibodies, for identifying

XX agents or cellular factors that bind to 121P2A3 or a particular structure

XX domain, and in various therapeutic and diagnostic contexts, including

XX cancer vaccines. The antibodies or T cells reactive with the product are

XX useful in passive or active immunisation, and in imaging methodologies

XX for the management of cancer. The sequences shown in ABB83466 - ABB95595

XX represent peptides from the 121P2A3 variants of the invention

XX Sequence 15 AA;

XX Query Match 35.4%; Score 34; DB 6; Length 15;

XX Best Local Similarity 40.0%; Pred. No. 2.3e+02;

XX Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

XX 2 DQKVDQFPQOHGLV 16

XX 1 ENKLDKRGVHQHQL 15

XX Human; 121P2A3; cytosolic; immunostimulant; vaccine; SSH;

KM humoral immune response; cellular immune response;

XX suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002MO-US011359.

XX 10-APR-2001; 2001US-0282739P.

XX 25-APR-2001; 2001US-0286630P.

XX 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI; 2003-092956/08.

XX Claim 13; Page 270; 362pp; English.

XX The invention relates to a novel composition comprising a substance that

XX modulates the status of a protein, 121P2A3. The composition of the

XX invention has cytostatic and immunostimulant activity, and is useful as a

XX vaccine. The 121P2A3 proteins and polynucleotides are useful for

XX eliciting humoral or cellular immune response. The polynucleotides are

XX useful for characterizing cytogenetic abnormalities of this chromosomal

XX locus, as tools that can be used to delineate cytogenetic abnormalities

XX in the chromosomal region that encodes 121P2A3 that may contribute to

XX malignant phenotype, and in assessing the status of 121P2A3 gene products

XX in normal versus cancerous tissues. The proteins are useful for

XX generating and characterizing domain-specific antibodies, for identifying

XX agents or cellular factors that bind to 121P2A3 or a particular structure

XX domain, and in various therapeutic and diagnostic contexts, including

XX cancer vaccines. The antibodies or T cells reactive with the product are

XX useful in passive or active immunisation, and in imaging methodologies

XX for the management of cancer. The sequences shown in ABB83466 - ABB95595

XX represent peptides from the 121P2A3 variants of the invention

XX Sequence 15 AA;

XX Query Match 35.4%; Score 34; DB 6; Length 15;

XX Best Local Similarity 40.0%; Pred. No. 2.3e+02;

XX Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

XX 2 DQKVDQFPQOHGLV 16

XX 1 ENKLDKRGVHQHQL 15



```
XX OS Homo sapiens.
XX PN WO000283068-A2.
XX PD 24-OCT-2002.
XX PF 09-APR-2002; 2002WO-US011359.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PR 22-JUN-2001; 2001US-0300373P.
XX PA (AGEN-) AGENSYS INC.
XX PI Challa-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX DR WPI; 2003-092956/08.
XX PT New composition comprising a substance that modulates the status of
XX PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of 121P2A3 gene products in normal
XX PT versus cancerous tissues.
XX PS Claim 13; Page 287; 362pp; English.
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterizing cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene products
XX CC in normal versus cancerous tissues. The proteins are useful for
XX CC generating and characterizing domain-specific antibodies, for identifying
XX CC agents or cellular factors that bind to 121P2A3 or a particular structure
XX CC domain, and in various therapeutic and diagnostic contexts, including
XX CC cancer vaccines. The antibodies or T cells reactive with the product are
XX CC useful in passive or active immunisation, and in imaging methodologies
XX CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX CC represent peptides from the 121P2A3 variants of the invention
XX SQ Sequence 15 AA;
SQ
Query Match 35.4%; Score 34; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 DGQKVDQFPQHGLV 16
Db 1 ENKKLDQRHVQHQL 15
RESULT 9
ABP95194
ID ABP95194 standard; peptide; 15 AA.
XX AC ABP95194;
XX DT 28-MAR-2003 (first entry)
XX DE HLA protein 121P2A3 peptide #11549.
XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO000283068-A2.
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XX PD 24-OCT-2002.
XX PF 09-APR-2002; 2002WO-US011359.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PR 22-JUN-2001; 2001US-0300373P.
XX PA (AGEN-) AGENSYS INC.
XX PI Challa-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX DR WPI; 2003-092956/08.
XX PT New composition comprising a substance that modulates the status of
XX PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of 121P2A3 gene products in normal
XX PT versus cancerous tissues.
XX PS Claim 13; Page 279; 362pp; English.
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterizing cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene products
XX CC in normal versus cancerous tissues. The proteins are useful for
XX CC generating and characterizing domain-specific antibodies, for identifying
XX CC agents or cellular factors that bind to 121P2A3 or a particular structure
XX CC domain, and in various therapeutic and diagnostic contexts, including
XX CC cancer vaccines. The antibodies or T cells reactive with the product are
XX CC useful in passive or active immunisation, and in imaging methodologies
XX CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX CC represent peptides from the 121P2A3 variants of the invention
XX SQ Sequence 15 AA;
SQ
Query Match 35.4%; Score 34; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 2 DGQKVDQFPQHGLV 16
Db 1 ENKKLDQRHVQHQL 15
RESULT 10
ADM96833
ID ADM96833 standard; peptide; 17 AA.
XX AC ADM96833;
XX DT 29-JUL-2004 (first entry)
XX DE Tissue factor VIIa (TFVIIa) peptide antagonist #249.
XX KW tissue factor VIIa; chronic thromboembolic disease;
XX KW fibrin formation; vascular disorders; deep venous thrombosis;
XX KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
XX OS Synthetic.
XX PN US200408767-A1.
XX PD 06-MAY-2004.
XX PF 30-JAN-2003; 2003US-0036257.
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XX 06-FEB-2002; 2002US-0355420P.
PR (GETH ) GENENTECH INC.
XX
XX Lazarus RA, Maun HR;
XX WPI; 2004-356247/33.
DR
XX New peptide, useful for preventing or treating chronic thromboembolic
PT diseases or disorders associated with fibrin formation including vascular
PT disorders, such as deep venous thrombosis, arterial thrombosis, and
PT stroke.
XX
XX Example 2; SEQ ID NO 255; 102pp; English.
XX
XX The invention relates to peptide antagonists of tissue Factor VIIa
CC (FVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
CC with the peptide in the presence of tissue factor and under conditions
CC that allow binding of the compound to FVIIa to occur. The peptides are
CC useful for preventing or treating chronic thromboembolic diseases or
CC disorders associated with fibrin formation including vascular disorders,
CC such as deep venous thrombosis, arterial thrombosis, stroke,
CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
CC peptide antagonist of the invention.
XX
XX Sequence 17 AA;
SQ
Query Match 35.4%; Score 34; DB 8; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 3 GQKVDQPPQ 12
Db 1 GEGVEEFPE 10
RESULT 11
ADRI0609
ID ADRI0609 standard; peptide; 18 AA.
XX
AC ADRI0609;
XX
DT 21-OCT-2004 (first entry)
XX
DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
XX
KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX
OS Canis familiaris.
XX
XX WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (1) that
CC

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CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (1) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE.
XX
XX Sequence 18 AA;
SQ
Query Match 35.4%; Score 34; DB 8; Length 18;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 IDGKVDQPP 11
Db 1 VDGGKATNTP 11
RESULT 12
ADL98126
ID ADL98126 standard; peptide; 10 AA.
XX
AC ADL98126;
XX
DT 17-JUN-2004 (first entry)
XX
DE Candida kefyr enone reductase peptide SEQ ID NO:9.
XX
KW enone reductase; enzyme; levodione; ketoisophorone; carotenoid;
XX Candida kefyr; Kluyveromyces marxianus.
XX
OS Kluyveromyces marxianus.
XX
XX WO2004027065-A2.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-EP010473.
XX
PR 23-SEP-2002; 2002EP-00021098.
XX
XX (STM ) DSM IP ASSETS BV.
XX
XX Karaoka M, Shimizu S;
XX
XX WPI; 2004-295422/27.
XX
XX New enone reductase, useful in improving the production process of
PT levodione, which is important in the synthesis of optically active
PT carotenoids.
XX
XX Example 1; SEQ ID NO 9; 31pp; English.
XX
XX The present invention describes an isolated DNA (1) comprising a
CC nucleotide sequence coding for an enzyme having enone reductase activity.
CC Also described: (1) a vector or a plasmid comprising (1); (2) a host cell
CC transformed or transfected by (1) or the vector or the plasmid of (1);
CC (3) a polypeptide encoded by (1); and (4) a process for the production of
CC levodione which comprises contacting ketoisophorone with the polypeptide
CC of (3) or with the host cell of (2) or a cell-free extract under
CC conditions for the production of levodione, e.g. at pH 4.0-9.0 and at a
CC temperature of 10-60 degrees Celsius for 5 minutes to 72 hours or at pH
CC 5.0-8.0 and at a temperature of 20-60 degrees Celsius for 15 minutes to
CC 48 hours. The DNA (1) and the encoded polypeptide can be used in
CC improving the production process of levodione, which is important in the

```

CC synthesis of optically active carotenoids. The present sequence  
CC represents a Candida kefyr (Kluyveromyces marxianus) enone reductase  
CC peptide, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 10 AA;

Query Match 34.4%; Score 33; DB 8; Length 10;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 POGGLVK 17  
| | | | |  
Db 4 POGGITK 10

RESULT 13  
ABP94247  
ID ABP94247 standard; peptide; 15 AA.  
XX  
XX ABP94247;  
XX

DT 28-MAR-2003 (first entry)  
XX

DE HLA protein 121P2A3 peptide #10602.  
XX

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
KW humoral immune response; cellular immune response;  
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
XX

OS Homo sapiens.  
XX

PN WO200283068-A2.  
XX

PD 24-OCT-2002.  
XX

PF 09-APR-2002; 2002WO-US011359.  
XX

PR 10-APR-2001; 2001US-0282739P.  
XX

PR 25-APR-2001; 2001US-028630P.  
XX

PR 22-JUN-2001; 2001US-0300373P.  
XX

PA (AGEN-) AGENSYS INC.  
XX

PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
XX  
XX WPI; 2003-092956/08.

PT New composition comprising a substance that modulates the status of  
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
PT responses or in assessing the status of 121P2A3 gene products in normal  
PT versus cancerous tissues.

PS Claim 13; Page 261; 362pp; English.  
XX

CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a protein, 121P2A3. The composition of the  
CC invention has cytostatic and immunostimulant activity, and is useful as a  
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
CC eliciting humoral or cellular immune response. The polynucleotides are  
CC useful for characterising cytogenetic abnormalities of this chromosomal  
CC locus, as tools that can be used to delineate cytogenetic abnormalities  
CC in the chromosomal region that encodes 121P2A3 that may contribute to  
CC malignant phenotype, and in assessing the status of 121P2A3 gene products  
CC in normal versus cancerous tissues. The proteins are useful for  
CC generating and characterising domain-specific antibodies, for identifying  
CC agents or cellular factors that bind to 121P2A3 or a particular structure  
CC domain, and in various therapeutic and diagnostic contexts, including  
CC cancer vaccines. The antibodies or T cells reactive with the product are  
CC useful in passive or active immunisation, and in imaging methodologies  
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595  
XX represent peptides from the 121P2A3 variants of the invention

SQ Sequence 15 AA;

Query Match 34.4%; Score 33; DB 6; Length 15;  
Best Local Similarity 42.9%; Pred. No. 3.3e+02;  
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 DQKVDQFPQHGL 15  
: | : | | | |  
Db 2 ENEKUDRQHVOHQL 15

RESULT 14  
ABP95554  
ID ABP95554 standard; peptide; 15 AA.  
XX  
XX ABP95554;  
XX

DT 28-MAR-2003 (first entry)  
XX

DE HLA protein 121P2A3 peptide #11909.  
XX

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
KW humoral immune response; cellular immune response;  
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
XX

OS Homo sapiens.  
XX

PN WO200283068-A2.  
XX

PD 24-OCT-2002.  
XX

PF 09-APR-2002; 2002WO-US011359.  
XX

PR 10-APR-2001; 2001US-0282739P.  
XX

PR 25-APR-2001; 2001US-028630P.  
XX

PR 22-JUN-2001; 2001US-0300373P.  
XX

PA (AGEN-) AGENSYS INC.  
XX

PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
XX  
XX WPI; 2003-092956/08.

PT New composition comprising a substance that modulates the status of  
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
PT responses or in assessing the status of 121P2A3 gene products in normal  
PT versus cancerous tissues.

PS Claim 13; Page 286; 362pp; English.  
XX

CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a protein, 121P2A3. The composition of the  
CC invention has cytostatic and immunostimulant activity, and is useful as a  
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
CC eliciting humoral or cellular immune response. The polynucleotides are  
CC useful for characterising cytogenetic abnormalities of this chromosomal  
CC locus, as tools that can be used to delineate cytogenetic abnormalities  
CC in the chromosomal region that encodes 121P2A3 that may contribute to  
CC malignant phenotype, and in assessing the status of 121P2A3 gene products  
CC in normal versus cancerous tissues. The proteins are useful for  
CC generating and characterising domain-specific antibodies, for identifying  
CC agents or cellular factors that bind to 121P2A3 or a particular structure  
CC domain, and in various therapeutic and diagnostic contexts, including  
CC cancer vaccines. The antibodies or T cells reactive with the product are  
CC useful in passive or active immunisation, and in imaging methodologies  
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595  
XX represent peptides from the 121P2A3 variants of the invention

Query Match 34.4%; Score 33; DB 6; Length 15;  
Best Local Similarity 42.9%; Pred. No. 3.3e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 2 DGQKVDQFPQHGL 15  
: : : : :  
Db 2 ENKLDQRQHVQHQL 15

Db 2 ENKLDQRQHVQHQL 15

Search completed: December 12, 2005, 21:52:05  
Job time : 111.333 secs

RESULT 15  
ABP94098  
ID ABP94098 standard; peptide; 15 AA.  
XX  
AC ABP94098;  
XX  
DT 28-MAR-2003 (first entry)  
XX  
DE HLA protein 121P2A3 peptide #10453.  
XX  
KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;  
KW humoral immune response; cellular immune response;  
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO200283068-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 09-APR-2002; 2002WO-US011359.  
XX  
PR 10-APR-2001; 2001US-0282739P.  
PR 25-APR-2001; 2001US-0286630P.  
PR 22-JUN-2001; 2001US-0300373P.  
XX  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Challa-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Alar DSH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
XX  
XX WPI; 2003-092956/08.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
PT responses or in assessing the status of 121P2A3 gene products in normal  
PT versus cancerous tissues.  
XX  
PS Claim 13; Page 258; 362pp; English.  
XX  
CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a protein, 121P2A3. The composition of the  
CC invention has cytostatic and immunostimulant activity, and is useful as a  
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
CC eliciting humoral or cellular immune response. The polynucleotides are  
CC useful for characterising cytogenetic abnormalities of this chromosomal  
CC locus, as tools that can be used to delineate cytogenetic abnormalities  
CC in the chromosomal region that encodes 121P2A3 that may contribute to  
CC malignant phenotype, and in assessing the status of 121P2A3 gene products  
CC in normal versus cancerous tissues. The proteins are useful for  
CC generating and characterising domain-specific antibodies, for identifying  
CC agents or cellular factors that bind to 121P2A3 or a particular structure  
CC domain, and in various therapeutic and diagnostic contexts, including  
CC cancer vaccines. The antibodies or T cells reactive with the product are  
CC useful in passive or active immunisation, and in imaging methodologies  
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595  
CC represent peptides from the 121P2A3 variants of the invention  
XX  
SQ Sequence 15 AA;

Query Match 34.4%; Score 33; DB 6; Length 15;  
Best Local Similarity 42.9%; Pred. No. 3.3e+02;  
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGQKVDQFPQHGL 15  
: : : : :  
: : : : :

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 12, 2005, 21:05:57 ; Search time 27 Seconds  
(without alignments)  
55.117 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQPPQHGHWKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 208455

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:  
1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/ECTUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfill1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	34	35.4	15	2	US-08-914-479A-11
2	32	33.3	10	1	US-08-151-574-3
3	32	33.3	10	1	US-08-419-448-3
4	32	33.3	10	2	US-09-233-510-3
5	30	31.2	11	1	US-08-486-839-8
6	30	31.2	11	2	US-09-151-011-8
7	30	31.2	11	2	US-09-343-623-8
8	29	30.2	10	1	US-08-166-195A-23
9	29	30.2	10	1	US-08-436-772-23
10	29	30.2	10	1	US-08-436-772-23
11	29	30.2	10	1	US-08-436-883B-23
12	29	30.2	11	1	US-08-486-839-12
13	29	30.2	11	2	US-09-151-011-12
14	29	30.2	11	2	US-09-343-623-12
15	29	30.2	11	2	US-09-977-827-13
16	29	30.2	15	1	US-08-006-341-2
17	29	30.2	15	1	US-09-511-625B-64
18	28	29.2	15	1	US-07-995-503A-10
19	28	29.2	15	1	US-08-590-510-10
20	28	29.2	15	1	US-08-390-790-10
21	28	29.2	15	1	US-08-390-509-10
22	28	29.2	15	2	US-09-149-860A-10
23	28	29.2	17	2	US-08-836-561-41
24	28	29.2	17	2	US-09-434-122-41
25	27	28.1	10	2	US-08-371-680-10
26	27	28.1	11	1	US-08-486-839-14
27	27	28.1	11	1	US-09-151-011-14

28	27	28.1	11	2	US-09-343-623-14	Sequence 14, Appl
29	27	28.1	11	2	US-09-977-827-15	Sequence 15, Appl
30	27	28.1	15	2	US-08-475-955-75	Sequence 75, Appl
31	27	28.1	15	2	US-07-867-819D-75	Sequence 75, Appl
32	27	28.1	16	2	US-09-701-588C-107	Sequence 107, Appl
33	26	27.1	11	1	US-08-486-839-13	Sequence 13, Appl
34	26	27.1	11	2	US-09-151-011-13	Sequence 13, Appl
35	26	27.1	11	2	US-09-343-623-13	Sequence 13, Appl
36	26	27.1	11	2	US-09-685-010-49	Sequence 49, Appl
37	26	27.1	11	2	US-09-977-827-14	Sequence 14, Appl
38	26	27.1	11	2	US-09-978-309A-49	Sequence 49, Appl
39	26	27.1	11	2	US-09-978-309A-84	Sequence 84, Appl
40	26	27.1	12	1	US-08-151-574-9	Sequence 9, Appl
41	26	27.1	12	1	US-08-196-940-3	Sequence 3, Appl
42	26	27.1	12	1	US-08-419-448-9	Sequence 9, Appl
43	26	27.1	12	2	US-09-233-510-9	Sequence 9, Appl
44	26	27.1	12	2	US-09-685-010-12	Sequence 12, Appl
45	26	27.1	12	2	US-09-685-010-17	Sequence 17, Appl

## ALIGNMENTS

```

RESULT 1
US-08-914-479A-11
; Sequence 11, Application US/08914479A
; Patent No. 6419932
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; FILE REFERENCE: 481112.404C2
; CURRENT APPLICATION NUMBER: US/08/914.479A
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 08/409,270
; PRIOR FILING DATE: 1995-03-23
; PRIOR APPLICATION NUMBER: 07/945,860
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NH2-terminal fragment of M protein for
; OTHER INFORMATION: constructing antigens, which elicit opsonic
; OTHER INFORMATION: antibodies in an immunized animal
US-08-914-479A-11

Query Match      35.4%; Score 34; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 25;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy      2  DGQKVDQPPQ 13
Db      1  DARSVNGEPR 12

RESULT 2
US-08-151-574-3
; Sequence 3, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F. M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; NUMBER OF SEQUENCES: 52

```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Morrison & Foerster  
;; STREET: 545 Middlefield Road, Suite 200  
;; CITY: Menlo Park  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94025-3471  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/151,574  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/688,578  
;; FILING DATE: 24-MAY-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Murashige, Kate H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 24615-20026.00  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-327-7250  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; FRAGMENT TYPE: N-terminal  
;;  
US-08-151-574-3

Query Match 33.3%; Score 32; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDEQFPQHG 14  
|||:|  
Db 2 VDERFPYTG 10

RESULT 3  
US-08-419-448-3  
; Sequence 3, Application US/08419448  
; Patent No. 5863533  
; GENERAL INFORMATION:  
; APPLICANT: Robert F.M. Van Gorcom  
; APPLICANT: Willem Van Hartingsveldt  
; APPLICANT: Petrus A. Van Paridon  
; APPLICANT: Annemarie E. Veenstra  
; APPLICANT: Rudolf G.M. Luttin  
; APPLICANT: Gerardus Sellen  
; TITLE OF INVENTION: Cloning and Expression of Microbial  
; TITLE OF INVENTION: Phytase  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/419,448  
;; FILING DATE: 10-APR-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Murashige, Kate H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 24615-20026.10  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-887-1500  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHEICAL: NO  
;; FRAGMENT TYPE: N-terminal  
;;  
US-08-419-448-3

Query Match 33.3%; Score 32; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDEQFPQHG 14  
|||:|  
Db 2 VDERFPYTG 10

RESULT 4  
US-09-233-510-3  
; Sequence 3, Application US/09233510  
; Patent No. 6350602  
; GENERAL INFORMATION:  
; APPLICANT: Robert F.M. Van Gorcom  
; APPLICANT: Willem Van Hartingsveldt  
; APPLICANT: Petrus A. Van Paridon  
; APPLICANT: Annemarie E. Veenstra  
; APPLICANT: Rudolf G.M. Luttin  
; APPLICANT: Gerardus Sellen  
; TITLE OF INVENTION: Cloning and Expression of Microbial  
; TITLE OF INVENTION: Phytase  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025-3471  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,510  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/688,578  
; FILING DATE: 24-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20026.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-327-7250  
; TELEFAX: 415-327-2951  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
FRAGMENT TYPE: N-terminal  
US-09-233-510-3

Query Match 33.3%; Score 32; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 35;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDQKVDQFP 14  
DB 2 DVDDIDWEP 10

RESULT 5  
US-08-486-839-8  
Sequence 8, Application US/08486839  
Patent No. 5928928  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: A human chitinase, its recombinant  
production, its use for decomposing chitin, its use  
in therapy or prophylaxis against infection diseases.  
TITLE OF INVENTION: 16  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron  
STREET: 350 Jericho Turnpike  
CITY: Jericho  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11758

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,839  
FILING DATE: 07 - June - 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Baron, Ronald J.  
REGISTRATION NUMBER: 29,281  
REFERENCE/DOCKET NUMBER: 294-26  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-08-486-839-8

Query Match 31.2%; Score 30; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 85;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
DB 2 DVDDIDWEP 11

RESULT 6  
US-09-151-011-8  
Sequence 8, Application US/09151011  
Patent No. 6057142  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: A Human Chitinase, Its Recombinant  
production, its use for decomposing chitin, its use in  
therapy or prophylaxis against infection diseases.  
TITLE OF INVENTION: 16  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron, LLP  
STREET: 6900 Jericho Turnpike  
CITY: Syosset  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11791

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/151,011  
FILING DATE: 10 - September - 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Morris, Robert C.  
REGISTRATION NUMBER: 42,910  
REFERENCE/DOCKET NUMBER: 294-32 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-09-151-011-8

Query Match 31.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 85;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
DB 2 DVDDIDWEP 11

RESULT 7  
US-09-343-623-8  
Sequence 8, Application US/09343623  
Patent No. 6303118  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A human chitinase, its recombinant  
production, its use for decomposing chitin, its use  
in therapy or prophylaxis against infection diseases.  
TITLE OF INVENTION: 16  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron  
STREET: 350 Jericho Turnpike  
CITY: Jericho  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11758

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/343,623  
FILING DATE:  
PRIOR APPLICATION DATA:

US-09-343-623-8  
Sequence 8, Application US/09343623  
Patent No. 6303118  
GENERAL INFORMATION:  
APPLICANT:

APPLICATION NUMBER: US/08/486,839  
FILING DATE: 07-June-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Baron, Ronald J.  
REGISTRATION NUMBER: 29,281  
REFERENCE/DOCKET NUMBER: 294-26  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-343-623-8

Query Match 31.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 85;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
|||:|:  
Db 2 DGVIDWEPF 11

RESULT 8  
US-09-977-827-8  
Sequence 8, Application US/09977827  
Patent No. 6896884  
GENERAL INFORMATION:  
APPLICANT: Aeris, Johannes Maria F.G.  
TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decont  
FILE REFERENCE: Docket 294-32 DIVII/CON  
CURRENT FILING DATE: 2001-10-15  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 8  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Autographa californica  
US-09-977-827-8

Query Match 31.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 85;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
|||:|:  
Db 2 DGVIDWEPF 11

RESULT 9  
US-08-166-195A-23  
Sequence 23, Application US/08166195A  
Patent No. 5480799  
GENERAL INFORMATION:  
APPLICANT: O'Rand, Michael G.  
APPLICANT: Widgren, Esther E.  
APPLICANT: Richardson, Richard T.  
APPLICANT: Lea, Isabel  
TITLE OF INVENTION: Sperm Antigen Corresponding to a  
NUMBER OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope  
CORRESPONDENCE ADDRESSES: 51  
ADDRESS: Kenneth D. Sibley  
STREET: P.O. Box 34009  
CITY: Charlotte  
STATE: No. 5480799th Carolina

COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/166,195A  
FILING DATE: 10 DEC 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5470/73  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-166-195A-23

Query Match 30.2%; Score 29; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 11e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVDQFP 10  
|||:|:  
Db 1 GAKVDQFP 8

RESULT 10  
US-08-436-772-23  
Sequence 23, Application US/08436772  
Patent No. 5814456  
GENERAL INFORMATION:  
APPLICANT: O'Rand, Michael G.  
APPLICANT: Widgren, Esther E.  
APPLICANT: Richardson, Richard T.  
APPLICANT: Lea, Isabel  
TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Kenneth D. Sibley  
STREET: P.O. Box 34009  
CITY: Charlotte  
STATE: No. 5814456th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,772  
FILING DATE: 08-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5470-738  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:



LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-436-772-23

Query Match 30.2% Score 29; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GQKVDQFP 10  
| | | | |  
Db 1 GAKVDDRF 8

RESULT 11  
US-08-436-883B-23  
Sequence 23, Application US/08436883B  
Patent No. 5820861  
GENERAL INFORMATION:  
APPLICANT: O'Rand, Michael G.  
APPLICANT: Widgren, Esther E.  
APPLICANT: Richardson, Richard T.  
APPLICANT: Lea, Isabel  
TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm  
TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sibley  
STREET: P.O. Box 34009  
CITY: Charlotte  
STATE: No. 5820861th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,883B  
FILING DATE: 08-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5470-73C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-436-883B-23

Query Match 30.2% Score 29; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GQKVDQFP 10  
| | | | |  
Db 1 GAKVDDRF 8

RESULT 12  
US-08-486-839-12  
Sequence 12, Application US/08486839  
Patent No. 5928928

GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A human chitinase, its recombinant  
TITLE OF INVENTION: production, its use for decomposing chitin, its use  
TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron  
STREET: 350 Jericho Turnpike  
CITY: Jericho  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11758  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,839  
FILING DATE: 07-June-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Baron, Ronald J.  
REGISTRATION NUMBER: 29,281  
REFERENCE/DOCKET NUMBER: 294-26  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
US-08-486-839-12

Query Match 30.2% Score 29; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DQKVDQFP 11  
| | | | |  
Db 2 DGLNLDQFP 11

RESULT 13  
US-09-151-011-12  
Sequence 12, Application US/09151011  
Patent No. 6057142  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A Human Chitinase, Its Recombinant  
TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use In  
TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases.  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron, LLP  
STREET: 6900 Jericho Turnpike  
CITY: Syosset  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11791  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/151,011

FILING DATE: 10 - September - 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Morris, Robert C.  
REGISTRATION NUMBER: 42,910  
REFERENCE/DOCKET NUMBER: 294-32 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-151-011-12

Query Match 30.2%; Score 29; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11  
||:|:|  
Db 2 DGLNLDWQYP 11

RESULT 14  
US-09-343-623-12  
Sequence 12, Application US/09343623  
Patent No. 6303118  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A human chitinase, its recombinant  
production, its use for decomposing chitin, its use  
TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron  
STREET: 350 Jericho Turnpike  
CITY: Jericho  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11758  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/343,623  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,839  
FILING DATE: 07-June-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Baron, Ronald J.  
REGISTRATION NUMBER: 29,281  
REFERENCE/DOCKET NUMBER: 294-26  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-343-623-12

Query Match 30.2%; Score 29; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11  
||:|:|  
Db 2 DGLNLDWQYP 11

RESULT 15  
US-09-977-827-13  
Sequence 13, Application US/09977827  
Patent No. 6896884  
GENERAL INFORMATION:  
APPLICANT: Aerts, Johannes Maria F.G.  
TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decomposing  
chitin, its use in therapy or prophylaxis against infectious diseases  
FILE REFERENCE: Docket 294-32 DIVI/CON  
CURRENT FILING DATE: 2001-10-15  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 13  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-977-827-13

Query Match 30.2%; Score 29; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11  
||:|:|  
Db 2 DGLNLDWQYP 11

Search completed: December 12, 2005, 21:20:09  
Job time : 28 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:19 ; Search time 95 Seconds  
(without alignments)  
79.168 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDEQFPQHGLVKQ 18

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 356231

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : Published\_Applications\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*\n2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*\n3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*\n4: /cgn2\_6/ptodata/1/pubppaa/US10a\_PUBCOMB.pep:\*\n5: /cgn2\_6/ptodata/1/pubppaa/US10b\_PUBCOMB.pep:\*\n6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	5	US-10-758-165-11
2	78	81.2	15	4	US-10-052-788-5
3	36	37.5	14	3	US-09-880-748-2449
4	36	37.5	14	4	US-10-293-418-2449
5	35	36.5	18	5	US-10-758-165-10
6	34	35.4	15	4	US-10-141-627-11
7	34	35.4	17	4	US-10-356-257-255
8	34	35.4	18	5	US-10-758-165-9
9	32	33.3	10	4	US-10-079-709-3
10	32	33.3	14	3	US-09-880-748-2446
11	32	33.3	14	3	US-09-880-748-2466
12	32	33.3	14	4	US-10-293-418-2446
13	32	33.3	14	4	US-10-293-418-2703
14	32	33.3	14	5	US-09-865-478-842
15	31	32.3	14	3	US-09-880-748-2146
16	31	32.3	14	3	US-09-880-748-2151
17	31	32.3	14	4	US-10-293-418-2146
18	31	32.3	14	4	US-10-293-418-2151
19	31	32.3	15	4	US-10-059-261-108
20	31	32.3	15	4	US-10-059-261-216
21	31	32.3	15	5	US-10-627-649-108
22	31	32.3	15	5	US-10-627-649-216
23	31	32.3	18	5	US-10-758-165-15
24	30	31.2	10	4	US-10-353-929-166
25	30	31.2	11	3	US-09-977-827-8
26	30	31.2	17	3	US-09-864-761-46580
27	29.5	30.7	17	4	US-10-356-257-314

28	29	30.2	11	3	US-09-977-827-13	Sequence 13, Appl
29	29	30.2	14	5	US-10-476-362-26	Sequence 26, Appl
30	29	30.2	15	4	US-10-282-960-23	Sequence 23, Appl
31	29	30.2	17	5	US-10-996-316-125	Sequence 125, Appl
32	28	29.2	11	4	US-10-432-234A-13	Sequence 13, Appl
33	28	29.2	11	4	US-10-362-527-52	Sequence 52, Appl
34	28	29.2	11	6	US-11-005-794-107	Sequence 107, Appl
35	28	29.2	13	4	US-10-415-165-21	Sequence 21, Appl
36	28	29.2	14	3	US-09-880-748-2366	Sequence 2366, Ap
37	28	29.2	14	3	US-09-880-748-2452	Sequence 2452, Ap
38	28	29.2	14	3	US-09-880-748-2545	Sequence 2545, Ap
39	28	29.2	14	3	US-10-293-418-2366	Sequence 2366, Ap
40	28	29.2	14	4	US-10-293-418-2452	Sequence 2452, Ap
41	28	29.2	14	4	US-10-293-418-2545	Sequence 2545, Ap
42	28	29.2	15	3	US-09-836-861-10	Sequence 10, Appl
43	28	29.2	15	4	US-10-084-813-1231	Sequence 1231, Ap
44	28	29.2	17	4	US-10-283-349-41	Sequence 41, Appl
45	28	29.2	17	4	US-10-225-567A-1964	Sequence 1964, Ap

## ALIGNMENTS

```
RESULT 1
US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match      100.0%; Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IDGQKVDEQFPQHGLVKQ 18
        ||| ||| ||| ||| |||
Db       1 IDGQKVDEQFPQHGLVKQ 18

RESULT 2
US-10-052-788-5
; Sequence 5, Application US/10052788
; Publication No. US20030087314A1
GENERAL INFORMATION:
; APPLICANT: Gerstwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence:epitope peptide  
OTHER INFORMATION: p5, middle portion of C2 of equine IGE epsilon  
OTHER INFORMATION: heavy chain  
US-10-052-788-5

Query Match 81.2%; Score 78; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6,7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQEPQHG 14  
Db 2 IDGQKVDQEPQHG 15

RESULT 3  
US-09-880-748-2449  
Sequence 2449, Application US/09880748  
Publication No. US2003005937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: P523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2449  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-2449

Query Match 37.5%; Score 36; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15  
Db 7 FPOHGL 12

RESULT 4  
US-10-293-418-2449  
Sequence 2449, Application US/10293418  
Publication No. US2003022396A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: P523P2  
CURRENT APPLICATION NUMBER: US/10/293,418  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2449  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-293-418-2449

Query Match 37.5%; Score 36; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15  
Db 7 FPOHGL 12

RESULT 5  
US-10-758-165-10  
Sequence 10, Application US/10758165  
Publication No. US20050196816A1  
GENERAL INFORMATION:  
APPLICANT: Hammerberg, Bruce  
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
FILE REFERENCE: 5051-661  
CURRENT APPLICATION NUMBER: US/10/758,165  
CURRENT FILING DATE: 2004-01-16  
PRIOR APPLICATION NUMBER: 60/440,472  
PRIOR FILING DATE: 2003-01-16  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 10  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-758-165-10

Query Match 36.5%; Score 35; DB 5; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 IDGQKVDQEPQHGIVKQ 18  
Db 1 VDGQKATNIFPYTAPGKQ 18

RESULT 6  
US-10-141-627-11  
Sequence 11, Application US/10141627  
Publication No. US20020176863A1  
GENERAL INFORMATION:  
APPLICANT: Dale, James B.  
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER  
FILE REFERENCE: 481112.404C3  
CURRENT APPLICATION NUMBER: US/10/141,627  
CURRENT FILING DATE: 2002-05-07  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: NH2-terminal fragment of M protein for  
OTHER INFORMATION: constructing antigens, which elicit opsonic  
OTHER INFORMATION: antibodies in an immunized animal  
US-10-141-627-11

Query Match 35.4%; Score 34; DB 4; Length 15;

Best Local Similarity 41.7%; Pred. No. 1.3e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 DQKVDQEPPOH 13  
Db 1 DAKSVNGEPFRH 12

## RESULT 7

US-10-356-257-255  
; Sequence 255, Application US/10356257  
; Publication No. US20040087767A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZARUS, ROBERT A.  
; APPLICANT: MAUN, HENRY R.  
; TITLE OF INVENTION: Fv1ta Antagonists  
; FILE REFERENCE: P1950R1  
; CURRENT APPLICATION NUMBER: US/10/356,257  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 60/355,420  
; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 355  
; SEQ ID NO 255  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-10-356-257-255

Query Match 35.4%; Score 34; DB 4; Length 17;  
Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GQKVDQEPPO 12  
Db 1 GEGVEEPPE 10

## RESULT 8

US-10-758-165-9  
; Sequence 9, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-758-165-9

Query Match 35.4%; Score 34; DB 5; Length 18;  
Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQVDEQFP 11  
Db 1 VDGQKATNIFP 11

## RESULT 9

US-10-079-709-3  
; Sequence 3, Application US/10079709  
; Publication No. US20030119163A1  
; GENERAL INFORMATION:

APPLICANT: Robert F. M. Van Gorcom  
APPLICANT: Willem Van Hartingsveldt  
APPLICANT: Petrus A. Van Paridon  
APPLICANT: Annemarie E. Veenstra  
APPLICANT: Rudolf G.M. Luttin  
APPLICANT: Gerardus Seiten  
TITLE OF INVENTION: Cloning and Expression of Microbial  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025-3471  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/079,709  
FILING DATE: 02-FEB-2002  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/233,510  
FILING DATE: 20-JAN-1999  
APPLICATION NUMBER: 07/688,578  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20026.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7250  
TELEFAX: 415-327-2951  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
US-10-079-709-3

Query Match 33.3%; Score 32; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VDEQFPQHG 14  
Db 2 VDERPPYTG 10

RESULT 10  
US-09-880-748-2446  
; Sequence 2446, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16

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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 2446
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2446
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Query Match          33.3%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      10 FPOHG 14
         |||||
Db       7 FPOHG 11
```

```
RESULT 11
US-09-880-748-2703
; Sequence 2703, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 2703
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2703
```

```
Query Match          33.3%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      10 FPOHG 14
         |||||
Db       7 FPOHG 11
```

```
RESULT 12
US-10-293-418-2446
; Sequence 2446, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
```

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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2446
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2446
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Query Match          33.3%; Score 32; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      10 FPOHG 14
         |||||
Db       7 FPOHG 11
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RESULT 13
US-10-293-418-2703
; Sequence 2703, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2703
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2703
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Query Match          33.3%; Score 32; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      10 FPOHG 14
         |||||
Db       7 FPOHG 11
```

```
RESULT 14
US-10-865-478-842
; Sequence 842, Application US/10865478
; Publication No. US20040235041A1
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Search completed: December 12, 2005, 21:29:24  
Job time : 96 secs

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; GENERAL INFORMATION:
; APPLICANT: Shimketer, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: csingle Nucleotide Polymorphisms for Known Genes
; FILE REFERENCE: 15866-534-CIP1
; CURRENT APPLICATION NUMBER: US/10/865,478
; PRIOR FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 09/443,199
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/442,129
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/442,849
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 842
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)...(0)
; OTHER INFORMATION: csnp translation
US-10-865-478-842

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```

Query Match      33.3%; Score 32; DB 5; Length 14;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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```

QY      2 DGGKVDGQFPQ 12
      |||:|:|
Db      3 DGGVDPPNP 13

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RESULT 15
US-09-880-748-2146
; Sequence 2146; Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2146
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2146

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```

Query Match      32.3%; Score 31; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      10 PPOHGL 15
      |||
Db      7 PPHGL 12

```

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:17:33 ; Search time 3 Seconds

(without alignments)  
33.507 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDQEPQHGIVKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 9754

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	37.5	14	US-11-054-515-2449	Sequence 2449, Ap
2	32	33.3	14	US-11-054-515-2446	Sequence 2446, Ap
3	32	33.3	14	US-11-054-515-2703	Sequence 2703, Ap
4	31	32.3	14	US-11-054-515-2146	Sequence 2146, Ap
5	31	32.3	14	US-11-054-515-2151	Sequence 2151, Ap
6	28	29.2	14	US-11-054-515-2366	Sequence 2366, Ap
7	28	29.2	14	US-11-054-515-2452	Sequence 2452, Ap
8	28	29.2	14	US-11-054-515-2545	Sequence 2545, Ap
9	28	29.2	18	US-10-518-341-5	Sequence 5, Appl
10	27	28.1	14	US-11-054-515-2406	Sequence 2406, Ap
11	26	27.1	14	US-11-054-515-2414	Sequence 2414, Ap
12	26	27.1	15	US-11-054-515-2429	Sequence 2429, Ap
13	26	27.1	14	US-11-106-932-134	Sequence 134, Appl
14	26	27.1	15	US-11-106-932-135	Sequence 135, Appl
15	26	27.1	18	US-10-503-575-77	Sequence 77, Appl
16	25	26.0	9	US-10-969-314-32	Sequence 32, Appl
17	25	26.0	14	US-10-503-575-25	Sequence 25, Appl
18	25	26.0	14	US-10-503-575-26	Sequence 26, Appl
19	25	26.0	14	US-10-503-575-27	Sequence 27, Appl
20	25	26.0	14	US-10-503-575-28	Sequence 28, Appl
21	25	26.0	14	US-10-503-575-29	Sequence 29, Appl
22	25	26.0	14	US-10-503-575-30	Sequence 30, Appl
23	25	26.0	14	US-10-503-575-31	Sequence 31, Appl
24	25	26.0	14	US-10-503-575-32	Sequence 32, Appl
25	25	26.0	14	US-11-054-515-2149	Sequence 2149, Ap

26	25	26.0	14	US-11-054-515-2152	Sequence 2152, Ap
27	25	26.0	14	US-11-054-515-2404	Sequence 2404, Ap
28	25	26.0	14	US-11-054-515-2427	Sequence 2427, Ap
29	25	26.0	14	US-11-054-515-2543	Sequence 2543, Ap
30	25	26.0	15	US-10-503-575-78	Sequence 78, Appl
31	25	26.0	15	US-11-106-932-65	Sequence 65, Appl
32	25	26.0	16	US-11-106-932-52	Sequence 52, Appl
33	24	25.0	9	US-11-097-864-41	Sequence 41, Appl
34	24	25.0	9	US-11-097-912-41	Sequence 41, Appl
35	24	25.0	10	US-11-097-864-77	Sequence 77, Appl
36	24	25.0	10	US-11-097-864-195	Sequence 195, Appl
37	24	25.0	10	US-11-097-912-77	Sequence 77, Appl
38	24	25.0	10	US-11-097-912-195	Sequence 195, Appl
39	24	25.0	14	US-10-503-575-45	Sequence 45, Appl
40	24	25.0	14	US-11-054-515-2393	Sequence 2393, Ap
41	24	25.0	14	US-11-054-515-2442	Sequence 2442, Ap
42	24	25.0	14	US-11-054-515-2570	Sequence 2570, Ap
43	24	25.0	14	US-11-054-515-2687	Sequence 2687, Ap
44	23	24.0	9	US-11-010-748A-334	Sequence 334, Appl
45	23	24.0	9	US-11-010-748A-346	Sequence 346, Appl

## ALIGNMENTS

RESULT 1  
US-11-054-515-2449  
; Sequence 2449, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFG2393  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; PRIOR FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2449  
; LENGTH: 14  
; TYPE: PR  
; ORGANISM: Homo sapiens  
US-11-054-515-2449  
Query Match 37.5%; Score 36; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 PFGHGL 15  
|||  
DB 7 PFGHGL 12  
RESULT 2

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US-11-054-515-2446
; Sequence 2446, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2446
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2446

Query Match          33.3%; Score 32; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 FPGHG 14
Db      7 FPGHG 11

RESULT 3
US-11-054-515-2703
; Sequence 2703, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2146
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2146

Query Match          33.3%; Score 32; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 FPGHG 14
Db      7 FPGHG 11
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```

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2703
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2703

Query Match          33.3%; Score 32; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 FPGHG 14
Db      7 FPGHG 11

RESULT 4
US-11-054-515-2146
; Sequence 2146, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2146
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2146

Query Match          33.3%; Score 31; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 FPGHGL 15
Db      7 FPGHGL 12

RESULT 5
US-11-054-515-2151
; Sequence 2151, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2151
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2151
```

```

Query Match      32.3%; Score 31; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 5,2;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      10 PPOHGL 15
         |||||
Db       7 FPOHGL 12
```

```

RESULT 6
US-11-054-515-2366
; Sequence 2366, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
```

```

; SEQ ID NO 2366
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2366
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```

Query Match      29.2%; Score 28; DB 7; Length 14;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      10 PPOHGLV 16
         |||||
Db       7 FPOHGLV 13
```

```

RESULT 7
US-11-054-515-2452
; Sequence 2452, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2452
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2452
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```

Query Match      29.2%; Score 28; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      10 PPOHGL 15
         |||||
Db       7 FPOHGL 12
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RESULT 8
US-11-054-515-2545
; Sequence 2545, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2545
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2545
```

```
Query Match          29.2%; Score 28; DB 7; Length 14;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      10  PPOHGLV 16
         ||: |||
Db       7  PPRHPLV 13
```

```
RESULT 9
US-10-518-341-5
; Sequence 5, Application US/10518341
; Publication No. US20050249744A1
; GENERAL INFORMATION:
; APPLICANT: VAN ELS, Cecile Antoinette Carola Maria
; APPLICANT: BOOG, Marie-Claire Josefa Pia
; TITLE OF INVENTION: MHC class II haplotype specific immunodominancy of
; TITLE OF INVENTION: peptides derived from RSV fusion (F) or attachment
; FILE REFERENCE: 28902.0014
; CURRENT APPLICATION NUMBER: US/10/518,341
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/NL03/00454
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02077461.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-10-518-341-5
```

```
Query Match          29.2%; Score 28; DB 6; Length 18;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      3  GQKVDQFPQ 12
         ||: |||
Db       1  GQNTTBEFYQ 10
```

```
RESULT 10
US-11-054-515-2406
```

```
; Sequence 2406, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2406
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2406
```

```
Query Match          28.1%; Score 27; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      10  PPOHG 14
         ||: |||
Db       7  PPHHG 11
```

```
RESULT 11
US-11-054-515-2414
; Sequence 2414, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
```

```

; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 2414
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2414

Query Match      27.1%; Score 26; DB 7; Length 14;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 FPOHGLV 16
DB      7 FPAHPLV 13

RESULT 12
US-11-054-515-2429
; Sequence 2429, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 2429
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2429

Query Match      27.1%; Score 26; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 FPOHGLV 16
DB      7 FPAHPLV 13

RESULT 13
US-11-106-932-134
; Sequence 134, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: HAYES, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
```

```

; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 134
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-134

Query Match      27.1%; Score 26; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 DQKXVD 7
DB      7 DGERVD 12

RESULT 14
US-11-106-932-135
; Sequence 135, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 135
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-932-135

Query Match      27.1%; Score 26; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 DQKXVD 7
DB      10 DGERVD 15

RESULT 15
US-10-503-575-77
; Sequence 77, Application US/10503575
; Publication No. US2005024823A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan Wouter
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
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; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 77  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-575-77

Query Match 27.1%; Score 26; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PPOH 13  
|||  
Db 1 PPOH 4

Search completed: December 12, 2005, 21:20:43  
Job time : 4 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: December 12, 2005, 21:18:48 ; Search time 10.6667 Seconds  
(without alignments)  
162.366 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDQEPQHGIVKQ 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	26.0	14	2	A56632 - neosulfakinin-II -
2	24	25.0	15	2	PT0090 - alpha-glucosidase
3	24	25.0	18	2	A61577 - 24k serine protein
4	23	24.0	11	1	GMR0L - leucosulfakinin -
5	23	24.0	11	2	A60656 - perisulfakinin - A
6	23	24.0	16	2	D49655 - T-cell-receptor be
7	23	24.0	16	2	C90981 - his operon leader
8	23	24.0	16	2	A85827 - his operon leader
9	23	24.0	18	2	S70340 - napin large chain
10	22	22.9	9	2	B39841 - dextranucrase (EC
11	22	22.9	11	2	A33917 - dihydrocrotonase (EC
12	22	22.9	18	2	S29379 - sorbitol dehydroge
13	21	21.9	7	2	A34818 - vicillin 72k chain
14	21	21.9	14	2	EC7075 - guanylate cyclase
15	21	21.9	15	2	A30330 - neuropeptide pep -
16	21	21.9	16	2	A49226 - major outer membra
17	21	21.9	17	2	A65274 - glutathione S-tran
18	21	21.9	17	2	G85956 - hypothetical prote
19	21	21.9	18	2	I55453 - zinc finger homeod
20	21	21.9	18	2	H75063 - hypothetical prote
21	20	20.8	10	2	S33844 - alpha-2-macroglobu
22	20	20.8	10	2	I48778 - small nuclear ribo
23	20	20.8	12	2	G60589 - sperm-activating p
24	20	20.8	12	2	S68402 - NAD(+) -glycohydrol
25	20	20.8	12	2	S68271 - major urinary prot
26	20	20.8	12	2	PN0170 - alcohol dehydrogen
27	20	20.8	13	2	S23640 - Ig kappa chain J s
28	20	20.8	13	2	S47357 - T-cell antigen rec
29	20	20.8	13	2	S47358 - T-cell antigen rec

30	20	20.8	14	2	PC4382 - dehydrin 4.5K poly
31	20	20.8	14	2	PQ0152 - 18k iron-sulfur pr
32	20	20.8	15	2	S51735 - T-cell receptor be
33	20	20.8	15	2	B49655 - T-cell-receptor be
34	20	20.8	15	2	PH0789 - T-cell receptor al
35	20	20.8	15	2	S71306 - heat shock protein
36	20	20.8	16	2	E49255 - T-cell receptor be
37	20	20.8	16	2	F49039 - T-cell receptor be
38	20	20.8	18	2	D49570 - plasma membrane ca
39	19.5	20.3	17	2	B36727 - cytochrome c554 -
40	19	19.8	11	2	A40693 - transgalin - sheep
41	19	19.8	11	2	PC2173 - triacylglycerol 11
42	19	19.8	11	2	QJ2307 - hypothetical 1.5K
43	19	19.8	14	2	C35141 - T-cell receptor de
44	19	19.8	14	2	S27140 - hypothetical prote
45	19	19.8	15	2	S14749 - 3-dehydroquinase -

## ALIGNMENTS

```

RESULT 1
A56632
neosulfakinin-II - flesh fly (Sarcophaga bullata)
N:Alternate names: Neb-SK-II
N:Contains: neosulfakinin-I (Neb-SK-I)
C:Species: Sarcophaga bullata
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: A56632
R:Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.
Comp. Biochem. Physiol. C 103, 135-142, 1992
A:Title: Isolation and primary structure of two sulfakinin-like peptides from the fleshf
F:6-14/Product: neosulfakinin-II #status experimental <NSK2>
F:9/Binding site: sulfate (Tyr) (covalent) #status predicted
F:14/Modified site: amidated carboxyl end (Phe) #status experimental

A:Accession: A56632
A:Molecule type: Protein
A:Residues: 1-14 <PON>
A:Cross-references: UNIPROT:P41493; UNIPARC:UPI000013054D
A:Experimental source: heads
A>Note: sequence extracted from NCBI backbone (NCBIP:120391)
C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F:1-14/Product: neosulfakinin-II #status experimental <NSK2>
F:6-14/Product: neosulfakinin-I #status experimental <NSK1>
F:9/Binding site: sulfate (Tyr) (covalent) #status predicted
F:14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match      26.0%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6; 1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      7 DEQPPHG 14
Db      3 EQFPDDYG 10

RESULT 2
PT0090
alpha-glucosidase (EC 3.2.1.20) - honeybee (fragment)
C:Species: Apis mellifera (honeybee)
C>Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: PT0090
R:Kimura, A.; Takata, M.; Fukushi, Y.; Mori, H.; Matsui, H.; Chiba, S.
Biosci. Biotechnol. Biochem. 61, 1091-1098, 1997
A:Title: A catalytic amino acid and primary structure of active site in Aspergillus nige
A:Reference number: PT0090; MUID:97399878; PMID:9255970
A:Accession: PT0090
A:Molecule type: protein
A:Residues: 1-15 <KIM>
A:Cross-references: UNIPROT:Q7M3W5; UNIPARC:UPI000017BF08
C:Keywords: glycosidase; hydrolase

Query Match      25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 9; 9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 IDGQKVD 7  
||| :||  
Db 2 IDGFRID 8

## RESULT 3

A61577  
24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)  
C/Species: Streptomyces fradiae  
C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: A61577  
R/Sinha, U.; Moliz, S.A.; Lad, P.J.  
Int. J. Biochem. 23, 979-984, 1991  
A/Title: Two new extracellular serine proteases from Streptomyces fradiae.  
A/Reference number: A61577; PMID:92155439; PMID:1786859  
A/Accession: A61577  
A/Molecule type: protein  
A/Residues: 1-18 <SIN>  
A/Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AE13  
C/Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 25.0%; Score 24; DB 2; Length 18;  
Best Local Similarity 27.3%; Pred. No. 1.2e+03;  
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDGQKVDQFP 11  
: ||| :  
Db 2 VGTTRAAQDFP 12

## RESULT 4

GMROL  
Leucosulfakinin - Madeira cockroach

N/Alternate names: LSK

C/Species: Leucophaea maderae (Madeira cockroach)

C/Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004

C/Accession: A01622

R/Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A/Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch

A/Reference number: A01622; PMID:86315858; PMID:3745893

A/Accession: A01622

A/Molecule type: protein

A/Residues: 1-11 <NAC>

A/Cross-references: UNIPROT:P04428; UNIPARC:UPI000012E960

C/Superfamily: gastrin

C/Keywords: amidated carboxyl end; hormone; sulfoprotein

F/6/Binding site: sulfate (Tyr) (covalent) #status experimental

F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 EQPQHG 14  
||| :||  
Db 1 EQFDYD 7

## RESULT 5

A60656  
perisulfakinin - American cockroach

C/Species: Periplaneta americana (American cockroach)

C/Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004

C/Accession: A60656

R/Venestra, J.A.

Neuropeptides 14, 145-149, 1989

A/Title: Isolation and structure of two gastrin/CKR-like neuropeptides from the American

A/Reference number: A60656; PMID:90137190; PMID:2615921

A/Accession: A60656

A/Molecule type: Protein

A/Residues: 1-11 <VEE>

A/Cross-references: UNIPROT:P36885; UNIPARC:UPI000012E962  
C/Comment: This neuropeptide stimulates hindgut contractions.  
C/Keywords: amidated carboxyl end; neuropeptide; sulfoprotein  
F/6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 EQPQHG 14  
||| :||  
Db 1 EQFDYD 7

## RESULT 6

D49655

T-cell-receptor beta chain variable region, TCR V beta (clone 2) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C/Accession: D49655

R/Grom, A.A.; Thompson, S.D.; Luvyink, L.; Passo, M.; Choi, E.; Glaes, D.N.

Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993

A/Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juveni

A/Reference number: A49655; PMID:94068553; PMID:8248215

A/Accession: D49655

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-16 <GRO>

A/Cross-references: UNIPARC:UPI000017C3CA

A/Experimental source: peripheral blood lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIP:140448)

C/Keywords: T-cell receptor

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 55.6%; Pred. No. 1.6e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DQQRVDQFP 10  
||| :|||  
Db 7 DRAPVNEQF 15

RESULT 7  
C90981  
his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RIMD (

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C/Accession: C90981

R/Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A/Reference number: A99629; PMID:21156231; PMID:11258796

A/Accession: C90981

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 <HAY>

A/Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI00000D08D2; GB:BA000007; PIDN:BA836242.1;

A/Experimental source: strain O157:H7, substrain RIMD 0509952

C/Genetics:

A/Gene: ECa2819

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QPQKH 13  
||| :||  
Db 5 QPQKH 9

## RESULT 8



A85827  
his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: A85827  
R:Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Dimmlanta, E.; Potamouelis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A85827  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-16 <STO>  
A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI00000080D2; GB:AE005174; NID:G12516199; F  
A:Experimental source: strain O157:H7, substrain EDL933  
A:Gene: hlyE

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 QPPOH 13  
| | |  
| | |  
Db 5 QPKQH 9

RESULT 9  
S70340  
napin large chain 11A - Swedish turnip (fragments)  
C:Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 31-Dec-2004  
C:Accession: S70340  
R:Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.  
Biochim. Biophys. Acta 1295, 34-43, 1996  
A:Title: Purification and sequencing of multiple forms of Brassica napus seed napin larg  
A:Reference number: S70340; MUID:96283791; PMID:8679671  
A:Accession: S70340  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12;13-18 <NEU>  
A:Cross-references: UNIPROT:Q39344; UNIPROT:Q9S9F0; UNIPARC:UPI000017B02E; UNIPARC:UPI00  
C:Superfamily: Alpha amylase inhibitor

Query Match 24.0%; Score 23; DB 2; Length 18;  
Best Local Similarity 36.4%; Pred. No. 1.8e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 4 QKVDQFPOHG 14  
| : : | | |  
| : : | | |  
Db 1 QQIQQQGQQG 11

RESULT 10  
B39841  
dextranucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)  
C:Species: Streptococcus sobrinus  
C:Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: B39841  
R:Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.  
J. Biol. Chem. 266, 8916-8922, 1991  
A:Title: Isolation and sequence of an active-site peptide containing a catalytic aspart  
A:Reference number: A39841; MUID:91224988; PMID:1827439  
A:Accession: B39841  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <MOO>  
A:Cross-references: UNIPROT:Q7M0L7; UNIPARC:UPI000017AC69  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 22.9%; Score 22; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 DQOKVD 7  
| | : | |  
| | : | |  
Db 1 DQVRVD 6

RESULT 11  
A33917  
dihydroxotriase (EC 3.5.2.3) - Chinese hamster (fragment)  
C:Species: Cricetus griseus (Chinese hamster)  
C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 07-Nov-1997  
C:Accession: A33917  
R:Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.;  
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989  
A:Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain an  
A:Reference number: A33917; MUID:89282776; PMID:2543974  
A:Accession: A33917  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-11 <SIM>  
A:Cross-references: UNIPARC:UPI0000176037; GB:M23652  
C:Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Ba  
arabamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phos  
C:Keywords: hydrolase

Query Match 22.9%; Score 22; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DQOKV 6  
| | | | |  
| | | | |  
Db 2 EQQKV 6

RESULT 12  
S29379  
sorbitol dehydrogenase - sheep  
C:Species: Ovis orientalis aries  
C:Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S29379  
R:Reiersen, H.; Sletten, K.; McKinley-McKee, J.S.  
Eur. J. Biochem. 211, 861-869, 1993  
A:Title: Affinity labelling of sorbitol dehydrogenase from sheep liver with alpha-bromo-  
A:Reference number: S29379; MUID:93170323; PMID:8436142  
A:Accession: S29379  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <REI>  
A:Cross-references: UNIPROT:Q9TR15; UNIPARC:UPI0000087DC1  
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 22.9%; Score 22; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 7 DEQFPOHG 14  
| : : | | |  
| : : | | |  
Db 10 DVHWQHG 17

RESULT 13  
A34818  
vicilin 72k chain - pigeon pea (fragment)  
C:Species: Cajanus cajan (pigeon pea)  
C:Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993  
C:Accession: A34818  
R:Maxwell, Y.R.; Maxwell, M.R.; Ranjekar, P.K.  
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990  
A:Title: Unusual denaturation properties of vicilin from Cajanus cajan.  
A:Reference number: A34818; MUID:90165956; PMID:2306256  
A:Accession: A34818  
A:Status: preliminary

A;Molecule type: protein  
A;Residues: 1-7 <MAW>  
A;Cross-references: UNIPARC:UPI000017B040

Query Match 21.9%; Score 21; DB 2; Length 7;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVDQ 9  
| : || :  
Db 1 GARVDQ 7

## RESULT 14

PC7075  
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: PC7075  
R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Matsui, T.; Watanabe, Y.;  
Electrophoresis 21, 1853-1871, 2000  
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t  
A;Reference number: PC7072  
A;Accession: PC7075  
A;Molecule type: protein  
A;Residues: 1-14 <TSU>  
A;Cross-references: UNIPROT:Q7M058; UNIPARC:UPI000017C675  
A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum  
C;Keywords: brain; phosphorus-oxygen lyase

Query Match 21.9%; Score 21; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 3e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KVDEQPPQ 12  
|| : || :  
Db 3 KVGDAPQ 10

## RESULT 15

A30330  
neuropeptide pep - California sea hare  
C;Species: Aplysia californica (California sea hare)  
C;Date: 02-Feb-1990 #sequence\_revision 02-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: A30330  
R;Lloyd, P.E.; Connolly, C.M.  
J. Neurosci. 9, 312-317, 1989  
A;Title: Sequence of pedal peptide: a novel neuropeptide from the central nervous system  
A;Reference number: A30330; PMID:8910403; PMID:2913209  
A;Accession: A30330  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <LLO>  
A;Cross-references: UNIPROT:Q7M3P8; UNIPARC:UPI000017BD9A  
C;Keywords: neuropeptide

Query Match 21.9%; Score 21; DB 2; Length 15;  
Best Local Similarity 30.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 VDEQPPQHL 15  
: | : || :  
Db 2 LDSVYGTTHGM 11

Search completed: December 12, 2005, 21:24:33  
Job time : 11.6667 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 12, 2005, 21:17:48 / Search time 61.6667 Seconds  
(without alignments)  
205.938 Million cell updates/sec

Title: US-10-758-165a-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQFPQHGLVKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 11298

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	31.2	16	Q7RPP5_PLAYO	Q7RPP5 plasmodium
2	29	30.2	13	Q9UPB7_HUMAN	Q9UPB7 homo sapien
3	28	29.2	14	Q9J1U5_MOUSE	Q9J1U5 mus musculi
4	28	29.2	18	Q8QFT3_CHICK	Q8QFT3 gallus gall
5	25	26.0	14	NSR2_SARBU	P81493 sarcophaga
6	25	26.0	15	COX5A_SCYCA	P83012 scylliorhinu
7	25	26.0	18	O12692_9PLVG	O12692 simian-huma
8	24	25.0	15	O5CLX6_SCHJA	O5CLX6 achistosoma
9	24	25.0	15	Q7M3M5_APIME	Q7M3M5 apis mellif
10	24	25.0	15	Q9R563_ECOLI	Q9R563 escherichia
11	24	25.0	18	Q4YL79_PLABE	Q4YL79 plasmodium
12	24	25.0	18	O5FBR5_SUNMU	O5FBR5 suncus murt
13	24	25.0	18	Q7M198_STRFR	Q7M198 streptomyce
14	23	24.0	11	LSK1_LEUMA	P04428 leucophaea
15	23	24.0	11	LSKP_PBRAM	P36885 periplaneta
16	23	24.0	14	P78359_HUMAN	P78359 homo sapien
17	23	24.0	15	CX1B_CONBE	P58624 conus betul
18	23	24.0	16	LPH1_ECO57	Q8X8T5 escherichia
19	23	24.0	18	O13167_XIRGL	O13167 xiphias gla
20	22	22.9	9	Q7M0L7_STRE	Q7M0L7 streptococc
21	22	22.9	10	Q5D4Q4_9RHO	Q5D4Q4 dechloromon
22	22	22.9	11	Q48933_MYCBO	Q48933 mycobacteri
23	22	22.9	11	Q79C20_MYCBO	Q79C20 mycobacteri
24	22	22.9	11	Q79C22_MYCTU	Q79C22 mycobacteri
25	22	22.9	13	Q39380_BRAOL	Q39380 braesica ol
26	22	22.9	15	ODP3_SOLTU	P81420 solanum tub
27	22	22.9	16	Q9TRHO_BOVIN	Q9TRHO bos taurus
28	22	22.9	18	RL24_PROOV	P20032 proteus vul
29	22	22.9	18	Q580F2_9TRYP	Q580F2 trypanosoma
30	22	22.9	18	Q4XFY5_PLACH	Q4XFY5 plasmodium
31	22	22.9	18	Q9TRIS_SHEEP	Q9TRIS ovis aries

32	22	22.9	18	Q8B133_IATX6	Q8B133 influenza a
33	21	21.9	14	GIGS_SPIOL	P55235 spinacia ol
34	21	21.9	14	Q9UNM9_HUMAN	Q9UNM9 homo sapien
35	21	21.9	14	Q7M058_MOUSE	Q7M058 mus musculi
36	21	21.9	14	Q65CH4_9GBMI	Q65CH4 tomato leaf
37	21	21.9	15	Q7M3P8_APLCA	Q7M3P8 aplysia cal
38	21	21.9	15	Q6LC05_PSEAE	Q6LC05 pseudomonas
39	21	21.9	16	Q9UC18_HUMAN	Q9UC18 homo sapien
40	21	21.9	16	Q94F61_WHEAT	Q94F61 triticum ae
41	21	21.9	16	Q44543_ANAVA	Q44543 anabaena va
42	21	21.9	16	Q9R5E9_HAESO	Q9R5E9 haemophilus
43	21	21.9	17	Q9S8U7_SOLTU	Q9S8U7 solanum tub
44	21	21.9	17	Q07270_MYCTU	Q07270 mycobacteri
45	21	21.9	17	Q8X4A4_ECO57	Q8X4A4 escherichia

## ALIGNMENTS

RESULT 1					
ID	Q7RPP5_PLAYO	PRELIMINARY;	PRT;	16 AA.	
AC	Q7RPP5;				
DT	01-MAR-2004 (TREMBLrel. 26, Created)				
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Hypothetical protein.				
GN	Name=PY01411;				
OS	Plasmodium yoelii yoelii.				
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
OX	NCBI_TaxID=73239;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=17XNL;				
RX	MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;				
RA	Carlton J.M., Angluoli S.V., Suh B.B., Kool T.W., Pextea M.,				
RA	Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,				
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,				
RA	Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,				
RA	Cho J.K., Quackenbush J., Sedegah M., Shoah A., Cummings L.M.,				
RA	Florens L., Yates J.R., Ili, Raine J.D., Sinden R.E., Harris M.A.,				
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Valdiva A.B.,				
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,				
RA	Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,				
RA	Carracci D.J.				
RT	"Genome sequence and comparative analysis of the model rodent malaria				
RT	parasite Plasmodium yoelii yoelii."				
RL	Nature 419:512-519(2002).				
CC	-!- CAUTION: The sequence shown here is derived from an				
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is				
CC	preliminary data				
DR	EMBL; AB01000372; EAA20742.1; -; Genomic.DNA.				
KW	Hypothetical protein.				
SQ	SEQUENCE 16 AA; 1778 MW; 22142D73EC2BE109 CRC64;				
Query Match					
	Best Local Similarity	31.2%	Score 30;	DB 2;	length 16;
	Matches	5;	Conservative	2;	Mismatches 1;
					Indels 0;
					Gaps 0;
QY	1 IDGQKVD 8				
DB	4 INGSKIDE 11				
RESULT 2					
ID	Q9UPB7_HUMAN	PRELIMINARY;	PRT;	13 AA.	
AC	Q9UPB7;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)				
DE	Inosine monophosphatase 2 (Fragment).				
GN	Name=IMP2;				

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9746349; PubMed=9322233; DOI=10.1038/sj.mp.4000325;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA DeGera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP-19p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., DeGera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF025882; AAD22136.1; -; Genomic DNA.
FT NON_TER 1
FT SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;
SQ
Query Match 30.2%; Score 29; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 8 DEOPFHGLVQK 18
Db 1 ERFPSHRFIAE 11

RESULT 3
Q9JUT5_MOUSE PRELIMINARY; PRT; 14 AA.
ID Q9JUT5_MOUSE PRELIMINARY;
AC Q9JUT5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 15, Last annotation update)
DE B-Raf protein (Fragment).
GN Name=B-raf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Barnier J.V., Papin C., Eychene A., Lecocq O.;
RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-
RT specific expression.";
RL J. Biochem. 270:23381-23389(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Barnier J.V.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276308; CAB81556.1; -; mRNA.
FT NON_TER 1
FT SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;
SQ
Query Match 29.2%; Score 28; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 DEOPFHGLVQK 18
Db 1 DEKPEVELDQD 12

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```

RESULT 4
Q8QFT3_CHICK PRELIMINARY; PRT; 18 AA.
ID Q8QFT3_CHICK PRELIMINARY;
AC Q8QFT3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sterol regulatory element binding protein 1 (Fragment).
GN Name=SRBP-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Asaef S., Pitel F., Morrison M., Alizadeh M., Gondret F., Diot C.,
RA Leclercq B., Vignal A., Douaire M., Lagarrigue S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ441122; CAD29619.1; -; Genomic DNA.
FT NON_TER 1
FT SEQUENCE 18 AA; 1947 MW; 3206A67750BFD7EA CRC64;
SQ
Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 DEOPFHGLVQK 18
Db 1 DSPLCNHGKVKQ 12

RESULT 5
NSK2_SARBU STANDARD; PRT; 14 AA.
ID NSK2_SARBU STANDARD;
AC P41493;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Neosulfakinin-2 (Neosulfakinin-II) (Neb-SK-II).
OS Sarcophaga bullata (Grey Flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga; Neobellieria.
OX NCBI_TaxID=7385;
RN [1]
RP PROTEIN SEQUENCE.
RA TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata.";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
RN [2]
RP SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR: A56632; A56632.
CC InterPro: IPR001651; Gastrin.
CC PROSITE: PS00259; GASTRIN; 1.
CC Amidaation: Direct protein sequencing: Neuropeptide; Sulfation.
FT MOD_RES 9
FT MOD_RES 14 9 Sulfotyrosine (Potential).
FT MOD_RES 14 14 Phenylalanine amide (Potential).
FT SEQUENCE 14 AA; 1796 MW; 8B4B06D5B61C62AA CRC64;
SQ

```

Query Match 26.0%; Score 25; DB 1; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 6.5e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 DEQFQHG 14  
 :|||:  
 :|||:  
 Db 3 EQQFDDYG 10

## RESULT 6

COX5A\_SCYCA STANDARD; PRT; 15 AA.  
 ID COX5A\_SCYCA  
 AC P83012;

DT 10-MAY-2005 (Rel. 47, Created)  
 DT 10-MAY-2005 (Rel. 47, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1) (Fragment).  
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 NCBI\_TaxId=7830;  
 RN NCBI [1]  
 RP PROTEIN SEQUENCE.

RC TISSUE=Rectal gland;  
 RX MEDLINE=21534268; PubMed=11676495; DOI=10.1006/dbrc.2001.5826;  
 RA Schurnans Stekhoven F.M.A.H., Fluk G., Wendelaar Bonga S.E.;  
 RT "N-terminal sequences of small ion channels in rectal glands of  
 sharks: a biochemical hallmark for classification and phylogeny?";  
 RL Biochem. Biophys. Res. Commun. 288:670-675(2001).  
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c  
 oxidase, the terminal oxidase in mitochondrial electron transport.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC GO: 0005739; Cytochromedion; IDA.

DR InterPro; IPR003204; Cyt\_c\_ox5a.

DR Pfam; PF02284; COX5A; 1.

KW Direct protein sequencing; Heme; Inner membrane; Iron; Membrane;  
 KW Metal-binding; Mitochondrion; Oxidoreductase.

FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1720 MW; 937518D7590B35C5 CRC64;

Query Match 26.0%; Score 25; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 7e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 QKVDEQF 10  
 :|||:  
 :|||:  
 Db 5 QETDEEF 11

## RESULT 7

O12692\_9PLVG PRELIMINARY; PRT; 18 AA.  
 ID O12692\_9PLVG  
 AC O12692;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Gag polypeptide (Fragment).

OS Name=gag;

OS Simian-human immunodeficiency virus.

OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
 OC Lentivirus; Primate lentivirus group.

OX NCBI\_TaxId=57667;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SHIVkul;

RX MEDLINE=97312452; PubMed=9168893; DOI=10.1006/viro.1997.8534;

RA Stephens E.B., Mukherjee S., Sahn M., Zhuge W., Raghavan R.,

RA Singh D.K., Leung K.K., Atkinson R.B., Li Z., Joag S.V., Liu Z.O.,

RA Narayan O.;

RT "A cell-free stock of simian-human immunodeficiency virus that causes

RT AIDS in pig-tailed macaques has a limited number of amino acid

RT substitutions in both SIVmac and HIV-1 regions of the genome and has

RT offered cytotropism.";

RT Virology 231:313-321(1997).

RL EMBL; U89249; AAC57878.1; -; Genomic DNA.

DR GO: 0019013; C:Viral nucleocapsid; IEA.

DR GO: 0005198; F:Structural molecule activity; IEA.

DR InterPro; IPR00071; Imm\_lentv\_matrix.

DR Pfam; PF00540; Gag\_p17; 1.

KW AIDS; Core protein; Polyprotein.

FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 1961 MW; E0647725D22E262B CRC64;

Query Match 26.0%; Score 25; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 8.5e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDGQKVD 8  
 :|||:  
 :|||:  
 Db 8 LSGKQAD 15

## RESULT 8

O5C1X6\_SCHJA PRELIMINARY; PRT; 15 AA.  
 ID O5C1X6\_SCHJA  
 AC O5C1X6;

DT 10-MAY-2005 (TREMBLrel. 30, Created)

DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)

DE Hypothetical protein.

OS Schistosoma japonicum (Blood fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;

OC Schistosomatoidea; Schistosomatidae; Schistosoma.

OX NCBI\_TaxId=6182;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Han Z.;

RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY810460; AAX26349.1; -; mRNA.

KW Hypothetical protein.

SQ SEQUENCE 15 AA; 1910 MW; F849301B576FB1D8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1e+04;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 QPFGHGVKQ 18  
 :|||:  
 :|||:  
 Db 6 QPHKKSIVKQ 15

## RESULT 9

Q7M3M5\_APIME PRELIMINARY; PRT; 15 AA.  
 ID Q7M3M5\_APIME  
 AC Q7M3M5;

DT 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Alpha-glucosidase (EC 3.2.1.20) (Fragment).

OS Apis mellifera (Honeybee).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

OC Apidae; Apis.

OX NCBI\_TaxId=7460;

```

RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=97399878; PubMed=9255970;
RA Kimura A., Taketa M., Fukushi Y., Mori H., Matsui H., Chiba S.;
RT "A catalytic amino acid and primary structure of active site in
RL Aspergillus niger alpha-glucosidase.";
DR Biosci. Biotechnol. Biochem. 61:1091-1098(1997).
PT PIR; PT0090; PT0090.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1686 MW; 85730BA8387CB741 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDGOKVD 7
DB 2 IDGFRID 8

RESULT 10
Q9RS63_ECOLI PRELIMINARY; PRT; 15 AA.
AC Q9RS63;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE 40 kDa porin homolog (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93328296; PubMed=8392972;
RA D'Arcy M., Soti R., Cockrell F.I.II., De Azavedo J., Louie M.,
RA Brunton J., Sherman P.;
RT "Multiple determinants of verotoxin-producing Escherichia coli O157:H7
RT attachment-effacement";
RL Infect. Immun. 61:3382-3391(1993).
SQ SEQUENCE 15 AA; 1699 MW; 2767AC9298F8754D CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGOKVD 7
DB 7 DGNKLD 12

RESULT 11
Q4YL79_PLABE PRELIMINARY; PRT; 18 AA.
AC Q4YL79;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
OR Names=PB400723.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berthian M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;

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RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAA101003787; CAA101022.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2206 MW; EBBABA563A3085A7 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 30.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 9 QPQHGVLVKQ 18
DB 1 KFPKYSMMHQ 10

RESULT 12
Q5FBR5_SUNMU PRELIMINARY; PRT; 18 AA.
AC Q5FBR5;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Thioedoxin (Fragment).
GN Name:TXN;
OS Suncus murinus (House shrew) (Musk shrew).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Soricidae;
OC Crociuidinae; Suncus.
OX NCBI_TaxID=9378;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TKU, WZ, and BAN; TISSUE=Kidney;
RX PubMed=15897627; DOI=10.1538/expan.54.173;
RA Adjei S., Sato A., Tanaka S., Kobayashi E., Tanaka K., Namikawa T.,
RA Ishikawa A.;
RT "Development and characterization of CATS markers for genetic linkage
RT mapping in the house musk shrew, Suncus murinus.";
RL Exp. Anim. 54:173-180(2005).
DR EMBL; AB167758; BAD89500.1; -; Genomic_DNA.
DR EMBL; AB167757; BAD89499.1; -; Genomic_DNA.
DR EMBL; AB167756; BAD93380.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2020 MW; D0B5FC66463A90F8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.3e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVIDE 8
DB 8 GQKVIDE 13

RESULT 13
Q7M198_STRFR PRELIMINARY; PRT; 18 AA.
AC Q7M198;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1906;
RN [1]
RP PROTEIN SEQUENCE.

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RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;
RA Saha U., Molt S.A., Lad P.J.;
RT "Two new extracellular serine proteases from streptomyces fradiae.";
RL Int. J. Biochem. 23:979-984(1991).
DR PIR; A61577; A61577.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 16 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 27.3%; Pred. No. 1.3e+04;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGKVFDEQFP 11
   :|:|:|
DB 2 VGGTRAAQDFP 12

RESULT 14
LSK1 LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05; Created)
DT 13-AUG-1987 (Rel. 05; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
DE Leucosulfakinin-1 (Leucosulfakinin-1) (LSK-1).
OS Leucophaea maderae (Maddira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatterioidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -1- FUNCTION: Changes the frequency and amplitude of contractions of
CC the hindgut. Inhibits muscle contraction of hindgut.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6
FT MOD_RES 11 Sulfotyrosine.
FT MOD_RES 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPQHG 14
   |||:|
DB 1 EQFEDYG 7

RESULT 15
LSKP PERAM STANDARD; PRT; 11 AA.
AC P3685;
DT 01-JUN-1994 (Rel. 29; Created)
DT 01-JUN-1994 (Rel. 29; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Perisulfakinin (Pea-SK-I).

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OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatterioidea;
OC Blattidae; Blattellae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinin.";
RL Neuropeptides 14:145-149(1989).
CC -1- FUNCTION: Stimulates hindgut contractions.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6
FT MOD_RES 11 Sulfotyrosine.
FT MOD_RES 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPQHG 14
   |||:|
DB 1 EQFEDYG 7

```

Search completed: December 12, 2005, 21:23:56  
Job time : 63.667 secs

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GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 97.6034 Seconds  
(without alignments)  
81.030 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQEPQHGLVKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1:	geneeqp1980s:*
2:	geneeqp1990s:*
3:	geneeqp2000s:*
4:	geneeqp2001s:*
5:	geneeqp2002s:*
6:	geneeqp2003as:*
7:	geneeqp2003bs:*
8:	geneeqp2004s:*
9:	geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	ADRI0611	Horse IGB
2	96	100.0	424	AAAM50103	AAAM50103 Equine Ig
3	96	100.0	424	AAAM50104	AAAM50104 Equine Ig
4	78	81.2	15	ADC64569	ADC64569 Horse Imm
5	63	65.6	569	ABP96585	ABP96585 Horse IGB
6	49	51.0	616	ADC00951	ADC00951 Enterohae
7	45	46.9	504	ABU27912	ABU27912 Protein e
8	45	46.9	685	ABR64268	ABR64268 Drosophil
9	45	46.9	1512	ADA33876	ADA33876 Actinecto
10	45	46.9	1536	ABR53009	ABR53009 Protein s
11	45	46.9	1536	ADK61916	ADK61916 Disease t
12	44	45.8	128	ABG05706	ABG05706 Novel hum
13	44	45.8	159	ABG05705	ABG05705 Novel hum
14	44	45.8	369	AAU65086	AAU65086 Proptonib
15	44	45.8	369	ABM61605	ABM61605 Proptonib
16	44	45.8	385	ABM65825	ABM65825 Proptonib
17	44	45.8	421	ABBS3051	ABBS3051 Escherich
18	44	45.8	616	ABM70417	ABM70417 Photocorb
19	44	45.8	686	ADL99373	ADL99373 Nanosturc
20	43	44.8	103	AAU58156	AAU58156 Proptonib
21	43	44.8	103	ABM54675	ABM54675 Proptonib
22	43	44.8	146	ADX77153	ADX77153 Plant ful
23	43	44.8	152	ADX72974	ADX72974 Plant ful
24	43	44.8	316	ADY26835	ADY26835 S. pulv

25	43	44.8	321	3	AAG35242	Aag35242 Zea maye
26	43	44.8	325	8	ADX66768	Adx66768 Plant ful
27	43	44.8	334	3	AAG33393	Aag33393 Zea maye
28	43	44.8	346	8	ADX69083	Adx69083 Plant ful
29	43	44.8	356	9	ADY26853	Ady26853 S. pulv
30	43	44.8	361	3	AAG44780	Aag44780 Zea maye
31	43	44.8	362	3	AAG33392	Aag33392 Zea maye
32	43	44.8	366	8	ADX66926	Adx66926 Plant ful
33	43	44.8	371	8	ADY79458	Ady79458 Plant ful
34	43	44.8	373	3	AAG35241	Aag35241 Zea maye
35	43	44.8	374	3	AAG44779	Aag44779 Zea maye
36	43	44.8	375	3	AAG33391	Aag33391 Zea maye
37	43	44.8	403	8	ADX71093	Adx71093 Plant ful
38	43	44.8	403	8	ADX94569	Adx94569 Plant ful
39	43	44.8	409	8	ADX77253	Adx77253 Plant ful
40	43	44.8	434	8	ADY11529	Ady11529 Plant ful
41	43	44.8	446	3	AAG44778	Aag44778 Zea maye
42	43	44.8	446	3	AAG35240	Aag35240 Zea maye
43	43	44.8	612	7	ABO76981	AbO76981 Pseudomon
44	43	44.8	654	5	ABBS4057	ABBS4057 Laccococc
45	43	44.8	1427	9	ABR39681	ABR39681 L. pneumo

## ALIGNMENTS

XX	RESULT 1
ADRI0611	
ID	ADRI0611 standard; peptide; 18 AA.
XX	
AC	ADRI0611;
XX	
DT	21-OCT-2004 (first entry)
DE	Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX	
KW	Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW	anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW	horse.
XX	
OS	Equus caballus.
XX	
PN	WO2004065936-A2.
XX	
PD	05-AUG-2004.
XX	
PF	15-JAN-2004; 2004WO-US003566.
XX	
PR	16-JAN-2003; 2003US-0440472P.
XX	
PA	(UNNC-) UNIV NORTH CAROLINA STATE.
XX	
PI	Hammerberg B;
XX	
DR	WPI: 2004-593545/57.
XX	
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful
PT	for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT	or treating asthma or anaphylactic shock.
XX	
PS	
XX	Example 6; Page 9; 14pp; English.
XX	
CC	The present invention relates to a novel monoclonal antibody (I) that
CC	specifically binds to a mammalian IGE epitope, where the epitope is
CC	between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The
CC	allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC	and corn allergens. The sample is a biological sample collected from a
CC	dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC	treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC	antibodies recognise epitopes on canine IGE corresponding to amino acid
CC	residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC	canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC horse IGE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 100.0%; Score 96; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IDGKVDQFPQHGVLVKQ 18  
 |||||  
 Db 1 IDGKVDQFPQHGVLVKQ 18

# RESULT 2

AAM50103 standard; protein; 424 AA.

XX AAM50103;

XX 02-SEP-2002 (first entry)

XX Equine IGE heavy chain constant region C-epsilon allotype A.

XX Cea; equine; horse; heavy chain; constant region; allotype a; IGE;  
 XX C-epsilon a; immunoglobulin E; antiallergic; allergy.

XX Equus caballus.

XX Key Location/Qualifiers  
 FT 1..97  
 FT Domain /note= "CH1 domain"  
 FT 98..205  
 FT Domain /note= "CH2 domain"  
 FT 206..312  
 FT Domain /note= "CH3 domain"  
 FT 313..424  
 FT Domain /note= "CH4 domain"

XX WO200250280-A2.

XX 27-JUN-2002.

XX 20-DEC-2001; 2001WO-DE004810.

XX 21-DEC-2000; 2000DE-01064415.

XX (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

XX Leibold W, Wagner B, Radbruch A;

XX WPI; 2002-508803/54.

XX N-PSDB; ABL61246.

XX DNA sequence encoding part of an equine immunoglobulin G, useful for  
 PT preparing isotype-specific antibodies for diagnosis and treatment of  
 PT allergy in horses.

XX Claim 1; Page 31-32; 37pp; German.

XX This invention describes a novel DNA (I) encoding the constant region  
 CC (CH) of the heavy chain of a horse immunoglobulin E (IGE) allotype. The  
 CC products of the invention are capable of neutralising IGE activity and  
 CC have antiallergic activity. The polynucleotides of the invention are used  
 CC to produce recombinant IGE (II), and this is used to raise specific  
 CC monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,  
 CC particularly of allergy in horses, and Mab can also be used for treatment  
 CC of allergies. (I) make possible production of isotype-specific  
 CC antibodies, important for precise evaluation of the immune response. This  
 CC sequence represents a fragment of the equine IGE heavy chain constant

CC region C-epsilon allotype a (Cea), used in the method of the invention  
 CC for IGE-isotype recombinant immunoglobulin production

XX Sequence 424 AA;

Query Match 100.0%; Score 96; DB 5; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IDGKVDQFPQHGVLVKQ 18  
 |||||  
 Db 145 IDGKVDQFPQHGVLVKQ 162

# RESULT 3

AAM50104 standard; protein; 424 AA.

XX AAM50104;

XX 02-SEP-2002 (first entry)

XX Equine IGE heavy chain constant region C-epsilon allotype b.

XX Ceb; equine; horse; heavy chain; constant region; allotype b; IGE;  
 XX C-epsilon b; immunoglobulin E; antiallergic; allergy.

XX Equus caballus.

XX Key Location/Qualifiers  
 FT 1..97  
 FT Domain /note= "CH1 domain"  
 FT 98..205  
 FT Domain /note= "CH2 domain"  
 FT 206..312  
 FT Domain /note= "CH3 domain"  
 FT 313..424  
 FT Domain /note= "CH4 domain"

XX WO200250280-A2.

XX 27-JUN-2002.

XX 20-DEC-2001; 2001WO-DE004810.

XX 21-DEC-2000; 2000DE-01064415.

XX (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

XX Leibold W, Wagner B, Radbruch A;

XX WPI; 2002-508803/54.

XX N-PSDB; ABL61247.

XX DNA sequence encoding part of an equine immunoglobulin G, useful for  
 PT preparing isotype-specific antibodies for diagnosis and treatment of  
 PT allergy in horses.

XX Claim 1; Page 34-36; 37pp; German.

XX This invention describes a novel DNA (I) encoding the constant region  
 CC (CH) of the heavy chain of a horse immunoglobulin E (IGE) allotype. The  
 CC products of the invention are capable of neutralising IGE activity and  
 CC have antiallergic activity. The polynucleotides of the invention are used  
 CC to produce recombinant IGE (II), and this is used to raise specific  
 CC monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,  
 CC particularly of allergy in horses, and Mab can also be used for treatment  
 CC of allergies. (I) make possible production of isotype-specific  
 CC antibodies, important for precise evaluation of the immune response. This  
 CC sequence represents a fragment of the equine IGE heavy chain constant  
 CC region C-epsilon allotype b (Ceb), used in the method of the invention  
 CC for IGE-isotype recombinant immunoglobulin production

SQ Sequence 424 AA;

Query Match 100.0%; Score 96; DB 5; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGVLVKQ 18  
 |||||  
 DB 145 IDGQKVDQFPQHGVLVKQ 162

RESULT 4

ADCC4569

ID ADC64569 standard; peptide; 15 AA.

AC ADC64569;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IgE, heavy chain immunogenic peptide P5.

KW Horse; immunoglobulin E, IgE; heavy chain; immunogen; allergy.

OS Equus caballus.

FN US2003087314-A1.

PD 08-MAY-2003.

PF 08-NOV-2001; 2001US-00052788.

PR 08-NOV-2001; 2001US-00052788.

PA (REGC ) UNIV CALIFORNIA.

PI Gerstwin LJ, Pettigrew HD, Kalina WV;

DR WPI; 2003-765437/72.

PT Immunogenic composition comprising an isolated equine immunoglobulin E  
 peptide that induces production of antibodies which specifically bind  
 to equine immunoglobulin E.

PS Example 1; Page 8; 14pp; English.

CC The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (SI-S6), 15 amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (SI)-(S6), an antibody that  
 CC specifically binds to equine IgE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (SI)-(S6), making an  
 CC antibody that specifically binds to equine IgE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-  
 CC (S6)), and collecting antiserum from the animal) and a kit for detection  
 CC of equine IgE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IgE. The  
 CC antibody is useful for detecting equine IgE protein in a biological  
 CC sample (serum) which involves contacting the sample with the antibody,  
 CC thus forming an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the  
 CC complex can be detected. The complex is detected using a second labelled  
 CC antibody. The peptides are useful for generating antibodies specific for  
 CC IgE which can serve as a diagnostic test for allergy. The present  
 CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic  
 CC peptide from the middle portion of the C2 region.

Sequence 15 AA;

Query Match 81.2%; Score 78; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 14  
 |||||  
 DB 2 IDGQKVDQFPQHG 15

RESULT 5

ABP96585

ID ABP96585 standard; protein; 569 AA.

AC ABP96585;

DT 28-MAY-2003 (first entry)

DE Horse IgE heavy chain amino acid sequence SEQ ID NO:30.

KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;

KW immune response; major histocompatibility complex; MHC; immunogenic;

KW antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;

KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;

KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;

KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;

KW urticaria hives.

OS Equus caballus.

FN WO2003015716-A2.

PD 27-FEB-2003.

PF 08-AUG-2002; 2002WO-US026986.

PR 13-AUG-2001; 2001US-0312120P.

PA (IGET-) IGE THERAPEUTICS INC.

PI Chen SA, Yang Y, Barankiewicz T, Chen Z;

DR WPI; 2003-268242/26.

PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IgE, by identifying peptide eliciting CTL response to IgE  
 PT peptides naturally presented by major histocompatibility complex class I  
 PT protein.

PS Example 7; Page 157-160; 187pp; English.

CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IgE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IgE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IgE peptides. C1-3 have antiallergic, antiaesthetic, immunosuppressive,  
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IgE, and in  
 CC vaccine. C1-3 can be used for modulating an IgE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as  
 CC hypersensitivity condition, IgE-mediated condition, IgE-mediated non-atopic  
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria

CC hives). The present sequence represents an IgE heavy chain amino acid  
CC sequence, which is given in an example from the present invention  
XX  
SQ Sequence 569 AA;

Query Match 65.6%; Score 63; DB 6; Length 569;  
Best Local Similarity 66.7%; Pred. No. 0.31;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQGLVQ 18  
Db 291 IEGQKVDQFPQGLVQ 308

RESULT 6  
ADCC0951  
ID ADC0951 standard; protein; 616 AA.

XX  
AC ADC0951;

XX  
DT 04-DEC-2003 (first entry)

XX  
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 996.

XX  
KM enterohaemorrhagic; anti-bacterial.

XX  
OS Escherichia coli; O157:H7.

XX  
PN JF2002355074-A.

XX  
PD 10-DEC-2002.

XX  
PF 24-JAN-2002; 2002JP-00015959.

XX  
PR 24-JAN-2001; 2001JP-00112010.

XX  
PA (UYTS-) UNIV TSUKUBA.

XX  
DR WPI; 2003-451640/43.

XX  
PT Enterohaemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule  
PT and a polypeptide and its use, a polypeptide, a vector and a host cell.

XX  
PS Claim 3; SEQ ID NO 996; 2067bp; Japanese.

XX The invention relates to a novel enterohaemorrhagic Escherichia coli  
CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention  
CC has anti-bacterial activity. The polypeptide can be used in detection  
CC and/or treatment of O157:H7 infection. The nucleotide sequence of the  
CC genome of Enterohaemorrhagic E. coli O157:H7 was determined. The present  
CC sequence represents an E. coli O157:H7-specific polypeptide of the  
CC invention.

XX  
SQ Sequence 616 AA;

Query Match 51.0%; Score 49; DB 7; Length 616;  
Best Local Similarity 50.0%; Pred. No. 58;  
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDQFPQ-HGVK 17  
Db 58 QKIDPEPPLTHGLIK 73

RESULT 7

ABU27912  
ID ABU27912 standard; protein; 504 AA.

XX  
AC ABU27912;

XX  
DT 19-JUN-2003 (first entry)

XX  
DE Protein encoded by prokaryotic essential gene #13439.

XX  
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Enterobacter cloacae.

XX  
PN WC000277183-A2.

XX  
PD 03-OCT-2002.

XX  
PF 21-MAR-2002; 2002MO-US009107.

XX  
PR 21-MAR-2001; 2001US-00815242.

XX  
PR 06-SEP-2001; 2001US-00948893.

XX  
PR 25-OCT-2001; 2001US-0342923P.

XX  
PR 08-FEB-2002; 2002US-00072851.

XX  
PR 06-MAR-2002; 2002US-0362699P.

XX  
PA (ELIT-) ELITRA PHARM INC.

XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RN, Xu HR;

XX  
DR WPI; 2003-029926/02.

XX  
DR N-PSDB; ACA31782.

XX  
PS Claim 25; SEQ ID NO 55836; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 504 AA;

Query Match 46.9%; Score 45; DB 6; Length 504;  
Best Local Similarity 53.3%; Pred. No. 2e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQGL 15  
Db 315 IDGERVDIQKPAHAI 329

```

RESULT 8
AB64268 standard; protein; 685 AA.
ID ABB64268
XX
AC ABB64268;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 19596.
XX
KM Drosophila developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX
OS WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX WPI; 2001-656660/75.
XX DR N-PSDB; ABL08371.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 19596; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 685 AA;

```

Query Match 46.9%; Score 45; DB 4; Length 685;  
 Best Local Similarity 53.3%; Pred. No. 2.9e+02;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Qy 3 GQKVDQFPQHGVLVK 17
   |||:|||||
Db 577 GQVGSNSTPFGVLVK 591

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RESULT 9
ADA33876
ID ADA33876 standard; protein; 1512 AA.
XX
AC ADA33876;
XX
DT 20-NOV-2003 (first entry)
XX
DE Acinetobacter baumannii protein #1037.
XX
KM Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
XX plant biocontrol agent.
XX

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OS Acinetobacter baumannii.
XX
XX US6562958-B1.
XX
PD 13-MAY-2003.
XX
PF 04-JUN-1999; 99US-00328352.
XX
PR 09-JUN-1998; 98US-0088701P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton G, Bush D;
XX
DR WPI; 2003-576092/54.
XX DR N-PSDB; ADA29750.
XX
PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 5163; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents the amino acid sequence of an A.
CC baumannii protein.
XX
SQ Sequence 1512 AA;

```

Query Match 46.9%; Score 45; DB 6; Length 1512;  
 Best Local Similarity 50.0%; Pred. No. 6.9e+02;  
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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Qy 3 GQKVDQFPQHGVLVK 18
   |||:|||||
Db 328 GDRTPDPLMPSHGVLVK 343

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RESULT 10
ABR53009
ID ABR53009 standard; protein; 1536 AA.
XX
AC ABR53009;
XX
DT 20-JUN-2003 (first entry)
XX
DE Protein sequence #SEQ ID 883.
XX
KM Multiprotein complex; eukaryote; drug target; diagnosis.
XX OS Saccharomycetes cerevisiae.
XX
XX EP1258494-A1.
XX
XX PN
XX PD 20-NOV-2002.
XX
XX PF 20-DEC-2001; 2001EP-00130253.
XX
XX PR 15-MAY-2001; 2001EP-00111774.
XX
XX PA (CELL-) CELLZOME AG.
XX
XX PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
XX Marzoch M, Schultz JD, Superti-Furga GD;
XX WPI; 2003-250078/25.
XX

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DR N-PSDB; ACC61051.  
XX  
XX New isolated protein complexes useful for diagnosing a disease or  
PT disorder, or as a target for an active agent of a pharmaceutical,  
PT preferably a drug target in the treatment or prevention of disease or  
PT disorder.  
XX  
XX Disclosure; SEQ ID NO 883; 177p + Sequence Listing; English.  
XX  
CC The invention relates to multiprotein complexes from eukaryotes. Proteins  
CC of the invention and DNA sequences encoding them are given in records  
CC AB52568-ABR33903 and ACC6610-ACC61944 respectively. The complexes are  
CC obtainable by using a protein as a bait and isolating the set of proteins  
CC which is attached thereto from cells. Such protein complexes may comprise  
CC up to 30 distinct proteins. Protein complexes of the invention are useful  
CC for diagnosing a disease or disorder, or as a target for an active agent  
CC of a pharmaceutical, preferably a drug target in the treatment or  
CC prevention of a disease or disorder. Note: The sequence data for this  
CC patent is not represented in the printed specification, but is based on  
CC sequence information supplied by the European Patent Office. The complete  
CC document is available on CD-ROM  
XX  
SQ Sequence 1536 AA;  
  
Query Match 46.9%; Score 45; DB 6; Length 1536;  
Best Local Similarity 53.3%; Pred. No. 7e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 IDGQKVDGPPQHL 15  
Db 1370 IDGTEVDGPPSPGI 1384  
  
RESULT 11  
ADK61916  
ID ADK61916 standard; protein; 1536 AA.  
XX  
AC ADK61916;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Disease treating protein complex-derived protein #84.  
XX  
KW protein complex; drug target; diagnosis.  
XX  
OS Unidentified.  
XX  
PN EPI338608-A2.  
XX  
PD 27-AUG-2003.  
XX  
PF 20-DEC-2002; 2002EP-00102902.  
XX  
PR 20-DEC-2001; 2001EP-00130253.  
XX  
PA (CELL-) CELLZOME AG.  
XX  
PI Bauer A, Gavin A, Superfi-Furga G, Kuester B, Schultz J;  
PI Merzloich M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
PI Michon A, Leutwein C, Rick J;  
XX  
XX WPI; 2003-638460/61.  
DR N-PSDB; ADK61917.  
XX  
XX  
XX New proteins and protein complexes from eukaryotes, useful as targets in  
PT drug screening, or in diagnosing or screening for the presence of a  
PT disease or disorder, or a predisposition for developing a disease or  
PT disorder in a subject.  
XX  
XX Disclosure; SEQ ID NO 167; 13pp; English.  
XX  
CC The invention relates to novel protein complexes comprising a first and a  
CC second protein, or its derivative, fragment, homologue or variant. The

CC proteins are selected from given protein complexes, which are not defined  
CC in the specification. The variants are encoded by nucleic acids that  
CC hybridize to the nucleic acids encoding the proteins under low stringency  
CC conditions. The protein complexes are useful as targets for an active  
CC agent of a pharmaceutical. These protein complexes are particularly  
CC useful as drugs targets for the treatment or preventing of a disease or  
CC disorder. The complexes and methods above are useful in diagnosing or  
CC screening for the presence of a disease or disorder or a predisposition  
CC for developing a disease or disorder in a subject. These are also useful  
CC in screening for a drug for treatment or prevention of a disease or  
CC disorder. The molecule that modulates the amount, activity or protein  
CC components of the complex is useful for the manufacture of a medicament  
CC for the treatment or prevention of a disease or disorder. This sequence  
CC corresponds to a protein of the invention. (Note: the sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained from the EPO in electronic format).  
XX  
SQ Sequence 1536 AA;  
  
Query Match 46.9%; Score 45; DB 7; Length 1536;  
Best Local Similarity 53.3%; Pred. No. 7e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 IDGQKVDGPPQHL 15  
Db 1370 IDGTEVDGPPSPGI 1384  
  
RESULT 12  
ABG05706  
ID ABG05706 standard; protein; 128 AA.  
XX  
AC ABG05706;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #5697.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS69893.  
XX  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
XX Claim 20; SEQ ID NO 36065; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is



CC presence or absence of *P. acnes* in a patient comprises contacting a  
 CC sample with a binding agent that binds to the proteins of the invention  
 CC and determining the amount of bound protein in the sample. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for *P. acnes* proteins. These antibodies can be used to  
 CC downregulate expression and activity of *P. acnes* polypeptides and  
 CC therefore treat *P. acnes* infections. The antibodies may also be used as  
 CC diagnostic agents for determining *P. acnes* presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 369 AA;

QY 3 GQKVDGQFPOH 13  
 Db 267 GRDIDDQFPRH 277  
 Query Match 45.8%; Score 44; DB 4; Length 369;  
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 15  
 ABM61605  
 XX ID ABM61605 standard; protein; 369 AA.  
 XX AC ABM61605;  
 XX DT 20-OCT-2003 (first entry)  
 XX DE Propionibacterium acnes transporter-related polypeptide #26281.  
 XX KM Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
 XX KW immunostimulant; immune response; vaccine.  
 XX OS Propionibacterium acnes.  
 XX PN WO2003033515-A1.  
 XX PD 24-APR-2003.  
 XX PF 11-OCT-2002; 2002WO-US032727.  
 XX PR 15-OCT-2001; 2001US-00978825.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;  
 XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
 XX PI Barth B, Vallieve-Douglas J;  
 XX WPI; 2003-381789/36.  
 XX N-PDB; ACF64587.

XX New Propionibacterium acnes polypeptides and polynucleotides encoding the  
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
 PT or for stimulating an immune response specific for a *P. acnes* protein.  
 XX Claim 3k; SEQ ID NO 26281; 1481bp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
 CC encoding a Propionibacterium acnes protein. The invention also relates to  
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
 CC immunogenic fragments of *P. acnes* polypeptides. The invention  
 CC additionally encompasses expression vectors and host cells comprising a  
 CC polynucleotide of the invention; antibodies against polypeptides of the  
 CC invention; fusion proteins comprising a polypeptide of the invention; a  
 CC method for stimulating an immune response specific for a *P. acnes*  
 CC polypeptide and an isolated T cell population comprising T cells prepared  
 CC via this method; a vaccine composition (comprising *P. acnes* polypeptides,  
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or

CC antigen-presenting cells that express the polypeptide); a method and kit  
 CC for detecting or determining the presence or absence of *P. acnes* in a  
 CC patient; and a method for inhibiting the development of *P. acnes* in a  
 CC patient. The *P. acnes* polypeptides, polynucleotides, antibodies, fusion  
 CC proteins, T cell populations or antigen-presenting cells that express the  
 CC polypeptides are useful for diagnosing, preventing or treating acne  
 CC vulgaris, or for stimulating an immune response specific for a *P. acnes*  
 CC protein. The polynucleotides can also be used as probes or primers for  
 CC nucleic acid hybridisation. The vaccine composition is useful for the  
 CC stimulation of an immune response against *P. acnes*, or for treating acne,  
 CC and the kit is useful for performing a diagnostic assay. The present  
 CC sequence represents a specifically claimed polypeptide which is predicted  
 CC to be encoded by an ORF (open reading frame) contained within the *P.*  
 CC acnes polynucleotides of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 369 AA;

QY 3 GQKVDGQFPOH 13  
 Db 267 GRDIDDQFPRH 277  
 Query Match 45.8%; Score 44; DB 6; Length 369;  
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Search completed: December 12, 2005, 20:30:32  
 Job time : 99.6034 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 24.5172 Seconds  
(without alignments)  
60.699 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQFPQHGVLKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/7\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/8\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/9\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	47.9	195	2	US-09-248-796A-19566
2	45	46.9	1512	2	US-09-328-352-5163
3	45	46.9	1536	2	US-09-487-558B-322
4	43	44.8	612	2	US-09-252-991A-25727
5	42	43.8	137	2	US-08-961-083-40
6	42	43.8	137	2	US-09-536-784-40
7	42	43.8	137	2	US-09-765-271-40
8	42	43.8	137	2	US-09-765-272A-40
9	42	43.8	185	2	US-09-583-110-5222
10	42	43.8	194	2	US-09-107-433-5104
11	42	43.8	229	2	US-09-134-000C-6247
12	42	43.8	359	1	US-08-307-382-2
13	42	43.8	359	1	US-08-366-779-2
14	42	43.8	359	1	US-08-478-727-2
15	42	43.8	359	1	US-08-473-508-2
16	42	43.8	359	1	US-08-789-936-2
17	42	43.8	359	1	US-08-833-610-6
18	42	43.8	359	2	US-08-834-033A-16
19	42	43.8	359	2	US-08-934-254-2
20	42	43.8	359	2	US-09-377-452-6
21	42	43.8	359	2	US-09-685-775-2
22	42	43.8	363	2	US-09-108-020-44
23	42	43.8	363	2	US-09-685-296-44
24	42	43.8	590	2	US-09-489-039A-8178
25	41	42.7	297	2	US-09-248-796A-25364
26	41	42.7	381	2	US-09-248-796A-17552
27	41	42.7	394	2	US-09-252-991A-32539

28	41	42.7	535	2	US-09-589-733C-18	Sequence 18, Appl
29	41	42.7	536	2	US-09-258-031C-77	Sequence 77, Appl
30	40.5	42.2	246	2	US-09-543-681A-8212	Sequence 8212, Ap
31	40	41.7	230	2	US-09-252-991A-25914	Sequence 25914, A
32	40	41.7	344	2	US-09-252-991A-30083	Sequence 30083, A
33	40	41.7	666	2	US-09-270-767-46736	Sequence 46736, A
34	39.5	41.1	79	2	US-09-248-796A-23915	Sequence 23915, A
35	39.5	41.1	912	1	US-08-951-871-2	Sequence 2, Appl1
36	39	40.6	195	2	US-09-252-991A-21451	Sequence 21451, A
37	39	40.6	271	1	US-08-152-019A-28	Sequence 28, Appl
38	39	40.6	336	1	US-07-667-276A-8	Sequence 8, Appl1
39	39	40.6	411	2	US-09-134-000C-3961	Sequence 3961, Ap
40	39	40.6	416	2	US-09-134-000C-6248	Sequence 6248, Ap
41	39	40.6	463	2	US-09-198-452A-115	Sequence 115, App
42	39	40.6	468	2	US-09-438-185A-100	Sequence 100, App
43	39	40.6	505	2	US-09-252-991A-29343	Sequence 29343, A
44	39	40.6	510	2	US-09-270-767-46399	Sequence 46399, A
45	39	40.6	1725	2	US-09-562-702A-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1
US-09-248-796A-19566
; Sequence 19566, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinlock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19566
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19566

Query Match      47.9%; Score 46; DB 2; Length 195;
Best Local Similarity 55.0%; Pred. No. 4.1;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY      1 IDGQKVDQFP--PQHGVLKQ 18
Db      34 MDGQKVDVLLPQPHKIKQ 53

RESULT 2
US-09-328-352-5163
; Sequence 5163, Application US/09328352
; Patent No. 6362958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5163
; LENGTH: 1512
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5163

Query Match      46.9%; Score 45; DB 2; Length 1512;
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Best Local Similarity 50.0%; Pred. No. 64;  
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 3 GQKVDQEPFOHGLVKQ 18  
Db 328 GDRTPDPLMPKHGLVSO 343

RESULT 3  
US-09-487-558B-322  
; Sequence 322, Application US/09487558B  
; Patent No. 6949356  
; GENERAL INFORMATION:  
; APPLICANT: Bueby, Robert  
; APPLICANT: Call, Brian  
; APPLICANT: Hecht, Peter  
; APPLICANT: Holtzman, Doug  
; APPLICANT: Madden, Kevin  
; APPLICANT: Maxon, Mary  
; APPLICANT: Milne, Todd  
; APPLICANT: No. 6949356man, Thea  
; APPLICANT: Royer, John  
; APPLICANT: Salama, Sofie  
; APPLICANT: Sherman, Amir  
; APPLICANT: Silva, Jeff  
; APPLICANT: Summers, Eric  
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
; FILE REFERENCE: 109272.130  
; CURRENT APPLICATION NUMBER: US/09/487,558B  
; CURRENT FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: US 60/487,558  
; PRIOR FILING DATE: 1999-10-20  
; NUMBER OF SEQ ID NOS: 446  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 322  
; LENGTH: 1536  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-487-558B-322

Query Match 46.9%; Score 45; DB 2; Length 1536;  
Best Local Similarity 53.3%; Pred. No. 65;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 IDGQKVDQEPFOHGL 15  
Db 1370 IDGTEVDEFEPSPEGI 1384

RESULT 4  
US-09-252-991A-25727  
; Sequence 25727, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 25727  
; LENGTH: 612  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-25727

Query Match 44.8%; Score 43; DB 2; Length 612;  
Best Local Similarity 44.4%; Pred. No. 50;

Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 IDGQKVDQEPFOHGLVKQ 18  
Db 401 VDRSVGSPSPQRMVPO 418

RESULT 5  
US-08-961-083-40  
; Sequence 40, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,083  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 137 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-961-083-40

Query Match 43.8%; Score 42; DB 2; Length 137;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 IDGQKVDQEPFO 12  
Db 93 IDGKTEVDEFPQ 104

RESULT 6  
US-09-536-784-40  
; Sequence 40, Application US/09536784  
; Patent No. 6573082  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA

ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/536,784  
FILING DATE: 30-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: OCT-30-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB340P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-536-784-40

Query Match 43.8%; Score 42; DB 2; Length 137;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQ 12  
| : | | | | |  
DB 93 IQGKTVQFPQ 104

RESULT 7  
US-09-765-271-40  
Sequence 40, Application US/09765271  
Patent No. 6887663  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,271  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/536,784  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/961,083  
FILING DATE: OCT-30-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB340P3  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-765-271-40

Query Match 43.8%; Score 42; DB 2; Length 137;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQ 12  
| : | | | | |  
DB 93 IQGKTVQFPQ 104

RESULT 8  
US-09-765-272A-40  
Sequence 40, Application US/09765272A  
Patent No. 6929930  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines  
NUMBER OF SEQUENCES: 454  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
COMPUTER: Dell Latitude C610  
OPERATING SYSTEM: Windows 2000  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,272A  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/961,083  
FILING DATE: OCT-30-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lyn J. Hymel  
REGISTRATION NUMBER: 45,414  
REFERENCE/DOCKET NUMBER: PB340P2C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 610-5790  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-765-272A-40

Query Match 43.8%; Score 42; DB 2; Length 137;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQ 12  
| : | | | | |  
DB 93 IQGKTVQFPQ 104

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RESULT 9
US-09-583-110-5222
: Sequence 5222, Application US/09583110
: Patent No 6659703
: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al.
: TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
: TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
: FILE REFERENCE: PATH00-07A
: CURRENT APPLICATION NUMBER: US/09/583,110
: PRIORITY FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/107,433
: PRIOR APPLICATION NUMBER: US 60/085,131
: PRIOR FILING DATE: 1998-05-12
: PRIOR APPLICATION NUMBER: US 60/051,553
: PRIOR FILING DATE: 1997-07-02
: NUMBER OF SEQ ID NOS: 5332
: SEQ ID NO 5222
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Streptococcus pneumoniae
: US-09-583-110-5222

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Query Match	43.8%	Score 42:	DB 2;	Length 185;
Best Local Similarity	66.7%	Pred. NO. 19;		
Matches 8;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	1	IDGOKVDSEQPQ	12
		:	
Db	112	I0GEKTVSEQPQ	123

RESULT 10  
 US-09-107-433-5104  
 : Sequence 5104, Application US/09107433  
 Patent No. 6800744  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEIC ACID AND  
 SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
 THERAPEUTICS  
 NUMBER OF SEQUENCES: 5206  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-ROM ISO9660  
 COMPUTER: <Unknown>  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: <Unknown>  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,433  
 FILING DATE: 30-Jun-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/085131  
 FILING DATE: May 12, 1998  
 APPLICATION NUMBER: 60/051553  
 FILING DATE: July 2, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinelli, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-011  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEFAX: (781)893-8277  
 INFORMATION FOR SEQ ID NO: 5104:

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?          SEQUENCE CHARACTERISTICS:
?             LENGTH: 194 amino acids
?             TYPE: amino acid
?             TOPOLOGY: linear
?             MOLECULE TYPE: protein
?             HYPOTHETICAL: YES
?             ORIGINAL SOURCE:
?             ORGANISM: Streptococcus pneumoniae
?
?             FEATURE:
?                 NAME/KEY: misc feature
?                 LOCATION: (B) LOCATION 1...194
?             SOURCE DESCRIPTION: SEQ ID NO: 5104
?
? JS-09-107-433-5104

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Query Match	43.8%	Score 42;	Length 194;
Best Local Similarity	66.7%	Pred. No. 20;	
Matches	8;	Conservative	1;
		Mismatches	3;
		Indels	0;
		Gaps	0

Qy	1	1DGOKVDEQFPQ	12
		:	
Db	121	1GGEKTVQFPQ	132

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RESULT 11
US-09-134-000C-6247
: Sequence 6247, Application US/09134000C
: Patent No. 6617156
: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
: TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 032796-032
: CURRENT APPLICATION NUMBER: US/09/134,000C
: PRIORITY FILING DATE: 1998-08-13
: PRIOR APPLICATION NUMBER: US 60/055,778
: PRIOR FILING DATE: 1997-08-15
: NUMBER OF SEQ. ID NOS: 6812
: SOFTWARE: Patentin version 3.1
: SEQ. ID NO. 6247
:
: LENGTH: 228
:
: TYPE: PRT
: ORGANISM: Enterococcus faecalis
US-09-134-000C-6247

```

Query Match	43.8%	Score 42	DB 2	Length 228
Best Local Similarity	87.5%	Pred. No. 24		
Matches 7	Conservative 1	Mismatches 0	Indels 0	Gaps 0

Qy	10	PFOHGLVK	17
		:	
Db	174	PFOHGLVK	181

RESULT 12  
US-08-307-382-2  
Sequence 2, Application US/06307282  
Patent No. 5552306  
GENERAL INFORMATION:  
APPLICANT: Thomas, Terry L.  
APPLICANT: Reddy, Avutu S.  
APPLICANT: Nuccio, Michael  
APPLICANT: Freysinet, Georges L.  
TITLE OF INVENTION: PRODUCTION OF GAMMA L'INOLENIC  
ACID BY A DELTA 6-DESATURASE  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 garden City plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:

RESULT 13  
US-08-366-779-2  
Sequence 2, Application US/08366779  
Patent No. 5614393  
GENERAL INFORMATION:  
APPLICANT: Thomas, Terry L.  
APPLICANT: Reddy, Avutu S.  
APPLICANT: Nuccio, Michael  
APPLICANT: Freysinet, Georges L.  
APPLICANT: Numbers, Andrew N.  
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  
TITLE OF INVENTION: DELTA 6-DESATURASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/366,779  
FILING DATE: 30-DEC-1994  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Presser, Leopold  
REGISTRATION NUMBER: 19,827  
REFERENCE/DOCKET NUMBER: 8383ZXXW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Review #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,727
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,382
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 07/817,919
FILING DATE: 08-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: McNulty, William E.
REGISTRATION NUMBER: 22,606
REFERENCE/DOCKET NUMBER: 83832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-478-727-2

Query Match      43.8%; Score 42; DB 1; Length 359;
Best Local Similarity 46.7%; Pred. No. 40;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0.

4 QKUDEQPPQHGLVKQ 18
|::|||::|::|::|
21 QRVDAFAEHLGTQR 35
```



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## OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 80.3793 Seconds  
(without alignments)  
93.568 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDQFPQHGLVKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:

1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	US-10-758-165-11	Sequence 11, Appl
2	96	100.0	424	US-10-451-078-2	Sequence 2, Appl
3	96	100.0	424	US-10-451-078-4	Sequence 4, Appl
4	78	81.2	15	US-10-052-788-5	Sequence 5, Appl
5	63	65.6	569	US-10-214-524-30	Sequence 30, Appl
6	45	46.9	178	US-10-424-599-146307	Sequence 146307,
7	45	46.9	504	US-10-282-122A-55836	Sequence 55836, A
8	45	46.9	685	US-11-097-143-19596	Sequence 19596, A
9	45	46.9	1536	US-09-801-368-322	Sequence 322, App
10	44	45.8	89	US-10-424-599-205669	Sequence 205669,
11	44	45.8	128	US-10-450-763-36065	Sequence 36065, A
12	44	45.8	130	US-10-424-599-145103	Sequence 145103,
13	44	45.8	159	US-10-450-763-36064	Sequence 36064, A
14	44	45.8	387	US-10-437-963-159933	Sequence 159933,
15	44	45.8	421	US-10-238-075-1472	Sequence 1472, Ap
16	43.5	45.3	718	US-10-017-161-784	Sequence 784, App
17	43	44.8	121	US-10-425-115-187877	Sequence 187877,
18	43	44.8	146	US-10-425-114-46519	Sequence 46519, A
19	43	44.8	149	US-10-425-115-210792	Sequence 210792,
20	43	44.8	152	US-10-425-114-42340	Sequence 42340, A
21	43	44.8	316	US-10-922-282-12	Sequence 12, Appl
22	43	44.8	325	US-10-425-114-37611	Sequence 37611, A
23	43	44.8	346	US-10-425-114-39926	Sequence 39926, A
24	43	44.8	356	US-10-922-282-30	Sequence 30, Appl
25	43	44.8	366	US-10-425-114-37769	Sequence 37769, A
26	43	44.8	371	US-10-425-114-48824	Sequence 48824, A
27	43	44.8	374	US-10-767-701-45372	Sequence 45372, A

28	43	44.8	374	US-10-425-115-216179	Sequence 216179,
29	43	44.8	374	US-10-425-115-216182	Sequence 216182,
30	43	44.8	375	US-10-767-701-42582	Sequence 42582, A
31	43	44.8	398	US-10-425-115-300080	Sequence 300080,
32	43	44.8	403	US-10-425-114-40459	Sequence 40459, A
33	43	44.8	403	US-10-425-114-57233	Sequence 57233, A
34	43	44.8	409	US-10-425-114-46619	Sequence 46619, A
35	43	44.8	434	US-10-425-114-67344	Sequence 67344, A
36	43	44.8	605	US-10-437-963-169342	Sequence 169342,
37	42	43.8	84	US-10-424-599-157014	Sequence 157014,
38	42	43.8	137	US-09-765-272-40	Sequence 40, Appl
39	42	43.8	137	US-11-106-649-40	Sequence 40, Appl
40	42	43.8	185	US-10-472-928-1980	Sequence 1980, Ap
41	42	43.8	191	US-10-474-776-661	Sequence 661, App
42	42	43.8	194	US-10-617-320-5104	Sequence 5104, Ap
43	42	43.8	199	US-10-282-122A-46126	Sequence 46126, A
44	42	43.8	218	US-10-369-493-2768	Sequence 2768, Ap
45	42	43.8	232	US-10-425-114-51771	Sequence 51771, A

## ALIGNMENTS

```

RESULT 1
US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match      100.0%; Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGLVKQ 18
      |||||
DB      1 IDGQKVDQFPQHGLVKQ 18

RESULT 2
US-10-451-078-2
; Sequence 2, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bettina, Wagner
; APPLICANT: Radbruch, Andreas
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
; TITLE OF INVENTION: Heavy Chain of an Equine IgE Allotype, Recombinant
; TITLE OF INVENTION: Immunoglobulin Obtained Using Them and Corresponding
; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 0310017aa
; CURRENT APPLICATION NUMBER: US/10/451,078
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 100 64 415.5
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2

```

```
SEQ ID NO 2
LENGTH: 424
TYPE: PRT
ORGANISM: Equus caballus
FEATURE:
NAME/KEY: Domain
LOCATION: (1)..(97)
OTHER INFORMATION: CH1 domain, IGE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (98)..(205)
OTHER INFORMATION: CH2 domain, IGE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (206)..(312)
OTHER INFORMATION: CH3 domain, IGE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (313)..(424)
OTHER INFORMATION: CH4 domain, IGE allotype a
US-10-451-078-2
```

```
Query Match          100.0%; Score 96; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 IDGQKVDQFPQHGVLVQ 18
Db      145 IDGQKVDQFPQHGVLVQ 162
```

```
RESULT 3
US-10-451-078-4
Sequence 4, Application US/10451078
Publication No. US20040115764A1
GENERAL INFORMATION:
APPLICANT: Leibold, Wolfgang
APPLICANT: Beltina, Wagner
APPLICANT: Radbruch, Andreas
TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
TITLE OF INVENTION: Heavy Chain of an Equine IGE Allotype, Recombinant
TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
FILE REFERENCE: 03100177a
CURRENT APPLICATION NUMBER: US/10/451,078
CURRENT FILING DATE: 2003-12-24
PRIOR APPLICATION NUMBER: PCT/DE01/04810
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: DE 100 64 415.5
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 424
TYPE: PRT
ORGANISM: Equus caballus
FEATURE:
NAME/KEY: Domain
LOCATION: (1)..(97)
OTHER INFORMATION: CH1 domain, IGE allotype b
FEATURE:
NAME/KEY: Domain
LOCATION: (98)..(205)
OTHER INFORMATION: CH2 domain, IGE allotype b
FEATURE:
NAME/KEY: Domain
LOCATION: (206)..(312)
OTHER INFORMATION: CH3 domain, IGE allotype b
FEATURE:
NAME/KEY: Domain
LOCATION: (313)..(424)
OTHER INFORMATION: CH4 domain, IGE allotype b
US-10-451-078-4
```

```
Query Match          100.0%; Score 96; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 IDGQKVDQFPQHGVLVQ 18
Db      145 IDGQKVDQFPQHGVLVQ 162
```

```
RESULT 4
US-10-052-788-5
Sequence 5, Application US/10052788
Publication No. US20030087314A1
GENERAL INFORMATION:
APPLICANT: Gereshwin, Laurel J.
APPLICANT: Pettigrew, Howard David
APPLICANT: Kalina, Warren V.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
FILE REFERENCE: 023070-121000US
CURRENT APPLICATION NUMBER: US/10/052,788
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
OTHER INFORMATION: P5, middle portion of C2 of equine IGE epsilon
OTHER INFORMATION: heavy chain
US-10-052-788-5
```

```
Query Match          81.2%; Score 78; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 IDGQKVDQFPQHG 14
Db      2 IDGQKVDQFPQHG 15
```

```
RESULT 5
US-10-214-524-30
Sequence 30, Application US/10214524
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Zhong
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: IGE-00101.P.1.1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 569
TYPE: PRT
ORGANISM: Horse (Equus caballus)
US-10-214-524-30
```

```
Query Match          65.6%; Score 63; DB 4; Length 569;
Best Local Similarity 66.7%; Pred. No. 0.12;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      1 IDGQKVDQFPQHGVLVQ 18
```



Db 291 IEGQKVDQFPQASMKQ 308

RESULT 6  
US-10-424-599-146307

; Sequence 146307, Application US/10424599  
; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223) B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 146307

; LENGTH: 178

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_103132C.1.dep  
US-10-424-599-146307

Query Match 46.9%; Score 45; DB 4; Length 178;  
Best Local Similarity 57.1%; Pred. No. 31;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 14

Db 152 VDSNVAVQFPQHG 165

RESULT 7

US-10-282-122A-55836

; Sequence 55836, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 55836  
; LENGTH: 504  
; TYPE: PRT  
; ORGANISM: Enterobacter cloacae  
US-10-282-122A-55836

Query Match 46.9%; Score 45; DB 4; Length 504;  
Best Local Similarity 53.3%; Pred. No. 99;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGL 15

Db 315 IDGERVDIQPAHAI 329

RESULT 8

US-11-097-143-19596

; Sequence 19596, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; FILE REFERENCE: CLO00728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 19596

; LENGTH: 685

; TYPE: PRT

; ORGANISM: DROSOPHILA

US-11-097-143-19596

Query Match 46.9%; Score 45; DB 6; Length 685;  
Best Local Similarity 53.3%; Pred. No. 1.4e+02;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKVDQFPQHGLVK 17

Db 577 GQVGSNSYFEGHVK 591

RESULT 9

US-09-801-368-322

; Sequence 322, Application US/09801368

; Patent No. US20020128250A1

; GENERAL INFORMATION:

```

; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 1536
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-322
```

```

Query Match          46.9%; Score 45; DB 3; Length 1536;
Best Local Similarity 53.3%; Pred. No. 3,4e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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QY      1  IDGQKVDQEPPOHGL 15
Db      1370  IDGTEVDEFEFSPBGI 1384
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```

RESULT 10
US-10-424-599-205669
; Sequence 205669, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205669
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) --(89)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27747C.1.pep
US-10-424-599-205669
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Query Match          45.8%; Score 44; DB 4; Length 89;
Best Local Similarity 58.3%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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```
QY      3  GQKVDQEPPOHGL 14
Db      46  GIKYDDKMPQHG 57
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```

RESULT 11
US-10-450-763-36065
; Sequence 36065, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36065
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36065
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Query Match          45.8%; Score 44; DB 5; Length 128;
Best Local Similarity 52.9%; Pred. No. 32;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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QY      2  DQGRPREQSPVHGLVQR 76
Db      60  DQGRPREQSPVHGLVQR 76
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```

RESULT 12
US-10-424-599-145103
; Sequence 145103, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145103
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102046C.1.pep
US-10-424-599-145103
```

```

Query Match          45.8%; Score 44; DB 4; Length 130;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3  GQKVDQEPPOHGL 15
Db      65  GQLQAEHLFPOHGL 77
```

```

RESULT 13
US-10-450-763-36064
; Sequence 36064, Application US/10450763
```

```
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 36064
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(159)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36064

Query Match          45.8%; Score 44; DB 5; Length 159;
Best Local Similarity 52.9%; Pred. No. 40;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGQKVDQFPQHGVLKQ 18
      |||:|||||:
Db      91 DQQRREQSPVHGVLQR 107

RESULT 14
US-10-437-963-154933
; Sequence 154933, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 154933
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54746C.1.pcp
US-10-437-963-154933

Query Match          45.8%; Score 44; DB 4; Length 387;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      6 VDEQFPQHGVL 15
      ::|||:
Db      302 IESFPQHGVL 311

RESULT 15
US-10-238-075-1472
; Sequence 1472, Application US/10238075
```

```
; Publication No. US20030148324A1
; GENERAL INFORMATION:
; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
; TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1472
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-1472

Query Match          45.8%; Score 44; DB 4; Length 421;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 7; Mismatches 0; Indels 2; Gaps 1;

QY      4 QKVDQFPQ--HGVLK 17
      ||::|||:||||:
Db      58 QKLEDFEPFTHGLIR 73

Search completed: December 12, 2005, 20:19:25
Job time : 80.3793 secs
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## OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.94828 Seconds  
(without alignments)  
34.094 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQFPQHGIVKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_New:\*  
1: /cgn2\_6/ptodata/1/pubpa/US09\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/1/pubpa/US06\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubpa/US07\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubpa/US08\_NEW\_PUB pep:\*  
5: /cgn2\_6/ptodata/1/pubpa/ECT\_NEW\_PUB pep:\*  
6: /cgn2\_6/ptodata/1/pubpa/US10\_NEW\_PUB pep:\*  
7: /cgn2\_6/ptodata/1/pubpa/US11\_NEW\_PUB pep:\*  
8: /cgn2\_6/ptodata/1/pubpa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	39.1	408	US-10-467-657-8004	Sequence 8004, Ap
2	37	38.5	423	US-11-074-176-4	Sequence 4, Appl
3	37	38.5	2004	US-10-467-657-84	Sequence 84, Appl
4	37	38.5	2004	US-10-467-657-6322	Sequence 6322, Ap
5	36	37.5	14	US-11-054-515-2449	Sequence 2449, Ap
6	36	37.5	249	US-11-054-515-774	Sequence 774, App
7	36	37.5	359	US-10-793-626-2454	Sequence 2454, Ap
8	36	37.5	445	US-10-467-657-3816	Sequence 3816, Ap
9	35.5	37.0	122	US-10-793-626-2212	Sequence 2212, Ap
10	35.5	37.0	179	US-10-793-626-1922	Sequence 1922, Ap
11	35.5	37.0	375	US-10-485-517-166	Sequence 166, App
12	35.5	37.0	724	US-10-793-626-3082	Sequence 3082, Ap
13	35	36.5	358	US-11-129-143-111	Sequence 111, App
14	35	36.5	444	US-10-131-826A-498	Sequence 498, App
15	35	36.5	444	US-11-071-580-1	Sequence 1, Appl
16	35	36.5	524	US-10-878-556A-152	Sequence 152, App
17	34	35.4	228	US-10-793-626-2936	Sequence 2936, Ap
18	34	35.4	228	US-10-793-626-3196	Sequence 3196, Ap
19	34	35.4	249	US-10-793-626-3298	Sequence 3298, Ap
20	34	35.4	256	US-10-793-626-1934	Sequence 1934, Ap
21	34	35.4	312	US-10-723-207-2	Sequence 2, Appl
22	34	35.4	451	US-10-467-657-516	Sequence 516, App
23	34	35.4	505	US-10-467-657-5148	Sequence 5148, Ap
24	34	35.4	588	US-11-184-380-5	Sequence 5, Appl
25	34	35.4	724	US-11-184-380-4	Sequence 4, Appl

26	34	35.4	1076	US-10-467-657-7916	Sequence 7916, Ap
27	34	35.4	2897	US-10-499-715-2	Sequence 2, Appl
28	33.5	34.9	202	US-10-467-657-1304	Sequence 1304, Ap
29	33.5	34.9	397	US-10-878-556A-189	Sequence 189, App
30	33	34.4	93	US-10-467-657-8835	Sequence 8835, Ap
31	33	34.4	110	US-10-467-657-8835	Sequence 8835, Ap
32	33	34.4	188	US-11-000-463-460	Sequence 460, App
33	33	34.4	188	US-10-467-657-8294	Sequence 932, App
34	33	34.4	193	US-10-467-657-8294	Sequence 2474, Ap
35	33	34.4	222	US-10-793-626-2474	Sequence 2474, Ap
36	33	34.4	222	US-10-793-626-2732	Sequence 2732, Ap
37	33	34.4	395	US-11-053-185-8	Sequence 8, Appl
38	33	34.4	401	US-11-053-185-6	Sequence 6, Appl
39	33	34.4	404	US-10-793-626-2638	Sequence 2638, Ap
40	33	34.4	428	US-11-055-822-606	Sequence 826, App
41	33	34.4	470	US-10-793-626-2496	Sequence 2496, Ap
42	33	34.4	578	US-11-083-800-2	Sequence 2, Appl
43	33	34.4	677	US-10-982-545-12	Sequence 12, Appl
44	33	34.4	696	US-10-793-626-2922	Sequence 2922, Ap
45	33	34.4	715	US-10-793-626-570	Sequence 570, App

## ALIGNMENTS

RESULT 1  
US-10-467-657-8004  
; Sequence 8004, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIANTANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqMan99, version 1.04  
; SEQ ID NO 8004  
; LENGTH: 408  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8004

Query Match 39.1%; DB 6; Length 408;  
Best Local Similarity 31.0%; Pred. No. 20;  
Matches 9; Conservative 6; Mismatches 3; Indels 11; Gaps 1;

QY 1 IDGQKVD-----EPPFGHIVKQ 18  
:||||:|||||:|  
DB 115 VDGQVDLAKDVAGFVSLDMQHGIVLR 143

RESULT 2  
US-11-074-176-4  
; Sequence 4, Application US/11074176  
; Publication No. US20050250135A1  
; GENERAL INFORMATION:  
; APPLICANT: Kjaenhammer, Todd R.  
; APPLICANT: Russell, William M.  
; APPLICANT: Altermann, Eric  
; APPLICANT: McAuliffe, Olivia  
; APPLICANT: Perill, Andrea Azcarate  
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding  
; FILE REFERENCE: 5051-694  
; CURRENT APPLICATION NUMBER: US/11/074,176  
; CURRENT FILING DATE: 2005-03-07

```
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
; US-11-074-176-4
```

```
Query Match          38.5%; Score 37; DB 7; Length 423;
Best Local Similarity 37.5%; Pred. No. 26;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 IDGQKVDQEPPOHGLV 16
        |||:|||||:|:|:
Db       379 VDGKKVDVDSLHSL 394
```

```
RESULT 3
; Sequence 84, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 84
; LENGTH: 2004
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-84
```

```
Query Match          38.5%; Score 37; DB 6; Length 2004;
Best Local Similarity 46.7%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 IDGQKVDQEPPOHGL 15
        |||:|||||:|:|:
Db       1618 VDGKKYBEGFDQRL 1632
```

```
RESULT 4
; Sequence 6322, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6322
; LENGTH: 2004
; TYPE: PRT
```

```
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-6322
```

```
Query Match          38.5%; Score 37; DB 6; Length 2004;
Best Local Similarity 46.7%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 IDGQKVDQEPPOHGL 15
        |||:|||||:|:~|
Db       1618 VDGKKYBEGFDQRL 1632
```

```
RESULT 5
; Sequence 2449, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2449
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-2449
```

```
Query Match          37.5%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      10 FPQHGL 15
        |||||
Db       7 FPQHGL 12
```

```
RESULT 6
; Sequence 774, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
```

```
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 774
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-774
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```
Query Match          37.5%; Score 36; DB 7; Length 249;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      10 PPOHGL 15
       |||||
Db       105 PPOHGL 110
```

```
RESULT 7
US-10-793-626-2454
; Sequence 2454, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2454
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2454
```

```
Query Match          37.5%; Score 36; DB 6; Length 359;
Best Local Similarity 41.2%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

```
QY      1 IDGKRVDEQFPQHGVLV 17
       :|:|:|:|:|:|:|:|:|
Db       65 LDETGIDIOFKNSGLIK 81
```

```
RESULT 8
US-10-467-657-3816
; Sequence 3816, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
```

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan9, version 1.04
; SEQ ID NO 3816
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3816
```

```
Query Match          37.5%; Score 36; DB 6; Length 445;
Best Local Similarity 57.1%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      3 GOKVDEQFPQHGVLV 16
       |||||
Db       398 GKCDVEVGHGCV 411
```

```
RESULT 9
US-10-793-626-2212
; Sequence 2212, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2212
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2212
```

```
Query Match          37.0%; Score 35.5; DB 6; Length 122;
Best Local Similarity 41.2%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
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```
QY      1 IDGKRVDEQFPQHGVLV 16
       :|:|:|:|:|:|:|:|:|
Db       52 LNKKTLKMIPEHGLV 68
```

```
RESULT 10
US-10-793-626-1922
; Sequence 1922, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1922
; LENGTH: 179
```

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-1922

Query Match 37.0%; Score 35.5; DB 6; Length 179;  
Best Local Similarity 41.2%; Pred. No. 17;  
Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 IDGQKVDQFPQH-GLV 16  
DB 38 LNKKKLKHMPHEGLV 54

RESULT 11  
US-10-485-517-166  
Sequence 166, Application US/10485517  
Publication No. US20050256299A1  
GENERAL INFORMATION:  
APPLICANT: University of Sheffield  
APPLICANT: Biosynexus Incorporated  
APPLICANT: Foster, Simon  
APPLICANT: Mond, James  
TITLE OF INVENTION: Antigenic Polypeptides  
FILE REFERENCE: P100629W0  
CURRENT APPLICATION NUMBER: US/10/485,517  
CURRENT FILING DATE: 2004-02-02  
PRIORITY APPLICATION NUMBER: GB 0118825.9  
PRIORITY FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: GB 0200349.9  
PRIOR FILING DATE: 2002-01-09  
NUMBER OF SEQ ID NOS: 424  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 166  
LENGTH: 375  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-10-485-517-166

Query Match 37.0%; Score 35.5; DB 6; Length 375;  
Best Local Similarity 44.4%; Pred. No. 41;  
Matches 8; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 2 DGQKVDQF-----POHG 14  
DB 242 DGRKAGEFPFAGANPMHG 259

RESULT 12  
US-10-793-626-3082  
Sequence 3082, Application US/10793626  
Publication No. US20050255478A1  
GENERAL INFORMATION:  
APPLICANT: KIMBERLY, WILLIAM JOHN  
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
FILE REFERENCE: P03480U5  
CURRENT APPLICATION NUMBER: US/10/793,626  
CURRENT FILING DATE: 2004-03-04  
PRIORITY APPLICATION NUMBER: 60/164,258  
PRIORITY FILING DATE: 1999-11-09  
NUMBER OF SEQ ID NOS: 4472  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3082  
LENGTH: 724  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-793-626-3082

Query Match 37.0%; Score 35.5; DB 6; Length 724;  
Best Local Similarity 44.4%; Pred. No. 88;  
Matches 8; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 2 DGQKVDQF-----POHG 14  
DB 591 DGRKAGEFPFAGANPMHG 608

RESULT 13  
US-11-129-143-111  
Sequence 111, Application US/11129143  
Publication No. US20050266518A1  
GENERAL INFORMATION:  
APPLICANT: BERRY, Alan  
APPLICANT: BRETZEL, Werner  
APPLICANT: HUMBERLIN, Markus  
APPLICANT: LOPEZ-ULIBARRI, Rual  
APPLICANT: MAYER, Anne F.  
APPLICANT: YELISEEV, Alexei A.  
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION  
FILE REFERENCE: C38435/121966  
CURRENT APPLICATION NUMBER: US/11/129,143  
CURRENT FILING DATE: 2005-05-13  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 111  
LENGTH: 358  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-11-129-143-111

Query Match 36.5%; Score 35; DB 7; Length 358;  
Best Local Similarity 26.7%; Pred. No. 47;  
Matches 4; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGL 15  
DB 333 VDKEKIDYDWTKHGI 347

RESULT 14  
US-10-131-826A-498  
Sequence 498, Application US/10131826A  
Publication No. US20050245730A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P0330R1C128  
CURRENT APPLICATION NUMBER: US/10/131,826A  
CURRENT FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113



Search completed: December 12, 2005, 20:19:49  
Job time : 2.94828 secs

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/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 498
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-498
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Query Match          36.5%; Score 35; DB 6; Length 444;
Best Local Similarity 35.7%; Pred. No. 60;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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QY      5 KVDQEPQHGIVKQ 18
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Db      341 KLDQKYMHEILRQ 354
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RESULT 15
US-11-071-580-1
/ Sequence 1, Application US/11071580
/ Publication No. US20050260708A1
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE GENOMICS, INC.
/ APPLICANT: YUE, Henry
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: BANDMAN, Olga
/ APPLICANT: LAL, Preeti
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: AZIMZAI, Yaida
/ APPLICANT: LU, Dyung Aina M.
/ APPLICANT: YANG, Junming
/ TITLE OF INVENTION: PROTEASES AND PROTEASE INHIBITORS
/ FILE REFERENCE: PF-0727 PCT
/ CURRENT APPLICATION NUMBER: US/11/071,580
/ CURRENT FILING DATE: 2005-03-04
/ PRIOR APPLICATION NUMBER: 60/147,986
/ PRIOR FILING DATE: 1999-08-09
/ PRIOR APPLICATION NUMBER: 60/160,807
/ PRIOR FILING DATE: 1999-10-21
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PERL Program
/ SEQ ID NO 1
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 088718CD1
US-11-071-580-1
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```
Query Match          36.5%; Score 35; DB 7; Length 444;
Best Local Similarity 35.7%; Pred. No. 60;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 KVDQEPQHGIVKQ 18
      ||:::|::|
Db      341 KLDQKYMHEILRQ 354
```

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 15.2069 Seconds  
(without alignments)  
113.888 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQFPQHGVLKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	51.0	616	2	E85508 hypothetical prote
2	49	51.0	616	2	E90657 hypothetical prote
3	47	49.0	721	2	UC7557 lipidosis - mouse
4	46	47.9	262	2	AC3034 inositol monophosp
5	46	47.9	297	2	E98251 similar to mcb177
6	45	46.9	1536	1	R8Y853 regulatory protei
7	43	44.8	105	2	T43322 hypothetical prote
8	43	44.8	284	2	G83358 probable ATP-bind
9	43	44.8	654	2	H86717 hypothetical prote
10	42	43.8	185	2	D95115 chlorodoxin family
11	42	43.8	191	2	H97984 conserved hypothet
12	42	43.8	218	2	S76407 phosphoribosylamh
13	42	43.8	271	2	T21777 hypothetical prote
14	42	43.8	359	2	T06532 pyruvate dehydroge
15	42	43.8	359	2	S35157 Delta6 fatty acid
16	42	43.8	702	2	E69498 hypothetical prote
17	42	43.8	817	2	T16409 hypothetical prote
18	42	43.8	1744	2	A54970 tendon, cardiac mu
19	41	42.7	133	2	H72459 probable ribosoma
20	41	42.7	287	1	S76736 hypothetical prote
21	41	42.7	305	2	F86744 tagatose-6-phospha
22	41	42.7	419	2	G84503 hypothetical prote
23	41	42.7	477	2	T37791 probable rna polym
24	41	42.7	535	2	T07969 probable reticuln
25	41	42.7	630	2	T31798 hypothetical prote
26	41	42.7	1020	2	AE0701 tetrathionate redu
27	41	42.7	1270	2	A96669 protein FIM19.11
28	41	42.7	2126	2	E70522 probable polyketid
29	40.5	42.2	237	2	AB0372 phosphoribosylamid

30	40	41.7	30	2	E71264 hypothetical prote
31	40	41.7	132	2	T46168 chlorodoxin-like p
32	40	41.7	156	2	T43834 cytochrome-c oxida
33	40	41.7	181	2	G89799 hypothetical prote
34	40	41.7	183	2	E64248 ribosome releasing
35	40	41.7	183	2	E83447 hypothetical prote
36	40	41.7	229	2	T21714 transcriptional regu
37	40	41.7	324	2	F83426 hypothetical prote
38	40	41.7	489	2	A96234 sugar ABC transpor
39	40	41.7	489	2	AC3052 hypothetical prote
40	40	41.7	493	2	AB2103 codyric acid synth
41	40	41.7	531	2	B97040 phage related prot
42	40	41.7	560	2	S27387 interferon alpha r
43	40	41.7	1243	2	T17390 vrik protein - Dic
44	40	41.7	6658	2	T13931 protection - fruit
45	39.5	41.1	576	2	AC1384 phosphomannomutase

## ALIGNMENTS

RESULT 1  
E85508 hypothetical protein 20260 [imported] - Escherichia coli (strain O157:H7, substrain EDL9  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: E85508  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potlamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: AB5480; MUID:21074935; PMID:11206551  
A:Accession: E85508  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-616 <STO>  
A:Cross-references: UNIPROT:O8X7U6; UNIPARC:UP100000D09F5; GB:AE005174; NID:G12512966; P  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: 20260  
C:Superfamily: uncharacterized conserved protein

Query Match 51.0%; Score 49; DB 2; Length 616;  
Best Local Similarity 50.0%; Pred. No. 3.4;  
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

QY 4 QKVDQFPQ-HGLVK 17  
||:||||:|  
Db 58 QKIDFPELTHGLIK 73

RESULT 2  
E90657 hypothetical protein E850229 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: E90657  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. G  
gaewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: E90657  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-616 <HAV>  
A:Cross-references: UNIPROT:O8X7U6; UNIPARC:UP100000D09F5; GB:BA000007; PIDN:BA033652.1;  
A:Experimental source: strain O157:H7, substrain R1MD 0509952  
C:Genetics:  
A:Gene: E850229  
C:Superfamily: uncharacterized conserved protein

Query Match 51.0%; Score 49; DB 2; Length 616;

Best Local Similarity 50.0%; Pred. No. 3.4;  
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

QY 4 QKVDQFPQ-HGLV 17  
|:|:|:|:|:|:|:  
Db 58 QKEDPEPELTHGLIK 73

## RESULT 3

JC7557

lipidosis - mouse

N:Alternate names: lipidosis-related protein

C:Species: Mus musculus (house mouse)

C&gt;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004

C/Accession: J07557

R:Moriya-Sato, A.; Hida, A.; Inagawa-Ogashira, M.; Wada, M.R.; Sugiyama, K.; Shimizu, J.

Biochem. Biophys. Res. Commun. 279, 62-68, 2000

A&gt;Title: Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.

A/Reference number: JC7557; MUID: 20563802; PMID:1112418

A/Contents: Brain

A/Accession: JC7557

A/Molecule type: mRNA

A/Residues: 1-721 &lt;MOR&gt;

A/Cross-references: UNIPROT:Q99PUS; UNIPARC:UPI000017A518

C/Comment: This protein possesses long-chain acyl-CoA synthetase activity and catalyzes

the impairment of fatty acid metabolism in X-linked adrenoleukodystrophy. This

in human X-linked adrenoleukodystrophy

C/Keywords: adrenoleukodystrophy

Query Match 49.0%; Score 47; DB 2; Length 721;

Best Local Similarity 53.3%; Pred. No. 8.9;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQGL 15  
|:|:|:|:|:|:|:  
Db 44 IDGQTLKESHSKL 58

## RESULT 4

AG3034

inositol monophosphatase family protein (imported) - Agrobacterium tumefaciens (strain C

C/Species: Agrobacterium tumefaciens

C&gt;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C/Accession: AG3034

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCell

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A&gt;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743153

A/Accession: AG3034

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-262 &lt;KOR&gt;

A/Cross-references: UNIPROT:Q8U945; UNIPARC:UPI0000164892; GB:AE008689; PIDN:AAL44693.1;

C/Genetics:

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

E98251  
similar to mlib1779.29 (probable monophosphatase gene) in mycobacterium leprae [imported]

C/Species: Agrobacterium tumefaciens

C&gt;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004

C/Accession: E98251

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A&gt;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: E98251

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-297 &lt;KOR&gt;

A/Cross-references: UNIPROT:Q8U945; UNIPARC:UPI00000237F; GB:AE007870; PIDN:AAK89535.1;

C/Genetics:

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

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C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

A/Map position: linear chromosome

C/Superfamily: suppressor protein subb

Oy 1 IDGQKVDQFQPHGL 15  
|||:|||||:  
Db 1370 IDGTEVDEBFSPGSI 1384

## RESULT 7

T42322  
hypothetical protein - phage SPPI  
C:Species: phage SPPI  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T42322  
R:Alonso, J.C.; Luder, G.; Siege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.  
Gene 204, 201-212, 1997  
A:Title: The complete nucleotide sequence and functional organization of Bacillus subtilis  
A:Reference number: 222137; MUID:98094274; PMID:9434185  
A:Accession: T42322  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-105 <ALD>  
A:Cross-references: UNIPROT:Q48482; UNIPARC:UPI000009B161; EMBL:X97918; PIDN:CAA6529.1

Query Match 44.8%; Score 43; DB 2; Length 105;  
Best Local Similarity 50.0%; Pred. No. 4.9;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFQPHGLVKQ 18  
|||:|||||:  
Db 5 INGQKIGEMFIRGRVDD 22

## RESULT 8

G83358  
probable ATP-binding component of ABC transporter PA2294 [imported] - Pseudomonas aerugi  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: G83358  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lam,  
J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: G83358  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-284 <STO>  
A:Cross-references: UNIPROT:Q91111; UNIPARC:UPI00000C5650; GB:AE004655; GB:AE004091; NID  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA2294

Query Match 44.8%; Score 43; DB 2; Length 284;  
Best Local Similarity 44.4%; Pred. No. 15;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFQPHGLVKQ 18  
|||:|||||:  
Db 73 VDGSRVSGSPGRKGVFQ 90

## RESULT 9

H86717  
hypothetical protein yhfB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H86717  
R:Boletijn, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: H86717  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-654 <STO>  
A:Cross-references: UNIPROT:Q9CH17; UNIPARC:UPI00000C68D4; GB:AE005176; PID:G12723660; P  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yhfB

Query Match 44.8%; Score 43; DB 2; Length 654;  
Best Local Similarity 43.8%; Pred. No. 39;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFQPHGLV 16  
|||:|||||:  
Db 441 IDHRRDDDFEHALL 456

## RESULT 10

D95115  
thioredoxin family protein [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: D95115  
R:Retelijn, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
neon, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.D.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A85000; MUID:21357209; PMID:11463916  
A:Accession: D95115  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-185 <KUR>  
A:Cross-references: UNIPROT:Q97R36; UNIPARC:UPI0000051693; GB:AE005672; PIDN:AAK75117.1,  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP1000

Query Match 43.8%; Score 42; DB 2; Length 185;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFQ 12  
|||:|||||:  
Db 112 IQGKTVQEPFQ 123

## RESULT 11

H97984  
conserved hypothetical protein spr0904 [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: H97984  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.,  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: H97984  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-191 <KUR>  
A:Cross-references: UNIPROT:O8DQ10; UNIPARC:UPI00000E3552; GB:AE007317; PIDN:AAK99708.1;  
C:Genetics:  
A:Gene: spr0904

Query Match 43.8%; Score 42; DB 2; Length 191;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFQ 12  
|||:|||||:

Db 118 IQGKTVQFPQ 129

## RESULT 12

S76407

phosphoribosylanthranilate isomerase (EC 5.3.1.24) - *Synechocystis* sp. (strain PCC 6803)  
C/Species: *Synechocystis* sp.  
A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C/Accession: S76407

R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A/Reference number: S74322; PMID:97061201; PMID:8905231

A/Accession: S76407

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-218 <KAN>

A/Cross-references: UNIPROT:P74435; UNIPARC:UPI0000137608; EMBL:D90915; GB:AB001339; NID

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Superfamily: phosphoribosylanthranilate isomerase; trpf homology

C/Keywords: intramolecular oxidoreductase; isomerase

F:6-210/Domain: trpf homology <TRF>

Query Match 43.8%; Score 42; DB 2; Length 218;

Best Local Similarity 50.0%; Pred. No. 17;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 QKVDQFPQGLVK 17

Db 95 QVQKQAFPOHRLIK 108

## RESULT 13

T21777

hypothetical protein F35E2.2 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T21777

R/Lennard, N.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19471

A/Accession: T21777

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-271 <WLL>

A/Cross-references: UNIPROT:O62225; UNIPARC:UPI0000079A2B; EMBL:Z81528; PIDD:CA804283.1;

A/Experimental source: clone F35E2

C/Genetics:

A/Gene: CESP:F35E2.2

A/Map position: 1

A/Introns: 32/2; 230/2

Query Match 43.8%; Score 42; DB 2; Length 271;

Best Local Similarity 80.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGQKVDEQFP 11

Db 74 DGQKVQVQFP 83

## RESULT 14

T06532

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - garden pea  
C/Species: *Pisum sativum* (garden pea)

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 12-Jul-2004

C/Accession: T06532

R/Luetthy, M.H.; Miernyk, J.A.; Randall, D.D.

submitted to the EMBL Data Library, April 1996

A/Description: cDNA encoding the *Pisum sativum* mitochondrial pyruvate dehydrogenase E1b

A/Reference number: Z15740

A/Accession: T06532

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-359 <LUE>

A/Cross-references: UNIPROT:P52904; UNIPARC:UPI0000130C28; EMBL:U56697; NID:g1336096; PII

C/Superfamily: pyruvate dehydrogenase, E1 component, beta subunit

C/Keywords: oxidoreductase

Query Match 43.8%; Score 42; DB 2; Length 359;

Best Local Similarity 70.0%; Pred. No. 29;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VDEQFPQGL 15

Db 285 VEEGFPOHGV 294

## RESULT 15

S35157

Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - *Synechocystis* sp.  
C/Species: *Synechocystis* sp.

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 15-Mar-2004

C/Accession: S35157; S76243

R/Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

Plant Mol. Biol. 22, 293-300, 1993

A/Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium *Synechocystis* sp.

A/Reference number: S35157; PMID:93283633; PMID:8389613

A/Accession: S35157

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-359 <RED>

A/Cross-references: UNIPARC:UPI0000032FF9; GB:L11421; NID:g349562; PIDD:AAA27286.1; PIDD:

R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A/Reference number: S74322; PMID:97061201; PMID:8905231

A/Accession: S76243

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-359 <KAN>

A/Cross-references: UNIPARC:UPI0000032FF9; EMBL:D90914; GB:AB001339; NID:g1653477; PIDD:

A/Experimental source: PCC 6803

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Superfamily: fatty acid desaturase/sphingolipid desaturase

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 43.8%; Score 42; DB 2; Length 359;

Best Local Similarity 46.7%; Pred. No. 29;

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 QKVDQFPQGLVKQ 18

Db 21 QVQVAFPAHGLTOR 35

Search completed: December 12, 2005, 20:42:53  
Job time : 17.2069 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 97.7586 Seconds  
(without alignments)  
129.907 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDEQFPQHGIVKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	53.1	1089	2	Q8VQF9_XENBV
2	50.5	52.6	1008	2	Q5GR68_ALCXH
3	50	52.1	271	2	Q4LMX1_9BIRK
4	50	52.1	283	2	Q88RC3_PSEPK
5	49	51.0	616	2	Q8X7U6_ECO57
6	48	50.0	345	2	Q61Y77_CABR
7	47	49.0	721	2	Q99PUS_MOUSE
8	47	49.0	724	2	Q6ZQ79_MOUSE
9	46	47.9	239	2	Q87979_BOBR
10	46	47.9	239	2	Q7W262_BOBR
11	46	47.9	262	2	Q8U945_AGR5
12	46	47.9	273	2	Q74BV7_GEOSL
13	46	47.9	297	2	Q7CTJ2_AGR5
14	46	47.9	408	2	Q8CLM8_YERPE
15	46	47.9	447	2	Q51J08_MAGGR
16	46	47.9	606	2	Q664Y3_YERPS
17	46	47.9	1164	2	Q6SLC8_COCH
18	45	46.9	301	2	Q75B28_ASHGO
19	45	46.9	342	2	Q5KY10_GEOKA
20	45	46.9	694	2	Q9GZ15_DROSOPHILA
21	45	46.9	783	2	Q7KUY7_DROME
22	45	46.9	840	2	Q9VXL1_DROME
23	45	46.9	970	2	Q4GZAB_YTRYP
24	45	46.9	1536	1	SIN3_YEAST
25	44	45.8	169	2	Q8DKM9_SYNEL
26	44	45.8	282	2	Q65WBL_MANSML
27	44	45.8	376	2	Q54LC6_DICDI
28	44	45.8	386	2	Q6TKU8_ECOLI
29	44	45.8	501	2	Q6ABQ0_PROAC
30	44	45.8	524	2	Q4NMW4_9DELIT
31	44	45.8	615	2	Q7N9G7_PHOHL

32	44	45.8	617	2	Q72NZ2_LEPIC
33	44	45.8	617	2	Q8F7H8_LEPIN
34	44	45.8	864	2	Q5AZ29_ASPEGLIUS
35	44	45.8	916	2	Q5B315_EMENT
36	44	45.8	1517	2	Q4T2E2_TETNG
37	43	44.8	105	2	Q48482_BPSPP
38	43	44.8	131	2	Q7RH83_PLAYO
39	43	44.8	201	2	Q8R7E4_THETN
40	43	44.8	235	2	Q7I123_BRARE
41	43	44.8	284	2	Q91111_PSEAE
42	43	44.8	314	1	HAT7_AEATH
43	43	44.8	363	2	Q7Q3M5_ANOGA
44	43	44.8	373	2	Q9ZQY3_MAIZE
45	43	44.8	374	2	Q9ZQY1_ZEA MAYE

## ALIGNMENTS

RESULT 1									
ID	Q8VQF9_XENBV	PRELIMINARY;	PRT;	1089 AA.					
AC	Q8VQF9;								
DT	01-MAR-2002 (TrEMBLrel. 20, Created)								
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)								
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)								
DE	Peptide synthetase Xpsa.								
GN	Name=xpsa;								
OS	Xenorhabdus bovienii.								
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;								
OC	Enterobacteriaceae; Xenorhabdus.								
OX	NCBI_TaxID=40576;								
RN	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=T228;								
RA	Pinyon R.A., Thomas C.J.;								
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AF455810; AAL57599.1; -; Genomic_DNA.								
DR	HSSP; P14687; 1AMU.								
DR	GO; GO:0048037; F:cofactor binding; IEA.								
DR	GO; GO:0016874; F:ligase activity; IEA.								
DR	GO; GO:0008152; P:metabolism; IEA.								
DR	InterPro; IPR010071; AA_adenyl_dom.								
DR	InterPro; IPR009081; ACP_like.								
DR	InterPro; IPR008973; AMP-bind.								
DR	InterPro; IPR001242; AMP-bind.								
DR	InterPro; IPR006163; Phosphateth_bind.								
DR	Pfam; PF00501; AMP-binding; 1.								
DR	Pfam; PF00668; Condensation; 2.								
DR	Pfam; PF00550; PP-binding; 1.								
DR	PRINTS; PR00154; AMPBINDING.								
DR	TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.								
DR	PROSITE; PS00075; ACP_DOMAIN; 1.								
DR	PROSITE; PS00455; AMP_BINDING; 1.								
SQ	SEQUENCE 1089 AA; 122986 MW; FF42CIA12506CBF9 CRC64;								
Query Match									
Best Local Similarity		53.1%;	Score 51;	DB 2;	Length 1089;				
Matches 9;		Conservative 2;	Mismatches 6;	Indels 0;	Gaps 0;				
QY	2 DGQKVDEQFPQHGIVKQ 18								
DB	470 DENKTDKEFPQHALIHQ 486								
RESULT 2									
ID	Q5GR68_ALCXH	PRELIMINARY;	PRT;	1008 AA.					
AC	Q5GR68;								
DT	10-MAY-2005 (TrEMBLrel. 30, Created)								
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)								
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)								
DE	Transposase.								

```

GN Name=tnpA;
OS Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxydans) .
OG Plasmid pAB1.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Achromobacter.
OX NCBI_TaxID=85698;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB;
RA Jencova V., Strnad H., Chodora Z., Ulbrich P., Hickey W.J., Paces V.;
RT "Chlorocatechol catabolic enzymes from Achromobacter xylosoxydans
RT AB.";
RL Int. Biodeterior. Biodegradation 54:175-181(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB;
RA Jencova V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ515144; CA147903.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:Transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR002513; Transposase_7.
DR Pfam; PF01526; Transposase_7; 1.
KM plasmid.
SQ SEQUENCE 1008 AA; 114816 MW; A9F92682878061B5 CRC64;

Query Match 52.6%; Score 50.5; DB 2; Length 1008;
Best Local Similarity 45.5%; Pred. No. 30;
Matches 10; Conservative 3; Mismatches 0; Indels 9; Gaps 1;

Qy 1 IDGQKVDQFPQHGVLVQ 13
Db 516 VDGKQLLTETAEKVDSEFPQH 537

RESULT 3
Q4LMX1_9BURK PRELIMINARY; PRT; 271 AA.
AC Q4LMX1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE ABC transporter.
GN ORNames=Bcen2424DRAFT_2386;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-PGP);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israeli S., Plutnick S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
SQ SEQUENCE 271 AA; 29686 MW; E9976D6F6E02527 CRC64;

Query Match 52.1%; Score 50; DB 2; Length 271;

```

```

Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVQ 18
Db 85 VDGQPVDPSPQRMGFQ 102

RESULT 4
Q88RC3_PSEPK PRELIMINARY; PRT; 283 AA.
AC Q88RC3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nitrate ABC transporter, ATP-binding protein, putative.
GN OrderedCusNames=PP0209;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22423050; PubMed=12534453;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzaz A., Uteerback T.R., Rizzo M., Lee K., Kosack D., Meestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
RA Kewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Thiemler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 44:799-808(2002).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE016774; AAN65842.1; -; Genomic_DNA.
DR HSSP; Q9YGA6; 1G29.
DR TIGR; PP0209; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016867; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF00006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Membrane; Nucleotide-binding;
KW Transport.
SQ SEQUENCE 283 AA; 31651 MW; DA1B21FCA2223A4A CRC64;

Query Match 52.1%; Score 50; DB 2; Length 283;
Best Local Similarity 55.6%; Pred. No. 9.5;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVQ 18
Db 73 VDGQPVDPSPQRMGFQ 90

RESULT 5
Q8X7U6_ECOS7 PRELIMINARY; PRT; 616 AA.
AC Q8X7U6; 07AH17;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE No significant matches (Hypothetical protein EC80229).

```



GN OrderedLocusNames=EC60229, z0260;  
OS *Escherichia coli* O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Escherichia*.  
NCBI\_TaxId=83334;  
RN (1)  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=O157:H7 / EDL93 / ATCC 700927 / EHEC;  
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
Postel G., Hackert J., Klink S., Boutin A., Shao Y., Miller L.,  
Grobeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
Apodaca J., Antantharam T.S., Lin J., Yen G., Schwartz D.C.,  
Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";  
RL Nature 409:529-533 (2001).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,  
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
Kuhara S., Shiba T., Hattori M., Shingawa H.;  
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*  
O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22 (2001).  
DR EMBL, AE005174; AAG54529.1; -; Genomic\_DNA.  
DR EMBL, BA000007; BAB3652.1; -; Genomic\_DNA.  
DR PIR, E85508; E85508.  
DR PIR, E90657; E90657.  
DR InterPro: IPR010272; DUF879\_bac.  
DR Pfam: PF05947; DUF879; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 616 AA; 71185 MW; 1FBC0A5128341E30 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 616;  
Best Local Similarity 50.0%; Pred. No. 32;  
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKQVDFQPO-HGLVY 17  
||:||||:||||:  
Db 58 QKEDDFPELTHGLIK 73

RESULT 6  
O61Y77 CAEBR  
ID O61Y77 CAEBR PRELIMINARY; PRT; 345 AA.  
AC O61Y77-  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Hypothetical protein CBG03674.  
GN Name=CBG03674;  
OS *Caenorhabditis briggsae*.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Felodierinae; *Caenorhabditis*.  
NCBI\_TaxId=6238;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC The C.briggsae Sequencing Consortium;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL, CAC0100016; CAC6129.1; -; Genomic\_DNA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR001254; Peptidase\_S1\_S6.  
DR InterPro: IPR001314; Peptidase\_S1A.  
DR Pfam, PF00089; Trypsin, 1.  
DR PRINTS, PR00722; CHYMOTRYPsin.  
DR SMART, SM00020; TRYP\_SPC, 1.  
DR PROSITE, PS50240; TRYPSIN\_DOM, 1.

KW Hypothetical protein.  
SQ SEQUENCE 345 AA; 38450 MW; 744C79ED3DB0408D CRC64;

Query Match 50.0%; Score 48; DB 2; Length 345;  
Best Local Similarity 50.0%; Pred. No. 25;  
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IDQKVDQFQNG 14  
:||||:||||:  
Db 80 VSGKVDQFQNG 93

RESULT 7  
O99PUS MOUSE  
ID O99PUS MOUSE PRELIMINARY; PRT; 721 AA.  
AC O99PUS-  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
DE Lipidosis-related protein Lipidosin (Mus musculus 2 days pregnant  
adult female oviduct cDNA, RIKEN full-length enriched library", full  
clone: E230019603 product: lipidosis-related protein lipidosin, full  
insert sequence).  
DE insert sequence).  
GN Name=Lpd; Synonyms=lpd;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=20563802; PubMed=11112418; DOI=10.1006/dbrc.2000.3897;  
RA Moriya-Sato A., Hida A., Inagawa-Ogasawara M., Wada M.R., Sugiyama K.,  
Shimizu J., Yabuki T., Seyama Y., Hashimoto N.;  
RT "Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.";  
RL Biochem. Biophys. Res. Commun. 279:62-68 (2000).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44 (1999).  
RN (3)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Pletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
Schriml L.W., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,  
Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,  
Brownstein M.D., Bult C., Fletcher C., Fujita M., Kamuya M., Lee N.H.,  
Lyons P., Marchionni L., Mashima J., Mazzaeili J., Mombaerts P.,  
Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,  
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
RN (4)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Baidarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirral L.M., Kanapin A., Matsuda H., Batalov S., Betsel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbini L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,  
 RA Grimmer S., Guetlinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard R.D., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nomata S., Okido T., Pavan W.J., Petrea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius U.V., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sanderlin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Walestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Alizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yaumishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 [5]  
 RP NUCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RL prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 [6]  
 RP NUCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Alizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Komno H., Akiyama J., Nishi K., Kikunaka T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaga S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 [7]  
 RP NUCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6J; TISSUE=Oviduct;  
 RA Adachi J., Alizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Konda M., Koya S.,  
 RA Kiyuhara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y.,  
 RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Taya T., Yaumishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 [8]  
 RP NUCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,  
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguailo N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [9]  
 RP NUCLEOTIDE SEQUENCE  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RA Director MGC Project;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 CC -i- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme  
 CC family.  
 DR EMBL: AB050554; BAB32783.1; -; mRNA.  
 DR EMBL: AK054103; BAC35657.1; -; mRNA.  
 DR EMBL: BC057322; AAC57322.1; -; mRNA.  
 DR PIR: JC7557; JC7557.  
 DR HSSP: P08659; 1ICI.  
 DR Ensembl: ENSMUSG00000032281; Mus musculus.  
 DR MGI: MGI:238656; Upd.  
 DR GO: GO:0003624; F: catalytic activity; IEA.  
 DR GO: GO:0008152; P: metabolism; IEA.  
 DR InterPro: IPR000873; AMP-bind.  
 DR Pfam: PF00501; AMP-binding; 1.  
 DR PRINTS: PR00154; AMPBINDING  
 DR PROSITE: PS00455; AMP\_BINDING; 1.  
 DR SEQUENCE 721 AA; 80425 MW; C3A8C91335984FE CRC64;  
 SQ  
 Query Match 49.0%; Score 47; DB 2; Length 721;  
 Best Local Similarity 53.3%; Pred. No. 81;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 IDGQVDEQFPQHGL 15  
 ||||| : : : |||||  
 Db 44 IDGQTLSKESPSHGL 58  
 RESULT 8  
 Q6Z079 MOUSE PRELIMINARY; PRT; 724 AA.  
 ID Q6Z079; AC Q6Z079;  
 AC Q6Z079;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE MKIAA0631 protein (Fragment).  
 GN Name=Ipd; Synonyms=MKIAA0631;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCB1; TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Brain;  
 RX PubMed=14621295.  
 RA Okazaki N., Kikuno R., Ohara R., Imamoto S., Koseki H., Hirooka S.,  
 RA Suga Y., Nagase T., Ohara O., Koga H.,  
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:  
 RT ii. the complete nucleotide sequences of 500 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of cDNA clones  
 RL randomly sampled from size-fractionated libraries.";  
 RL DNA Res. 10:167-180 (2003).

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CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL: AK129179; BAC97989.1; -; mRNA.
DR MGI: MGI:2385656; Lpd.
DR GO: GO:0003824; F: catalytic activity; IEA.
DR GO: GO:0008152; F: metabolism; IEA.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP BINDING; 1.
FT NON TER
SQ SEQUENCE 724 AA; 80795 MW; 3E5875777B7E5560 CRC64;

Query Match 49.0%; Score 47; DB 2; Length 724;
Best Local Similarity 53.3%; Pred. No. 81;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGQKVDQFPQHG 15
DB 47 IDGQKVDQFPQHG 61

RESULT 9
O87979_BORBR PRELIMINARY; PRT; 239 AA.
AC O87979;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein BblP51.06.
GN Name=BblP51.06;
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=518;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CN7635E;
RX MEDLINE=99346157; PubMed=10417135;
RA Preston A., Allen A.G., Cadisch J., Thomas R., Stevens K.,
RA Churcher C.M., Badcock K.L., Parkhill J., Barrett B., Maskell D.J.,
RA "Genetic Basis for lipopolysaccharide O-antigen biosynthesis in
RA Bordetella.";
RT Infect. Immun. 67:3763-3767(1999).
DR EMBL: AJ007747; CA07645.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 239 AA; 27358 MW; 79CE20279B9C08C2 CRC64;

Query Match 47.9%; Score 46; DB 2; Length 239;
Best Local Similarity 53.8%; Pred. No. 38;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 GQKVDQFPQHG 15
DB 182 GQKVDQFPQHG 194

RESULT 10
O7W262_BORPA PRELIMINARY; PRT; 239 AA.
AC O7W262;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein wbpM.
GN Name=wbpM; OrderedLocustName=BPP0129;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=519;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;

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RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Chevreach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Mole S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640423; CAE39870.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 239 AA; 27359 MW; F5AC4AE7759C0622 CRC64;

Query Match 47.9%; Score 46; DB 2; Length 239;
Best Local Similarity 53.8%; Pred. No. 38;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 GQKVDQFPQHG 15
DB 182 GQKVDQFPQHG 194

RESULT 11
O8U945_AGR5 PRELIMINARY; PRT; 262 AA.
AC O8U945;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Inositol monophosphatase family protein.
GN OrderedLocustName=Atu3885;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxId=176299;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Sebubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. St.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kuyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreppan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL: AE009319; AAL44693.1; -; Genomic_DNA.
DR PIR: AG3034;
DR PIR: E98251; E98251.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004437; F:inositol or phosphatidylinositol phosphatase. . .; IEA.
DR InterPro: IPR011809; His_9_proposed.
DR InterPro: IPR000760; Inositol_P.
DR Pfam: PF00459; Inositol_P_1.
DR PRINTS: PR00378; INOSPHPTASE.
DR ProDom: PD023420; Inositol_P_1.
DR TIGRPFAM: TIGR02067; his_9_proposed; 1.
DR PROSITE: PS00629; IMP_1; 1.
KW Complete proteome.
SQ SEQUENCE 262 AA; 28813 MW; 5E7607DC3A3E31D CRC64;

Query Match 47.9%; Score 46; DB 2; Length 262;

```

Best Local Similarity 54.5%; Pred. No. 41;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQPOHGLV 16  
:::|||||:  
Db 59 IEEFPQHGIL 69

## RESULT 12

074BV7 GEOSL PRELIMINARY; PRT; 273 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE Transport-associated domain protein.

OC OrderedLocustNames=GSU1925;  
OS Geobacter sulfurreducens.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;  
OC Geobacteraceae; Geobacter.  
OX NCBI\_TaxID=35554;  
RN [1]

## RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PCA / ATCC 51573;  
RX PubMed=14671304; DOI=10.1126/science.1088727;  
RA Meehe B.A., Nelson K.E., Eissen J.A., Paulsen I.T., Nelson W.C.,  
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,  
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,  
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,  
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,  
RA Van Aken S.E., Lovley D.R., Fraser C.M.;  
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface  
environments."  
RL Science 302:1967-1969(2003).  
DR EMBL: AE017180; AAR35301.1; -, Genomic\_DNA.  
DR TIGR: GSU1925; -,  
DR InterPro: IPR007055; TAD.  
DR Pfam: PF04972; BON; 1.  
DR PROSITE: PS50914; BON; 1.  
KM Complete proteome.  
SQ SEQUENCE 273 AA; 31128 MW; 0449EB5A7B1A346 CRC64;

Query Match 47.9%; Score 46; DB 2; Length 273;

Best Local Similarity 44.4%; Pred. No. 43;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IDGKXVDEQPOHGLVQ 18  
:::|||||:  
Db 30 VDGKRIAEIAPRYGLDKR 47

## RESULT 13

07CTU2 AGRTS PRELIMINARY; PRT; 297 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE AGR\_1\_1926P.

OC OrderedLocustNames=AGR\_1\_1926;  
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
OX NCBI\_TaxID=176299;  
RN [1]

## RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Cereon;  
RX MEDLINE=1608551; PubMed=11743194; DOI=10.1126/science.1066803;  
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
RA Houcillo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,  
RA Houmiel K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,  
RA Wollam C., Allinger W., Doughy D., Scott C., Lappas C., Markelz B.,

RA Flanagan C., Crowell C., Guron J., Lomo C., Sear C., Strub G.,  
RA Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
RT Agrobacterium tumefaciens C58."  
RL Science 294:2323-2328(2001).

DR EMBL: AE008295; AAK89535.1; -, Genomic DNA.  
DR GO: GO:0016787; F:hydrolase activity; IEA.  
DR GO: GO:0004437; F:inostol or phosphatidylinositol phosphatas. . .; IEA.  
DR InterPro: IPR011809; His\_9\_proposed.  
DR InterPro: IPR000760; Inostol\_P.  
DR Pfam: PF00459; Inostol\_P.1.\_.  
DR PRINTS: PR00378; INOSPHTASE.  
DR Prodom: PD023420; Inostol\_P.1.  
DR TIGRFAMs: TIGR02067; his\_9\_proposed; 1.  
DR PROSITE: PS00629; IMP 1; 1.  
SQ SEQUENCE 297 AA; 33042 MW; 83E08201E4508B1E CRC64;

Query Match 47.9%; Score 46; DB 2; Length 297;

Best Local Similarity 54.5%; Pred. No. 47;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQPOHGLV 16  
:::|||||:  
Db 94 IEEFPQHGIL 104

## RESULT 14

08CLW8 YERPE PRELIMINARY; PRT; 408 AA.

DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DE Hypothetical.

GN OrderedLocustNames=Y0040;  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]

## RP NUCLEOTIDE SEQUENCE.

RC STRAIN=KIM5 / Biovar Medinevalis;  
RX MEDLINE=22137863; PubMed=12142430;  
RX DOI=10.1128/JB.184.16.4601-4611.2002;  
RA Deng W., Burtland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,  
RA Perry R.D.;  
RT "Genome sequence of Yersinia pestis KIM."  
RL J. Bacteriol. 184:4601-4611(2002).  
DR EMBL: AE013605; AAM83635.1; -, Genomic\_DNA.  
DR InterPro: IPR010272; DUF879\_bac.  
DR Pfam: PF05947; DUF879; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 408 AA; 46728 MW; 7E02D4E0003D39DB CRC64;

Query Match 47.9%; Score 46; DB 2; Length 408;

Best Local Similarity 53.3%; Pred. No. 66;  
Matches 8; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QXVDEQPOHGLV 16  
:::|||||:  
Db 57 EKXIDQFPELTGHL 71

## RESULT 15

051J08 MAGR PRELIMINARY; PRT; 447 AA.

DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Hypothetical protein.  
GN ORFNames=MG09895.4;  
OS Magnaporthe grisea 70-15.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.  
CX NCBI\_TaxID=242507;

RP NUCLEOTIDE SEQUENCE.  
[1]

RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
RC STRAIN=70-15;  
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,  
RA Bayul T., Biltsheteyn B., Bloom T., Biye J., Boguslavskiy L.,  
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,  
RA Calvo S., Camarata J., Campo K., Chang J., Cheesetang Y., Citroen M.,  
RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
RA Dorjee K., Dorrie L., Dufley N., Dupes A., Ekins T., Engels R.,  
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Fitzgerald M., Foley K., Gage D., Galagan J., Garin G., Gnerre S.,  
RA Gnrke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
RA Horan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseis M., Karlsson E.,  
RA Kells C., Kieu A., Kismar P., Kodira C., Kulbokas E., Labutti K.,  
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
RA Lindblad-coh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,  
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
RA Manning J., Marabella R., Maru K., Matthews C., Mancini E.,  
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menus L.,  
RA Mesirov J., Mihailev A., Minova T., Mikkelsen T., Mienga V., Moru K.,  
RA Moses J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okrawo O., O'leary S., Omotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
RA Rella R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stebson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,  
RA Tenzing P., Testaye S., Theodore J., Thoulitsang Y., Topham K.,  
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,  
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
RA Zimmer A., Zody M., Lander E.;  
RT "The genome sequence of Magnaporthe grisea."  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Zhu H., Blackmon B.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL: AACU01001744; EAA46674.1; -; Genomic\_DNA.  
DR Hypothetical protein.  
KW SEQUENCE 447 AA; 48757 MW; 9BD8DC0B87A2F1CB CRC64;

## Query Match

Best Local Similarity 47.9%; Score 46; DB 2; Length 447;  
Matches 11; Conservative 4; Mismatches 2; Indels 10; Gaps 1;

OY 2 DGQ-----KVDEQFPQHGIVKQ 18  
DB 27 DGQTTVTKSTSDDELDDQEPQTGIIVKQ 53

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:53:01 ; Search time 181 Seconds  
(without alignments)  
41.268 Million cell updates/sec

Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDGQVMDVLDSTASTTQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 808799

Minimum DB seq length: 0  
Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*
9:	Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	17	ADRI0616	Human IGE
2	51	61.4	13	ABR25916	Abj00228 Human IGE
3	51	61.4	13	ABR25914	Abj00228 Human IGE
4	51	61.4	13	ABR25917	Abj00228 Human IGE
5	51	61.4	13	ABR20872	Abj00228 Human IGE
6	51	61.4	13	ABR51028	Abj00228 Human IGE
7	51	61.4	13	AAU16642	Abj00228 Human IGE
8	51	61.4	13	AAU16641	Abj00228 Human IGE
9	51	61.4	13	ABU00312	Abj00228 Human IGE
10	51	61.4	13	ABU00312	Abj00228 Human IGE
11	51	61.4	13	ABU00224	Abj00228 Human IGE
12	51	61.4	13	ABU00226	Abj00228 Human IGE
13	51	61.4	16	ABU00542	Abj00228 Human IGE
14	51	61.4	9	ABR25907	Abj00228 Human IGE
15	47	56.6	9	ABR20867	Abj00228 Human IGE
16	47	56.6	9	ABR51023	Abj00228 Human IGE
17	47	56.6	9	ABU16632	Abj00228 Human IGE
18	47	56.6	9	ABU00217	Abj00228 Human IGE
19	47	56.6	9	ABU10893	Abj00228 Human IGE
20	47	56.6	9	ADM39798	Abj00228 Human IGE
21	47	56.6	9	ADM64140	Abj00228 Human IGE
22	47	56.6	9	ADM73528	Abj00228 Human IGE
23	47	56.6	9	ADR12820	Abj00228 Human IGE
24	47	56.6	10	ABR25929	Abj00228 Human IGE

25	47	56.6	10	AAU16654	Abj00228 Human IGE
26	47	56.6	10	ABU00228	Abj00228 Human IGE
27	47	56.6	10	ABR25902	Abj00228 Human IGE
28	47	56.6	10	ABR10902	Abj00228 Human IGE
29	47	56.6	10	ADM39807	Abj00228 Human IGE
30	47	56.6	10	ADM64149	Abj00228 Human IGE
31	47	56.6	10	ADM73537	Abj00228 Human IGE
32	47	56.6	10	ADR12829	Abj00228 Human IGE
33	47	56.6	14	ABU00540	Abj00228 Human IGE
34	47	51.8	9	ABR25907	Abj00228 Human IGE
35	42	50.6	9	ABR25902	Abj00228 Human IGE
36	41	49.4	10	ABR25907	Abj00228 Human IGE
37	37	44.6	13	ABU00541	Abj00228 Human IGE
38	34	41.0	7	ABR25923	Abj00228 Human IGE
39	34	41.0	7	AAU16648	Abj00228 Human IGE
40	34	41.0	7	ABU00227	Abj00228 Human IGE
41	34	41.0	17	ADR23403	Abj00228 Human IGE
42	34	41.0	17	ADR23080	Abj00228 Human IGE
43	33	39.8	17	AAU68511	Abj00228 Human IGE
44	33	39.8	17	AAU68255	Abj00228 Human IGE
45	33	39.8	17	AAU68364	Abj00228 Human IGE

## ALIGNMENTS

RESULT 1  
ID ADR10616 standard; peptide, 17 AA.  
XX  
AC ADR10616;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Human IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 16.  
XX  
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
XX human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
XX (UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hammerberg B;  
XX  
DR WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian IGE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
CC either pig or human epsilon-chains of IgE. The present sequence is the  
CC human IgE 3.76 recognition site.

XX Sequence 17 AA;

Query Match 100.0%; Score 83; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17  
Db 1 EDGQVMDVDLSTASTTQ 17

RESULT 2  
AAB25916  
ID AAB25916 standard; peptide; 13 AA.

XX AAB25916;

DT 05-JAN-2001 (first entry)

XX P1 mimotope peptide P15P SEQ ID NO:10.

XX Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.

XX Homo sapiens.

XX WO200050460-A1.

XX 31-AUG-2000.

XX 22-FEB-2000; 2000WO-EP001455.

XX 25-FEB-1999; 99GB-00004405.  
PR 29-MAR-1999; 99GB-00007151.  
PR 07-MAY-1999; 99GB-00010537.  
PR 07-MAY-1999; 99GB-00010538.  
PR 07-AUG-1999; 99GB-00018594.  
PR 07-AUG-1999; 99GB-00018603.  
PR 07-SEP-1999; 99GB-00021046.  
PR 07-SEP-1999; 99GB-00021047.  
PR 29-OCT-1999; 99GB-00025619.  
PR 23-NOV-1999; 99GB-00027698.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Basolac;

XX WPI; 2000-572073/53.

PT Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.

XX Disclosure; Page 9; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IgE), or its mimotope. Also described are: (i) an  
CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (1a) capable of being recognised by (IV); (6) an immunogen  
CC (1ia) comprising (1a); and (7) producing (III) by producing (II). (I) can

CC have antiallergic and immunosuppressive activities, and can be used as a  
CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful  
CC in medicine and in the manufacture of medicaments for treating and  
CC preventing allergies. (IV) is useful for identifying mimotopes of P1, in  
CC medicine and also in manufacturing medicaments for treating allergies.

CC (I) is useful in diagnostics and in the affinity purification of  
CC circulating anti-IgE antibodies from blood. (I), (II) and (III) are useful  
CC for treating a patient susceptible to or suffering from allergies. (IV)  
CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
CC peptide sequences which are used in the exemplification of the present  
CC invention

XX Sequence 13 AA;

Query Match 61.4%; Score 51; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10  
Db 3 EDGQVMDVDL 12

RESULT 3  
AAB25914  
ID AAB25914 standard; peptide; 13 AA.

XX AAB25914;

DT 05-JAN-2001 (first entry)

XX P1 mimotope peptide P15 SEQ ID NO:8.

XX Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;  
KW allergic disease; immunophylaxis; immunotherapy; antiallergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;  
KW allergy; atopy.

XX Homo sapiens.

XX WO200050460-A1.

XX 31-AUG-2000.

XX 22-FEB-2000; 2000WO-EP001455.

XX 25-FEB-1999; 99GB-00004405.  
PR 29-MAR-1999; 99GB-00007151.  
PR 07-MAY-1999; 99GB-00010537.  
PR 07-MAY-1999; 99GB-00010538.  
PR 07-AUG-1999; 99GB-00018594.  
PR 07-AUG-1999; 99GB-00018603.  
PR 07-SEP-1999; 99GB-00021046.  
PR 07-SEP-1999; 99GB-00021047.  
PR 29-OCT-1999; 99GB-00025619.  
PR 23-NOV-1999; 99GB-00027698.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Basolac;

XX WPI; 2000-572073/53.

XX Peptides useful for treating, preventing and ameliorating allergic  
PT diseases, comprising an isolated surface exposed group of a specific  
PT domain from immunoglobulin E.

XX Claim 14; Page 9; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of



Query	Match	Best Local Similarity	Score 51;	DB 3;	Length 13;
Matches	10;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	1 EDGQVMDVDL 10				
Db	3 EDGQVMDVDL 12				
RESULT 4					
AAB25917					
ID	AAB25917	standard;	peptide;	13 AA.	
XX	AAB25917;				
AC					
XX					
DT	05-JAN-2001	(first entry)			
XX					
DE	P1	mimotope peptide P15g SEQ ID NO:11.			
XX					
KW	Epitope:	mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;			
KM	allergic disease; immunophylaxis; immunotherapy; anti-allergic;				
KW	immunosuppressive; vaccine; histamine release inhibitor; immunogen;				
XX	allergy; atopy.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200050460-A1.				
XX					
PD	31-AUG-2000.				
XX					
PF	22-FEB-2000;	2000WO-EP001455.			
XX					
PR	25-FEB-1999;	99GB-00004405.			
XX					
PR	29-MAR-1999;	99GB-00007151.			
XX					
PR	07-MAY-1999;	99GB-00010537.			
XX					
PR	07-MAY-1999;	99GB-00010538.			
XX					
PR	07-AUG-1999;	99GB-00018594.			
XX					
PR	07-AUG-1999;	99GB-00018603.			
XX					
PR	07-SEP-1999;	99GB-00021046.			
XX					
PR	07-SEP-1999;	99GB-00021047.			
XX					
PR	29-OCT-1999;	99GB-00025619.			
XX					
PR	23-NOV-1999;	99GB-00027698.			
XX					
PA	(SMIT ) SMITKLIN BECHAM BIOLOGICALS.				
XX	(PEPT-) PEPTIDE THERAPEUTICS LTD.				
PI	Dyeon M., Friede M., Greenwood J., Hewitt E., Lamont A., Mason S;				
XX	Randall R., Turnell WG., Van Mechelen MP., Vinals Y De BassolsC;				
XX					
DR	WPI: 2000-572073/53.				
XX					

```

pt domain from immunoglobulin E.
ps Claim 14, Page 9; 12pp; English.
cc The present invention describes a peptide (I) comprising an isolated
cc surface exposed group/epitope (E1) of C-epsilon-2 domain (D) of
cc immunoglobulin E (IgE), or its mimotope. Also described are: (1) an
cc immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)
cc for treating allergies comprising (II); (3) a ligand (IV) capable of
cc recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);
cc (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen
cc (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can
cc have anti-allergic and immunosuppressive activities, and can be used as a
cc vaccine and histamine release inhibitor. (I), (II) and (III) are useful
cc in medicine and in the manufacture of medicaments for treating and
cc preventing allergies. (IV) is useful for identifying mimotopes of p1, in
cc medicine and also in manufacturing medicaments for treating allergies.
cc (I) is useful in diagnostics and in the affinity purification of
cc circulating anti-IgE antibodies from blood. (I), (III) and PC are useful
cc for treating a patient susceptible to or suffering from allergies. (IV)
cc is also useful in diagnosing atopy. AAB5907 to AAB2609 represent
cc peptide sequences which are used in the exemplification of the present
cc invention
cc
sq Sequence 13 AA;
qy Query Match 61.4%; Score 51; DB 3; Length 13;
Db Best local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 EDGQVMDVDL 10
| | | | | | | |
3 EDGQVMDVDL 12
RESULT 5
AAB20872 standard; peptide; 13 AA.
AAC AAB20872;
DT 03-JAN-2001 (first entry)
DE Antiallergy peptide mimotope sequence SEQ ID NO:10.
XX
XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;
KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;
KM malaria; cytotoxic; antiallergic; nootropic; neuroprotective;
KN protozoacide; Alzheimer's disease; allergy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 13 /note= "amidated"
FT .
XX WO200050077-A1.
XX PN 31-AUG-2000.
XX PD 22-FEB-2000; 2000WO-EP001457.
XX PF 25-FEB-1999; 99GB-00004405.
XX PR 25-FEB-1999; 99GB-00004408.
XX PR 25-FEB-1999; 99GB-00004412.
XX PR 13-AUG-1999; 99GB-00019260.
XX
XX (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.
XX Coeste M, Lobet Y, Van-Mechelen MP, Veriest C;
XX WPI, 2000-572040/53.
XX
```

PT Immunogens and vaccine comprising the immunogen useful for preventing and  
PT treating infectious diseases e.g. malaria and chronic disease e.g.  
XX cancer, comprises peptide and carrier from protein D of influenzae.  
XX  
PS Claim 10; Page 38; 53pp; English.  
XX  
CC The present invention describes an immunogen (I) comprising a peptide  
CC (1a) and a carrier (1b) derived from protein D of Haemophilus influenzae  
CC or its fragment. Also described are: (1) a vaccine comprising (I), and an  
CC excipient; (2) preparation of (I), comprising conjugating a peptide to  
CC protein D or its fragment; and (3) preparation of a vaccine of (1),  
CC comprising formulating (I) with an excipient. (I) has cytostatic,  
CC antiallergic, neutrotropic, neuroprotective and protozoacide activities. (I)  
CC and the vaccine are useful for the manufacture of a medicament for  
CC preventing and treating infectious diseases such as malaria or chronic  
CC disease such as cancer, Alzheimer's disease or allergy in a patient.  
CC Unlike prior art immunogens, (I) induces high levels of antipeptide  
CC immune responses while inducing a moderate humoral response against the  
CC carrier. The present sequence represents a specifically claimed mimotope  
CC peptide sequence, which can be used in an immunogen of the present  
CC invention  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 61.4%; Score 51; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 EDGQVMDVDL 10  
Db 3 EDGQVMDVDL 12  
XX  
RESULT 6  
ID AAB51028 standard; peptide; 13 AA.  
XX  
AC AAB51028;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE IGE peptide #6.  
XX  
KM Vaccine; immunoglobulin E; IGE; anti-allergy.  
XX  
OS Mammalia.  
XX  
PN WO200074716-A2.  
XX  
PD 14-DEC-2000.  
XX  
PF 06-JUN-2000; 2000WO-EP005164.  
XX  
PR 08-JUN-1999; 99GB-00013327.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Prieels J;  
XX  
DR WPI; 2001-091150/10.  
XX  
PT New vaccine comprising allergy peptides linked by an inert carrier,  
PT useful for boosting an anti-allergy immune response in an individual  
PT susceptible to an allergic response.  
XX  
PS Claim 5; Page 20; 26pp; English.  
XX  
CC The present invention relates to a composition comprising allergy  
CC peptides linked by an inert carrier. The allergy peptides are derived  
CC from immunoglobulin E (IGE) or IGE receptor. The present peptide is one  
CC such peptide from IGE. The composition is useful as a vaccine or for  
CC manufacturing a medicament for the prophylaxis or treatment of allergy.  
CC In particular, for boosting an anti-allergy immune response in an

CC individual susceptible to an allergic response  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 61.4%; Score 51; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 EDGQVMDVDL 10  
Db 3 EDGQVMDVDL 12  
XX  
RESULT 7  
ID AAU16642 standard; peptide; 13 AA.  
XX  
AC AAU16642;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Peptide P15q derived as mimotope of Cepsilon2 region of human IGE.  
XX  
KM Human; linkage technology; conjugated compound; carrier vehicle; epitope;  
KM Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IGE mediated disease;  
KM antibody response.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN WO200145745-A2.  
XX  
PD 28-JUN-2001.  
XX  
PF 21-DEC-2000; 2000WO-GB004935.  
XX  
PR 21-DEC-1999; 99GB-00030233.  
XX  
PR 22-FEB-2000; 2000GB-00004096.  
XX  
PR 22-AUG-2000; 2000GB-00020707.  
XX  
PR 22-AUG-2000; 2000GB-00020708.  
XX  
PA (ACAM-) ACAM-BIS RES LTD.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Flinn N, Johnson T;  
XX  
DR WPI; 2001-521967/57.  
XX  
PT A linkage comprising an immunogenic conjugate useful treatment of IGE  
PT mediated diseases.  
XX  
PS Example 4; Page 21; 48pp; English.  
XX  
CC The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.  
CC macromolecules, polymers, dendrimers, proteins) to produce biological and  
CC immunological constructs. The invention provides a method for linking an  
CC epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a  
CC pharmaceutical composition or a vaccine. The invention describes peptides  
CC derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4  
CC regions of human immunoglobulin E (IGE) which are used to produce  
CC conjugated compounds. The compounds or compositions of the invention are  
CC useful in the manufacture of a medicament for the treatment of IGE  
CC mediated diseases. The invention allows for controlled conjugation of a  
CC peptide epitope (antigen) to a protein so as to form an immunogenic  
CC conjugate which may be able to raise a protective antibody response in an  
CC animal or human patient. AAU16632-AAU16913 represent peptides derived  
CC from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human  
CC IGE  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 61.4%; Score 51; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10  
DB 3 EDGQVMDVDL 12

## RESULT 8

AAU16639  
ID AAU16639 standard; peptide; 13 AA.

AC AAU16639;

DT 07-NOV-2001 (first entry)

DE Peptide P15 derived as mimotope of Cepsilon2 region of human IGE.

XX Human; linkage technology; conjugated compound; carrier vehicle; epitope;  
KW Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IGE mediated disease;  
KW antibody response.

OS Homo sapiens.

OS Synthetic.

PN MO200145745-A2.

PD 28-JUN-2001.

PF 21-DEC-2000; 2000WO-GB004935.

PR 21-DEC-1999; 99GB-00030233.

PR 22-FEB-2000; 2000GB-00004096.

PR 22-AUG-2000; 2000GB-00020707.

PR 22-AUG-2000; 2000GB-00020708.

PA (ACAM-) ACAMBIS RES LTD.

PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Flinn N, Johnson T;

DR WPI; 2001-521967/57.

PT A linkage comprising an immunogenic conjugate useful treatment of IGE  
mediated diseases.

PS Example 4; Page 21; 48pp; English.

CC The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.  
CC macromolecules, polymers, dendrimers, proteins) to produce biological and  
CC immunological constructs. The invention provides a method for linking an  
CC epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a  
CC pharmaceutical composition or a vaccine. The invention describes peptides  
CC derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4  
CC regions of human immunoglobulin E (IGE) which are used to produce  
CC conjugated compounds. The compounds or compositions of the invention are  
CC useful in the manufacture of a medicament for the treatment of IGE  
CC mediated diseases. The invention allows for controlled conjugation of a  
CC peptide epitope (antigen) to a protein so as to form an immunogenic  
CC conjugate which may be able to raise a protective antibody response in an  
CC animal or human patient. AAU16632-AAU16913 represent peptides derived  
CC from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human  
CC IGE  
CC  
CC

SQ Sequence 13 AA;

Query Match 61.4%; Score 51; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10  
DB 3 EDGQVMDVDL 12

DB 3 EDGQVMDVDL 12

## RESULT 9

AAU16641  
ID AAU16641 standard; peptide; 13 AA.

AC AAU16641;

DT 07-NOV-2001 (first entry)

DE Peptide P15P derived as mimotope of Cepsilon2 region of human IGE.

XX Human; linkage technology; conjugated compound; carrier vehicle; epitope;  
KW Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IGE mediated disease;  
KW antibody response.

OS Homo sapiens.

OS Synthetic.

PN MO200145745-A2.

PD 28-JUN-2001.

PF 21-DEC-2000; 2000WO-GB004935.

PR 21-DEC-1999; 99GB-00030233.

PR 22-FEB-2000; 2000GB-00004096.

PR 22-AUG-2000; 2000GB-00020707.

PR 22-AUG-2000; 2000GB-00020708.

PA (ACAM-) ACAMBIS RES LTD.

PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Flinn N, Johnson T;

DR WPI; 2001-521967/57.

PT A linkage comprising an immunogenic conjugate useful treatment of IGE  
mediated diseases.

PS Example 4; Page 21; 48pp; English.

CC The present invention relates to linkage methodology for use in the  
CC conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.  
CC macromolecules, polymers, dendrimers, proteins) to produce biological and  
CC immunological constructs. The invention provides a method for linking an  
CC epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a  
CC pharmaceutical composition or a vaccine. The invention describes peptides  
CC derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4  
CC regions of human immunoglobulin E (IGE) which are used to produce  
CC conjugated compounds. The compounds or compositions of the invention are  
CC useful in the manufacture of a medicament for the treatment of IGE  
CC mediated diseases. The invention allows for controlled conjugation of a  
CC peptide epitope (antigen) to a protein so as to form an immunogenic  
CC conjugate which may be able to raise a protective antibody response in an  
CC animal or human patient. AAU16632-AAU16913 represent peptides derived  
CC from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human  
CC IGE  
CC  
CC

SQ Sequence 13 AA;

Query Match 61.4%; Score 51; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10  
DB 3 EDGQVMDVDL 12

RESULT 10  
ABJ00312

ID ABJ00312 standard; peptide; 13 AA.  
XX  
AC ABJ00312;  
XX  
DT 02-SEP-2002 (first entry)  
XX  
DE Human IGE cyclic immunogenic peptide SEQ ID NO: 96.  
XX  
KM Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;  
KW vaccine; anti-allergic; cyclic.  
XX  
OS Homo sapiens.  
XX  
PN WO200216409-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-EP009576.  
XX  
PR 22-AUG-2000; 2000GB-00020717.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
PI Friede M, Mason S, Turnell WG, Vinals Y Baesolsc;  
XX WPI; 2002-489648/52.  
XX  
DR Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
PT  
XX  
PS Claim 4; Page 11; 45pp; English.  
XX  
CC The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a cyclic peptide immunogen derived  
CC from human immunoglobulin E (IGE) suitable for use in the invention  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 61.4%; Score 51; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQVMDVDL 10  
Db 3 EDGQVMDVDL 12  
XX  
RESULT 11  
ABJ00224  
ID ABJ00224 standard; peptide; 13 AA.  
XX  
AC ABJ00224;  
XX  
DT 02-SEP-2002 (first entry)  
XX  
DE Human IGE immunogenic peptide SEQ ID NO: 8.  
XX  
KM Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;  
KW vaccine; anti-allergic.  
XX  
OS Homo sapiens.  
XX  
PN WO200216409-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-EP009576.  
XX  
PR 22-AUG-2000; 2000GB-00020717.  
XX

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
PI Friede M, Mason S, Turnell WG, Vinals Y Baesolsc;  
XX WPI; 2002-489648/52.  
XX  
DR Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
PT  
XX  
PS Claim 4; Page 9; 45pp; English.  
XX  
CC The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IGE) suitable to be cyclised and used in the invention  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 61.4%; Score 51; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQVMDVDL 10  
Db 3 EDGQVMDVDL 12  
XX  
RESULT 12  
ABJ00226  
ID ABJ00226 standard; peptide; 13 AA.  
XX  
AC ABJ00226;  
XX  
DT 02-SEP-2002 (first entry)  
XX  
DE Human IGE immunogenic peptide SEQ ID NO: 10.  
XX  
KM Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;  
KW vaccine; anti-allergic.  
XX  
OS Homo sapiens.  
XX  
PN WO200216409-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 17-AUG-2001; 2001WO-EP009576.  
XX  
PR 22-AUG-2000; 2000GB-00020717.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
PI Friede M, Mason S, Turnell WG, Vinals Y Baesolsc;  
XX WPI; 2002-489648/52.  
XX  
DR Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.  
PT  
XX  
PS Claim 4; Page 9; 45pp; English.  
XX  
CC The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IGE) suitable to be cyclised and used in the invention  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 61.4%; Score 51; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDVDL 10  
| | | | | | | | | |  
DB 3 EDGQVMDVDL 12

## RESULT 13

ABJ00542  
ID ABJ00542 standard; peptide; 16 AA.

XX AC ABJ00542;

XX DT 02-SEP-2002 (first entry)

XX DE Human IGE cyclic immunogenic peptide SEQ ID NO: 326.

XX KW Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;  
XX RV vaccine; anti-allergic; cyclic.

XX OS Homo sapiens.

XX PN WO200216409-A2.

XX PD 28-FEB-2002.

XX PE 17-AUG-2001; 2001WO-EP009576.

XX PR 22-AUG-2000; 2000GB-00020717.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
(PEPT-) PEPTIDE THERAPEUTICS LTD.

XX P1 Friede M, Mason S, Turnell WG, Vinals Y BassolsC;

XX DR WPI; 2002-489648/52.

PT Conjugate for use in vaccine for treatment of allergy, comprises  
PT disulfide bridge cyclized peptide and immunogenic carrier.

XX PS Claim 4; Page 16; 45pp; English.

CC The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulfide bridge cyclized peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a cyclic peptide immunogen derived  
CC from human immunoglobulin E (IGE) suitable for use in the invention

XX SQ Sequence 16 AA;

Query Match 61.4%; Score 51; DB 5; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.081;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDVDL 10  
| | | | | | | | | |  
DB 3 EDGQVMDVDL 12

## RESULT 14

AAB25907  
ID AAB25907 standard; peptide; 9 AA.

XX AC AAB25907;

XX DT 05-JAN-2001 (first entry)

XX DE IGE C-epsilon-2 domain surface exposed epitope peptide P1 SEQ ID NO:1.

XX KW Epitope; mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;  
KW allergic disease; immunotherapy; anti-allergic;  
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;

KW allergy; atopy.

XX OS Homo sapiens.

XX PN WO200050460-A1.

XX PD 31-AUG-2000.

XX PF 22-FEB-2000; 2000WO-EP001455.

XX PR 25-FEB-1999; 99GB-00004405.

XX PR 29-MAR-1999; 99GB-00007151.

XX PR 07-MAY-1999; 99GB-00010537.

XX PR 07-MAY-1999; 99GB-00010538.

XX PR 07-AUG-1999; 99GB-00018594.

XX PR 07-AUG-1999; 99GB-00018603.

XX PR 07-SEP-1999; 99GB-00021046.

XX PR 07-SEP-1999; 99GB-00021047.

XX PR 29-OCT-1999; 99GB-00025619.

XX PR 23-NOV-1999; 99GB-00027698.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
(PEPT-) PEPTIDE THERAPEUTICS LTD.

XX P1 Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;  
Randal R, Turnell WG, Van Mechelen MP, Vinals Y De BassolsC;

XX DR WPI; 2000-572073/53.

XX PT Peptides useful for treating, preventing and ameliorating allergic  
XX diseases, comprising an isolated surface exposed group of a specific  
XX domain from immunoglobulin E.

XX PS Claim 2; Page 5; 129pp; English.

CC The present invention describes a peptide (I) comprising an isolated  
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of  
CC immunoglobulin E (IGE), or its mimotope. Also described are: (1) an  
CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)  
CC for treating allergies comprising (II); (3) a ligand (IV) capable of  
CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);  
CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen  
CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can  
CC have anti-allergic and immunosuppressive activities, and can be used as a  
CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful  
CC in medicine and in the manufacture of medicaments for treating and  
CC preventing allergies. (IV) is useful for identifying mimotopes of PI, in  
CC medicine and also in manufacturing medicaments for treating allergies.

CC (I) is useful in diagnostics and in the affinity purification of  
CC circulating anti-IGE antibodies from blood. (I), (II) and (III) are useful  
CC for treating a patient susceptible to or suffering from allergies. (IV)  
CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent  
CC peptide sequences which are used in the exemplification of the present  
XX invention

XX SQ Sequence 9 AA;

Query Match 56.6%; Score 47; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDVD 9  
| | | | | | | | | |  
DB 1 EDGQVMDVD 9

## RESULT 15

AAB20867  
ID AAB20867 standard; peptide; 9 AA.

XX AC AAB20867;

XX DT 03-JAN-2001 (first entry)

```

XX Immunoglobulin E epitope immunogenic peptide SEQ ID NO:5.
DE
XX
XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;
KM prostate cancer; Haemophilus influenzae; vaccine; infectious disease;
KM malaria; cytostatic; antiallergic; neurotropic; neuroprotective;
KM protozoacide; Alzheimer's disease; allergy.
XX
XX Homo sapiens.
OS
XX WO200050077-A1.
PN
XX
XX 31-AUG-2000.
PD
XX
XX 22-FEB-2000; 2000WO-EP001457.
PF
XX
XX 25-FEB-1999; 99GB-00004405.
PR 25-FEB-1999; 99GB-00004408.
PR 25-FEB-1999; 99GB-00004412.
PR 13-AUG-1999; 99GB-00019260.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Coeste M, Lobet Y, Van-Mechelen MP, Verriest C;
PI
XX WPI; 2000-572040/53.
XX
XX Immunogens and vaccine comprising the immunogen useful for preventing and
PT treating infectious diseases e.g. malaria and chronic disease e.g.
XX cancer, comprises peptide and carrier from protein D of influenzae.
XX
XX Claim 9; Page 37; 53pp; English.
PS
XX
XX The present invention describes an immunogen (I) comprising a peptide
CC (Ia) and a carrier (Ib) derived from protein D of Haemophilus influenzae
CC or its fragment. Also described are: (1) a vaccine comprising (I) and an
CC excipient; (2) preparation of (I), comprising conjugating a peptide to
CC protein D or its fragment; and (3) preparation of a vaccine of (I),
CC comprising formulating (I) with an excipient. (I) has cytostatic,
CC antiallergic, neurotropic, neuroprotective and protozoacide activities. (I)
CC and the vaccine are useful for the manufacture of a medicament for
CC preventing and treating infectious diseases such as malaria or chronic
CC disease such as cancer, Alzheimer's disease or allergy in a patient.
CC Unlike prior art immunogens, (I) induces high levels of antipeptide
CC immune responses while inducing a moderate humoral response against the
CC carrier. The present sequence represents a specifically claimed
CC immunoglobulin E (IgE) epitope immunogenic peptide sequence, which can be
CC used in an immunogen of the present invention
XX
XX
SQ Sequence 9 AA;

```

```

Query Match          56.6%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EDGQVMDVD 9
   |||||
Db 1 EDGQVMDVD 9

```

Search completed: December 12, 2005, 22:08:38  
 Job time : 182 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:24:05 / Search time 45 Seconds  
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Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDQGVMDVLDLSTATTQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

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Minimum DB seq length: 0  
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Maximum Match 100%  
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3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/BCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	33.8	14	2	US-08-526-136-25	Sequence 25, Appl
2	28	33.7	7	US-09-842-164A-12	Sequence 12, Appl
3	28	33.7	10	US-08-447-411-46	Sequence 46, Appl
4	28	33.7	10	US-08-662-227-3	Sequence 3, Appl
5	28	33.7	10	US-09-017-947-3	Sequence 3, Appl
6	28	33.7	10	US-09-925-442-3	Sequence 3, Appl
7	28	33.7	13	US-08-162-081B-13	Sequence 13, Appl
8	28	33.7	13	US-08-780-872-13	Sequence 13, Appl
9	28	33.7	13	US-09-085-957-13	Sequence 13, Appl
10	28	33.7	16	PCT-US91-02942-91	Sequence 91, Appl
11	27	32.5	10	US-08-724-548-28	Sequence 28, Appl
12	27	32.5	10	US-07-978-674B-28	Sequence 28, Appl
13	27	32.5	12	US-09-238-448-8	Sequence 8, Appl
14	27	32.5	14	US-09-010-317-60	Sequence 60, Appl
15	27	32.5	15	US-08-906-769-179	Sequence 179, App
16	27	32.5	15	US-08-906-616-179	Sequence 179, App
17	27	32.5	15	US-08-639-075A-179	Sequence 179, App
18	27	32.5	15	US-09-004-731-68	Sequence 68, Appl
19	27	32.5	15	US-09-012-431-179	Sequence 179, App
20	27	32.5	15	US-08-749-699-68	Sequence 68, Appl
21	27	32.5	15	US-09-012-692-179	Sequence 179, App
22	27	32.5	15	US-08-906-613-179	Sequence 68, Appl
23	27	32.5	15	US-09-004-729-68	Sequence 68, Appl
24	27	32.5	15	US-09-071-252-33	Sequence 33, Appl
25	26	31.3	10	US-09-010-317-73	Sequence 73, Appl
26	26	31.3	10	US-09-010-317-74	Sequence 74, Appl
27	26	31.3	12	US-08-617-929-32	Sequence 32, Appl

28	26	31.3	14	1	US-08-617-929-31	Sequence 31, Appl
29	26	31.3	14	2	US-09-010-317-103	Sequence 103, App
30	26	31.3	15	1	US-08-528-057-18	Sequence 18, Appl
31	26	31.3	16	1	US-08-845-926-20	Sequence 20, Appl
32	26	31.3	16	2	US-09-351-286-20	Sequence 20, Appl
33	26	31.3	17	2	US-10-394-980-72	Sequence 72, Appl
34	25	30.1	9	2	US-09-743-467-11	Sequence 11, Appl
35	25	30.1	10	2	US-08-724-548-29	Sequence 29, Appl
36	25	30.1	10	2	US-07-978-674B-29	Sequence 29, Appl
37	25	30.1	10	2	US-09-743-467-12	Sequence 12, Appl
38	25	30.1	13	1	US-08-463-115-102	Sequence 102, App
39	25	30.1	13	1	US-08-465-388-102	Sequence 102, App
40	25	30.1	14	1	US-08-480-793-1	Sequence 1, Appl
41	25	30.1	14	4	PCT-US92-05825A-1	Sequence 1, Appl
42	25	30.1	15	2	US-08-912-560-3	Sequence 3, Appl
43	25	30.1	16	2	US-09-914-831-9	Sequence 9, Appl
44	24	28.9	10	1	US-08-198-962-4	Sequence 4, Appl
45	24	28.9	10	1	US-08-682-412B-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-526-136-25  
; Sequence 25, Application US/08526136  
; Patent No. 6107089  
; GENERAL INFORMATION:  
; APPLICANT: Towle, Christine A. et al.  
; TITLE OF INVENTION: ANNEXIN XI  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/526,136  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/214,036  
; FILING DATE:  
; APPLICATION NUMBER: 07/837,775  
; FILING DATE: February 13, 1992  
; APPLICATION NUMBER: 07/764,465  
; FILING DATE: September 23, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/099001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14  
; TYPE: amino acid  
; STRANDEDNESS: N/A  
; TOPOLOGY: N/A  
; US-08-526-136-25  
  
Query Match 39.8%; Score 33; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 24;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQWMDVDL 10  
| | | : | : |  
Db 1 EDGSDVIDYEL 10

## RESULT 2

US-09-842-164A-12  
; Sequence 12, Application US/09842164A  
; Patent No. 6544754  
; GENERAL INFORMATION:  
; APPLICANT: INOUE, SATOSHI  
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN  
; FILE REFERENCE: 206497US0  
; CURRENT APPLICATION NUMBER: US/09/842,164A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: JP 2000-125053  
; PRIOR FILING DATE: 2000-04-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Oplophorus graciliorostriis  
US-09-842-164A-12

Query Match 33.7%; Score 28; DB 2; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQWMDVD 9  
| | | : | : |  
Db 1 GDVMDMD 7

## RESULT 3

US-08-447-411-46  
; Sequence 46, Application US/08447411  
; Patent No. 5773243  
; GENERAL INFORMATION:  
; APPLICANT: FRITZINGER, DAVID C.  
; APPLICANT: BREDEHORST, REINHARD  
; APPLICANT: VOGEL, CARL-WILHELM  
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,411  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/043,747  
; FILING DATE: 07-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5773243man F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-101-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-447-411-46

Query Match 33.7%; Score 28; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQWMDVDL 10  
| | | : | : |  
Db 1 EDGFIADSDI 10

## RESULT 4

US-08-662-227-3  
; Sequence 3, Application US/08662227  
; Patent No. 5922320  
; GENERAL INFORMATION:  
; APPLICANT: VOGEL, CARL-WILHELM  
; APPLICANT: BREDEHORST, REINHORST  
; APPLICANT: KOCK, MICHAEL  
; APPLICANT: FRITZINGER, DAVID  
; TITLE OF INVENTION: RECOMBINANT PROCVF  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESS: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/662,227  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 1126-0107-0X  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-662-227-3

Query Match 33.7%; Score 28; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQWMDVDL 10  
| | | : | : |  
Db 1 EDGFIADSDI 10

## RESULT 5

US-09-017-947-3  
; Sequence 3, Application US/09017947



Patent No. 6303754  
GENERAL INFORMATION:  
APPLICANT: VOGEL, CARL-WILHELM  
APPLICANT: BREDEHORST, REINHORST  
APPLICANT: KOCK, MICHAEL  
APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCVF  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,947  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/662,227  
FILING DATE: 14-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-017-947-3

Query Match 33.7%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10  
|||:|:  
Db 1 EDGFADSIDI 10

RESULT 6  
US-09-925-442-3  
Sequence 3, Application US/0925442  
Patent No. 6607897  
GENERAL INFORMATION:  
APPLICANT: VOGEL, CARL-WILHELM  
APPLICANT: BREDEHORST, REINHORST  
APPLICANT: KOCK, MICHAEL  
APPLICANT: FRITZINGER, DAVID  
TITLE OF INVENTION: RECOMBINANT PROCVF  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/925,442  
FILING DATE: 10-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/017,947  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-0107-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-925-442-3

Query Match 33.7%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10  
|||:|:  
Db 1 EDGFADSIDI 10

RESULT 7  
US-08-162-081B-13  
Sequence 13, Application US/08162081B  
Patent No. 5824492  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayiotu, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-162-081B-13

Query Match 33.7%; Score 28; DB 1; Length 13;  
Best Local Similarity 44.4%; Pred. No. 1.6e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDGQVMDVD 9  
:||||: :|  
Db 1 DDGQLPHID 9

RESULT 8  
US-08-780-872-13  
Sequence 13, Application US/08780872  
Patent No. 5846824  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Orsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-780-872-13

Qy 1 EDGQVMDVD 9  
:||||: :|  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 DDGQLPHID 9

RESULT 9  
US-09-085-957-13  
Sequence 13, Application US/09085957  
Patent No. 6274327  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Orsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,957  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/780,872  
FILING DATE: 09-JAN-1997  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-085-957-13

Query Match 33.7%; Score 28; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 1.6e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDGQVMDVD 9  
:||||: :|  
Db 1 DDGQLPHID 9

RESULT 10  
PCT-US91-02942-91  
Sequence 91, Application PC/TUS9102942  
GENERAL INFORMATION:  
APPLICANT: ROTHLEIN, ROBERT  
APPLICANT: ADAIR, JOHN R  
APPLICANT: ATHWAL, DILJEET S  
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Keseler, Goldstein & Fox

STREET: 1225 Connecticut Ave. NW Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02942  
FILING DATE: 19910429  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9009549.8  
FILING DATE: 27-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: FOX, SAM L  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 1011.0586600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 466-0800  
TELEFAX: (202) 833-8716  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US91-02942-91

Query Match 33.7%; Score 28; DB 4; Length 16;  
Best Local Similarity 53.8%; Pred. No. 2e+02;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQVMDVLDLAST 15  
Db 2 GCGTIVTVSSAST 14

RESULT 11  
US-08-724-548-28  
Sequence 28, Application US/08724548  
Patent No. 5830637  
GENERAL INFORMATION:  
APPLICANT: Frank, Ronald  
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR  
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joseph T. Eisele  
ADDRESSEE: Kane, Daisimer, Sullivan, Kurucz,  
ADDRESSEE: Levy, Eisele and Richard  
STREET: 711 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-4059  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" DISKETTE  
COMPUTER: IBM-XT COMPATIBLE  
OPERATING SYSTEM: DOS 3.3:  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,548  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/978,674  
FILING DATE: 03/22/93  
ATTORNEY/AGENT INFORMATION:  
NAME: EISELE, JOSEPH T.  
REGISTRATION NUMBER: 25,331  
REFERENCE/DOCKET NUMBER: 2727-68 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 687-6000  
TELEFAX: (212) 682-3485  
TELEX: (212) 426767  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE: Internal fragment  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
US-08-724-548-28

Query Match 32.5%; Score 27; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EDGQVMDVDL 10  
Db 1 DDGPGLDXDL 10

RESULT 12  
US-07-978-674B-28  
Sequence 28, Application US/07978674B  
Patent No. 6040423  
GENERAL INFORMATION:  
APPLICANT: Frank, Ronald  
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF  
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR  
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL  
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND  
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joseph T. Eisele  
ADDRESSEE: Kane, Daisimer, Sullivan, Kurucz,  
ADDRESSEE: Levy, Eisele and Richard  
STREET: 711 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-4059  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" DISKETTE  
COMPUTER: IBM-XT COMPATIBLE  
OPERATING SYSTEM: DOS 3.3:  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/978,674B  
FILING DATE:  
CLASSIFICATION:

```

: FILING DATE: 03/22/93
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: EISELE, JOSEPH T.
: REGISTRATION NUMBER: 25,331
: REFERENCE/DOCKET NUMBER: 2727-68 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 687-6000
: TELEFAX: (212) 682-3485
: TELEX: (212) 426767
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 residues
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: Peptide
: HYPOTHEetical:
: ANTI-SENSE:
: FRAGMENT TYPE: internal fragment
: ORIGINAL SOURCE:
: ORGANISM:
: STRAIN:
: INDIVIDUAL ISOLATE:
: DEVELOPMENTAL STAGE:
: HAPLOTYPE:
: TISSUE TYPE:
: CELL LINE:
: ORGANELLE:
: IMMEDIATE SOURCE:
: US-07-978-674B-28

Query Match      32.5%; Score 27; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLD 10
Db      1 DDGPGLDXDL 10

RESULT 13
US-09-238-448-8
: Sequence 8, Application US/09238448
: Patent No. 6238925
: GENERAL INFORMATION:
: APPLICANT: Sampson, Hugh A.
: TITLE OF INVENTION: Method for Determining Likelihood of Developing
: FILE REFERENCE: HS 100
: CURRENT APPLICATION NUMBER: US/09/238,448
: CURRENT FILING DATE: 1999-01-28
: EARLIER APPLICATION NUMBER: 60/073,171
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 8
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-238-448-8

Query Match      32.5%; Score 27; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVM 6
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Db      5 EDGRVM 10

RESULT 14
US-09-010-317-60
: Sequence 60, Application US/09010317
: Patent No. 6685943
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
: APPLICANT: Patti, Joseph M.
: APPLICANT: House-Pompeo, Karen L.
: APPLICANT: Speziale, Pietro
: APPLICANT: John, Danny
: APPLICANT: McGavin, Martin J.
: TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/010,317
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/036,139
: FILING DATE: 21-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: TAMK.189
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-418-3000
: TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 60:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
US-09-010-317-60

Query Match      32.5%; Score 27; DB 2; Length 14;
Best Local Similarity 25.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDLST 12
Db      1 QGQNVLDIDFDS 12

RESULT 15
US-08-906-769-179
: Sequence 179, Application US/08906769
: Patent No. 6077687
: GENERAL INFORMATION:
: APPLICANT: Grieve, Robert B.
: APPLICANT: Rushlow, Keith E.
: APPLICANT: Wu Hunter, Shirley
: APPLICANT: Frank, Glenn R.
: APPLICANT: Stiegler, Gary
: APPLICANT: Gaines, Patrick J.
: APPLICANT: Silver, Gary
```

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID  
TITLE OF INVENTION: MOLECULES AND USES THEREOF  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McInloch  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,769  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/639,075  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-25-C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 179:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-906-769-179

Query Match 32.5%; Score 27; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVDLIST 12  
| | | | |  
| | | | |  
Db 6 DVDIST 11

Search completed: December 12, 2005, 21:52:52  
Job time : 46 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:46:41 ; Search time 159 Seconds

(without alignments)  
44.674 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83

Sequence: 1 EDGQVMDVLDLSTASTTQ 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 345637

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA Main:

1: /cgn2\_6/ptodata1/pubpaa/US07\_PUBSCOMB.pep.\*

2: /cgn2\_6/ptodata1/pubpaa/US08\_PUBSCOMB.pep.\*

3: /cgn2\_6/ptodata1/pubpaa/US09\_PUBSCOMB.pep.\*

4: /cgn2\_6/ptodata1/pubpaa/US10\_PUBSCOMB.pep.\*

5: /cgn2\_6/ptodata1/pubpaa/US10B\_PUBSCOMB.pep.\*

6: /cgn2\_6/ptodata1/pubpaa/US11\_PUBSCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	US-10-758-165-16	Sequence 16, Appl
2	51	61.4	13	US-10-362-527-8	Sequence 8, Appl
3	51	61.4	13	US-10-362-527-10	Sequence 10, Appl
4	51	61.4	13	US-10-362-527-96	Sequence 96, Appl
5	51	61.4	13	US-11-005-794-8	Sequence 8, Appl
6	51	61.4	13	US-11-005-794-10	Sequence 10, Appl
7	51	61.4	13	US-11-005-794-11	Sequence 11, Appl
8	51	61.4	16	US-10-362-527-326	Sequence 326, App
9	47	56.6	9	US-10-082-014-273	Sequence 273, App
10	47	56.6	9	US-10-372-076-127	Sequence 127, App
11	47	56.6	9	US-10-362-527-1	Sequence 1, Appl
12	47	56.6	9	US-10-732-862A-141	Sequence 141, App
13	47	56.6	9	US-10-677-074-127	Sequence 127, Appl
14	47	56.6	9	US-11-005-794-1	Sequence 1, Appl
15	47	56.6	10	US-10-144-188-60	Sequence 60, Appl
16	47	56.6	10	US-10-082-014-282	Sequence 282, App
17	47	56.6	10	US-10-372-076-136	Sequence 136, App
18	47	56.6	10	US-10-362-527-12	Sequence 12, App
19	47	56.6	10	US-10-732-862A-150	Sequence 150, App
20	47	56.6	10	US-10-677-074-136	Sequence 136, App
21	47	56.6	10	US-11-005-794-23	Sequence 23, Appl
22	47	56.6	14	US-10-362-527-324	Sequence 324, App
23	41	49.4	10	US-10-144-188-55	Sequence 55, Appl
24	37	46.6	13	US-10-362-527-325	Sequence 325, App
25	34	41.0	7	US-10-362-527-11	Sequence 11, Appl
26	34	41.0	7	US-11-005-794-17	Sequence 17, Appl
27	33	39.8	17	US-09-988-493-175	Sequence 175, App

28	33	39.8	17	4	US-10-014-340-12	Sequence 12, Appl
29	33	39.8	17	4	US-10-014-340-500	Sequence 500, App
30	33	39.8	17	4	US-10-700-340-4	Sequence 4, Appl
31	33	39.8	17	5	US-10-652-779-62	Sequence 62, Appl
32	31	37.3	14	4	US-10-308-128-112	Sequence 112, App
33	29	34.9	10	3	US-09-572-270A-1084	Sequence 1084, App
34	29	34.9	10	3	US-09-572-270A-1086	Sequence 1086, App
35	29	34.9	11	4	US-10-362-527-49	Sequence 49, Appl
36	29	34.9	11	6	US-11-005-794-104	Sequence 104, Appl
37	29	34.9	14	4	US-10-137-867-36	Sequence 36, Appl
38	29	34.9	14	4	US-10-308-128-147	Sequence 147, App
39	29	34.9	16	3	US-09-791-378-101	Sequence 101, App
40	29	34.9	16	3	US-09-791-378-326	Sequence 326, App
41	29	34.9	16	3	US-09-826-290-230	Sequence 230, App
42	29	34.9	16	3	US-09-826-290-341	Sequence 341, App
43	29	34.9	16	3	US-09-826-290-398	Sequence 398, App
44	29	34.9	16	3	US-09-791-393-48	Sequence 48, Appl
45	29	34.9	16	3	US-09-791-389-48	Sequence 48, Appl

#### ALIGNMENTS

```
RESULT 1
US-10-758-165-16
; Sequence 16, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440.472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-758-165-16

Query Match      100.0%; Score 83; DB 5; Length 17;
Beer Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVLDLSTASTTQ 17
        |||||
DB      1 EDGQVMDVLDLSTASTTQ 17

RESULT 2
US-10-362-527-8
; Sequence 8, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y De Bassols, Carleota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362.527
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
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; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-8

Query Match          61.4%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 3
US-10-362-527-10
; Sequence 10, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-10

Query Match          61.4%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 4
US-10-362-527-96
; Sequence 96, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IGF peptide
US-10-362-527-96

Query Match          61.4%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 5
US-11-005-794-8
; Sequence 8, Application US/11005794
; Publication No. US20050214285A1
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judithly
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mason, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paullette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-2 Domain of IGF, Antagonists Thereof, and Their
; TITLE OF INVENTION: Therapeutic Uses
; FILE REFERENCE: B45172
; CURRENT APPLICATION NUMBER: US/11/005,794
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/914,088
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9907151.6
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9910537.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9910538.9
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9918594.4
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918603.3
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-11-005-794-8

Query Match          61.4%; Score 51; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 6
US-11-005-794-10
; Sequence 10, Application US/11005794
; Publication No. US20050214285A1
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
```



```

; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judithy
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mason, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paulette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-2 Domain of IGF, Antagonists Thereof, and Their
; TITLE OF INVENTION: Therapeutic Uses
; FILE REFERENCE: B45172
; CURRENT APPLICATION NUMBER: US/11/005,794
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/914,088
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9907151.6
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9910537.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9910538.9
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9918594.4
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918603.3
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-11-005-794-10

Query Match      61.4%; Score 51; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDL 10
Db      3 EDGQVMDVDL 12

RESULT 7
US-11-005-794-11
; Sequence 11, Application US/11005794
; Publication No. US20050214285A1
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judithy
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mason, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paulette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-2 Domain of IGF, Antagonists Thereof, and Their
; FILE REFERENCE: B45172
; CURRENT APPLICATION NUMBER: US/11/005,794
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/914,088
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
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; PRIOR APPLICATION NUMBER: GB 9907151.6
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9910537.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9910538.9
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9918594.4
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918603.3
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-11-005-794-11

Query Match      61.4%; Score 51; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDL 10
Db      3 EDGQVMDVDL 12

RESULT 8
US-10-362-527-326
; Sequence 326, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IGF peptide
US-10-362-527-326

Query Match      61.4%; Score 51; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDL 10
Db      3 EDGQVMDVDL 12

RESULT 9
US-10-082-014-273
; Sequence 273, Application US/10082014
; Publication No. US20030185858A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
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FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 273
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-014-273

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 10
US-10-372-076-127
; Sequence 127, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Mark
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 127
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-076-127

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 11
US-10-362-527-1
; Sequence 1, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y De Bassols, Carloia
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
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NUMBER OF SEQ ID NOS: 328
; SOFTWARE: PassSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-1

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 12
US-10-732-862A-141
; Sequence 141, Application US/10732862A
; Publication No. US20040146524A1
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: Lyons, Katelynne J.
; APPLICANT: Jay, Haron J.
; TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICC-136.0 (4564-88881)
; CURRENT APPLICATION NUMBER: US/10/732,862A
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,123
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 141
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-862A-141

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 13
US-10-677-074-127
; Sequence 127, Application US/10677074
; Publication No. US20040156863A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Mark
; APPLICANT: Schmidt, Annette Elisabeth
; APPLICANT: Scober, Detlef
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/677,074
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 10/372,076
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
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;; PRIOR FILING DATE: 2002-02-22  
;; NUMBER OF SEQ ID NOS: 308  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 127  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-677-074-127

Query Match                    56.6%;    Score 47;    DB 4;    Length 9;  
Best Local Similarity    100.0%;    Pred. No. 1.7e+06;  
Matches    9;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

OY                    1 EDGQVMDVD 9  
                     |||||  
Db                    1 EDGQVMDVD 9

RESULT 14  
US-11-005-794-1  
;; Sequence 1, Application US/11005794  
;; Publication No. US20050214285A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dyson, Michael  
;; APPLICANT: Friede, Martin  
;; APPLICANT: Greenwood, Judith  
;; APPLICANT: Hewitt, Ellen  
;; APPLICANT: Lamont, Alan  
;; APPLICANT: Mason, Sean  
;; APPLICANT: Randall, Roger  
;; APPLICANT: Turnell, William Gordon  
;; APPLICANT: Van Mechelen, Marcelle Paulette  
;; APPLICANT: Vinals y de Bassols, Carlota  
TITLE OF INVENTION: Epitopes or Mimotopes Derived from the  
TITLE OF INVENTION: C-Epsilon-2 Domain of Ige, Antagonists Thereof, and Their  
FILE REFERENCE: B45172  
CURRENT APPLICATION NUMBER: US/11/005,794  
CURRENT FILING DATE: 2004-12-07  
PRIOR APPLICATION NUMBER: US/09/914,088  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: GB 9904405.9  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: GB 9907151.6  
PRIOR FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: GB 9910537.1  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: GB 9910538.9  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: GB 9918594.4  
PRIOR FILING DATE: 1999-08-07  
PRIOR APPLICATION NUMBER: GB 9918603.3  
NUMBER OF SEQ ID NOS: 193  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimeric  
US-11-005-794-1

Query Match                    56.6%;    Score 47;    DB 6;    Length 9;  
Best Local Similarity    100.0%;    Pred. No. 1.7e+06;  
Matches    9;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

OY                    1 EDGQVMDVD 9  
                     |||||  
Db                    1 EDGQVMDVD 9

RESULT 15

US-10-144-188-60  
;; Sequence 60, Application US/10144188  
;; Publication No. US20030170212A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Cai, Zeling  
;; APPLICANT: Jackson, Michael R.  
;; APPLICANT: Peterson, Per A.  
;; APPLICANT: Shi, Weixing  
;; APPLICANT: Kong, Yan  
;; APPLICANT: Degraw, Juli  
TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specific  
TITLE OF INVENTION: For No. US20030170212A1-Tumor Antigens To Treat Autoimmune And A  
FILE REFERENCE: PRI0010 ORT-1627  
CURRENT APPLICATION NUMBER: US/10/144,188  
CURRENT FILING DATE: 2002-05-13  
PRIOR APPLICATION NUMBER: 60/291,300  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 60  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide antigen  
US-10-144-188-60

Query Match                    56.6%;    Score 47;    DB 4;    Length 10;  
Best Local Similarity    100.0%;    Pred. No. 0.27;  
Matches    10;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

OY                    4 QVMDVLDSTA 13  
                     |||||  
Db                    1 QVMDVLDSTA 10

Search completed: December 12, 2005, 22:05:13  
Job time : 160 secs

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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:52:16 ; Search time 11 Seconds  
(without alignments)  
8.630 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83

Sequence: 1 EDGQWMDVLDLSTATTQ 17

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 9353

Minimum DB seq length: 0  
Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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8: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	27.7	9	7	US-11-010-748A-423
2	23	27.7	9	7	US-11-010-748A-424
3	23	27.7	9	7	US-11-010-748A-429
4	23	27.7	9	7	US-11-010-748A-435
5	23	27.7	9	7	US-11-010-748A-436
6	23	27.7	9	7	US-11-010-748A-440
7	23	27.7	9	7	US-11-097-864-475
8	23	27.7	9	7	US-11-097-912-475
9	23	27.7	15	7	US-11-106-932-134
10	23	27.7	15	7	US-11-106-932-134
11	23	27.7	17	7	US-11-010-748A-418
12	23	27.7	17	7	US-11-010-748A-430
13	23	27.7	17	7	US-11-119-249-8
14	22	26.5	12	7	US-11-084-554-4
15	22	26.5	12	6	US-10-986-501-287
16	22	26.5	13	6	US-10-511-559-1068
17	22	26.5	13	6	US-10-511-559-1069
18	22	26.5	14	6	US-10-467-657-8761
19	22	26.5	15	6	US-10-467-657-8749
20	22	26.5	17	7	US-11-011-666-7
21	21	25.3	9	7	US-11-010-748A-891
22	21	25.3	9	7	US-11-010-748A-895
23	21	25.3	9	7	US-11-010-748A-897
24	21	25.3	9	7	US-11-010-748A-901
25	21	25.3	9	7	US-11-010-748A-904

26	21	25.3	9	7	US-11-097-864-482	Sequence 482, App
27	21	25.3	9	7	US-11-097-912-482	Sequence 482, App
28	21	25.3	10	7	US-11-054-515-3180	Sequence 3180, Ap
29	21	25.3	15	7	US-11-054-515-3083	Sequence 3083, Ap
30	21	25.3	16	7	US-11-089-764-69	Sequence 69, Appl
31	21	25.3	17	7	US-11-010-748A-890	Sequence 890, Appl
32	20	24.1	9	7	US-11-097-864-454	Sequence 454, App
33	20	24.1	9	7	US-11-097-864-569	Sequence 569, App
34	20	24.1	9	7	US-11-097-912-454	Sequence 454, App
35	20	24.1	9	7	US-11-097-912-569	Sequence 569, App
36	20	24.1	10	7	US-11-097-864-502	Sequence 502, App
37	20	24.1	10	7	US-11-097-864-510	Sequence 510, App
38	20	24.1	10	7	US-11-097-864-613	Sequence 613, App
39	20	24.1	10	7	US-11-097-912-502	Sequence 502, App
40	20	24.1	10	7	US-11-097-912-540	Sequence 540, App
41	20	24.1	10	7	US-11-097-912-613	Sequence 613, App
42	20	24.1	11	7	US-11-054-515-3177	Sequence 3177, Ap
43	20	24.1	12	6	US-10-467-657-8948	Sequence 8948, Ap
44	20	24.1	13	6	US-10-511-559-813	Sequence 813, App
45	20	24.1	13	6	US-10-511-559-886	Sequence 886, App

#### ALIGNMENTS

RESULT 1  
US-11-010-748A-423  
; Sequence 423, Application US/11010748A  
; Publication No. US20050244421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: MOIL, Heidrun  
; APPLICANT: SCHARM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 423  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 418  
US-11-010-748A-423  
Query Match 27.7% ; Score 23 ; DB 7 ; Length 9 ;  
Best Local Similarity 66.7% ; Pred. No. 2.8e+04 ;  
Matches 4 ; Conservative 1 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;  
QY 1 EDGQW 6  
Db 2 EDGNVL 7  
RESULT 2  
US-11-010-748A-424  
; Sequence 424, Application US/11010748A  
; Publication No. US20050244421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: MOIL, Heidrun  
; APPLICANT: SCHARM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A

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; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 418
US-11-010-748A-424

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 3
US-11-010-748A-429
; Sequence 429, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 418
US-11-010-748A-429

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 4
US-11-010-748A-435
; Sequence 435, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
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; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 435
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 430
US-11-010-748A-435

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 5
US-11-010-748A-436
; Sequence 436, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 436
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 430
US-11-010-748A-436

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 6
US-11-010-748A-440
; Sequence 440, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
```

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; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 440
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 430
US-11-010-748A-440
```

```
Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 EDGOVM 6
         |||:|
Db      2 EDGNVL 7
```

```
RESULT 7
; Sequence 475, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 475
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-475
```

```
Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      4 QVMDVLDST 12
         :|||:|
Db      1 RVRDVELLT 9
```

```
RESULT 8
US-11-097-912-475
; Sequence 475, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
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; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 475
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-475
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Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      4 QVMDVLDST 12
         :|||:|
Db      1 RVRDVELLT 9
```

```
RESULT 9
US-11-106-932-50
; Sequence 50, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; PRIOR FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-106-932-50
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```
Query Match      27.7%; Score 23; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      7 DVDLSTAS 14
         |||:|
Db      7 DTDSTKTS 14
```

```
RESULT 10
US-11-106-932-134
; Sequence 134, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; PRIOR FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 15
; TYPE: PRT
```

ORGANISM: Homo sapiens  
US-11-106-932-134

Query Match 27.7%; Score 23; DB 7; Length 15;  
Best Local Similarity 50.0%; Pred. No. 74;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DQGVMDVD 9  
|||:  
Db 7 DGERVDFD 14

RESULT 11  
US-11-010-748A-418

Sequence 418, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:

APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang

APPLICANT: MOLL, Heidrun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE

FILE REFERENCE: MER-136

CURRENT APPLICATION NUMBER: US/11/010,748A

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/EP03/06251

PRIOR FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: EP02013423.5

PRIOR FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 926

SOFTWARE: PatentIn version 3.1

SEQ ID NO 418

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: CD64 peptide fragment

US-11-010-748A-418

Query Match 27.7%; Score 23; DB 7; Length 17;  
Best Local Similarity 66.7%; Pred. No. 86;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQGVV 6  
|||:  
Db 2 EDGNVL 7

RESULT 12  
US-11-010-748A-430

Sequence 430, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:

APPLICANT: Merck Patent GmbH

APPLICANT: STRITTMAYER, Wolfgang

APPLICANT: MOLL, Heidrun

APPLICANT: SCHARR, Burkhard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE

FILE REFERENCE: MER-136

CURRENT APPLICATION NUMBER: US/11/010,748A

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/EP03/06251

PRIOR FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: EP02013423.5

PRIOR FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 926

SOFTWARE: PatentIn version 3.1

SEQ ID NO 430

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: CD64 peptide fragment

US-11-010-748A-430

Query Match 27.7%; Score 23; DB 7; Length 17;  
Best Local Similarity 66.7%; Pred. No. 86;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQGVV 6  
|||:  
Db 2 EDGNVL 7

RESULT 13  
US-11-119-249-8

Sequence 8, Application US/11119249  
Publication No. US20050261190A1  
GENERAL INFORMATION:

APPLICANT: SK Corp.

APPLICANT: Ewha Womans University

APPLICANT: LEE, Kong-Joo

APPLICANT: KIM, Hee-Jung

APPLICANT: CHO, Jeong Woo

APPLICANT: KIM, Eunhee

APPLICANT: SONG, Eun Joo

APPLICANT: MAENG, Cheol Young

TITLE OF INVENTION: PAS ASSOCIATED FACTOR 1

FILE REFERENCE: 12120-02USA

CURRENT APPLICATION NUMBER: US/11/119,249

CURRENT FILING DATE: 2005-04-29

PRIOR APPLICATION NUMBER: US 60/566,966

PRIOR FILING DATE: 2004-04-29

PRIOR APPLICATION NUMBER: US 60/590,327

PRIOR FILING DATE: 2004-07-21

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.3

SEQ ID NO 8

LENGTH: 17

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE: OTHER INFORMATION: Protein spots

US-11-119-249-8

Query Match 27.7%; Score 23; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DLSTA 13  
|||:  
Db 10 DLSTA 14

RESULT 14  
US-11-084-554-4

Sequence 4, Application US/11084554  
Publication No. US20050260679A1  
GENERAL INFORMATION:

APPLICANT: Kellermann, Stryd-Ai

APPLICANT: Green, Larry L.

APPLICANT: Korvet, Walter

TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

FILE REFERENCE: ABGENIX.100A

CURRENT APPLICATION NUMBER: US/11/084,554

CURRENT FILING DATE: 2005-03-17

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR FILING DATE: 2004-03-19

PRIOR APPLICATION NUMBER: 60/574,661

PRIOR FILING DATE: 2004-05-24

NUMBER OF SEQ ID NOS: 266

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 12

TYPE: PRT



```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-084-554-4
```

```
Query Match          26.5%; Score 22; DB 7; Length 12;
Best Local Similarity 83.3%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      10 LSTAST 15
        |||||:
Db       4 LSTASS 9
```

```
RESULT 15
US-10-986-501-287
; Sequence 287, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OR INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ01JP2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 287
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-287
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```
Query Match          26.5%; Score 22; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      5 VMDVDLST 12
        |||||:
Db       3 VMDTRSRST 10
```

Search completed: December 12, 2005, 22:05:30  
Job time : 12 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 22:02:32 ; Search time 37 Seconds  
(without alignments)  
44.208 Million cell updates/sec

Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDGQVMDVLDLSTATTQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0  
Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	26.5	15	2	PH1631
2	22	26.5	15	2	S20410
3	22	26.5	17	4	IS1887
4	21.5	25.9	16	2	S02473
5	21	25.3	13	2	B61458
6	21	25.3	13	2	A61458
7	21	25.3	16	2	PI0137
8	20	24.1	10	2	G58501
9	20	24.1	11	2	PS0259
10	20	24.1	15	2	S70719
11	20	24.1	15	2	PQ0778
12	20	24.1	16	2	A42291
13	19	22.9	10	2	GXH1
14	19	22.9	12	2	PN0160
15	19	22.9	13	2	PQ0491
16	19	22.9	13	2	S47381
17	19	22.9	13	2	D56661
18	19	22.9	14	2	PH1332
19	19	22.9	15	2	A18304
20	19	22.9	15	2	S29487
21	19	22.9	15	2	PH0750
22	19	22.9	17	2	S71864
23	19	22.9	17	2	S71327
24	19	22.9	17	2	D48138
25	18	21.7	10	2	C26997
26	18	21.7	12	2	A28856
27	18	21.7	12	2	PT0216
28	18	21.7	13	2	A33660
29	18	21.7	13	2	S66235

30	18	21.7	15	2	D38925	seed storage prote
31	18	21.7	15	2	PI0154	glycoprotein - log
32	18	21.7	15	2	A53594	calnexin - mouse (
33	18	21.7	15	2	A26997	unspecific monooxy
34	18	21.7	16	2	C39509	mannose-specific 1
35	18	21.7	16	2	S65430	pyrogallol hydroxy
36	18	21.7	17	2	PS0384	Ig heavy chain V r
37	18	21.7	17	2	S58660	H+-transporting tw
38	18	21.7	17	2	S28839	RNA-binding protei
39	18	21.7	17	2	C22595	bombolitin III - A
40	17	20.5	6	2	PT0604	T-cell receptor be
41	17	20.5	6	2	PT0657	T-cell receptor be
42	17	20.5	7	2	PT0543	T-cell receptor be
43	17	20.5	8	2	S21288	lectin - potato (f
44	17	20.5	8	2	A28719	thymic humoral fac
45	17	20.5	10	2	S10926	inhibin beta-A cha

## ALIGNMENTS

## RESULT 1

PH1631  
Ig H chain V-D-J region (clone B-lees 202) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1631  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1631  
A:Molecule type: DNA  
A:Residues: 1-15 <LFV>  
A:Cross-references: UNIPARC:UPI000017C699  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match  
Best Local Similarity 66.7%; Pred. No. 1.6e+03; Length 15;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DQVMD 7  
Db 9 DQVMD 14

## RESULT 2

S20410  
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)  
N:Alternate names: LHCI protein kinase  
C:Species: chloroplast Spinacia oleracea (spinach)  
C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: S20410  
R:Gal, A.; Herrmann, R.G.; Iotepelch, F.; Ohad, I.  
FEBS Lett. 298, 33-35, 1992  
A>Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyroc

A:Reference number: S20410; MUID:92183623; PMID:1544419

A:Accession: S20410

A:Molecule type: protein

A:Residues: 1-15 <GAL>

A:Cross-references: UNIPROT:Q9T2K8; UNIPARC:UPI000008E40D

C:Genetics:

A:Genome: chloroplast

C:Function:

A:Description: is responsible for the regulation of energy distribution between photosyn

A>Note: does not exhibit redox-controlled activation

C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphot

Query Match  
Best Local Similarity 62.5%; Pred. No. 1.6e+03; Length 15;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 DVDLSTAS 14  
 Db 6 DVEKSTLS 13

## RESULT 3

hypothetical EMSR1/FLI1 mutant fusion protein, type 1 - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000  
 C/Accession: 151887  
 R/Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulsnoff, M.G.; Link, M.P.; Mc  
 Am, J. Patbol. 143, 1294-1300, 1993  
 A/Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripher  
 A/Reference number: 151887; PMID:9405652; PMID:8238248  
 A/Accession: 151887  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-17 <DOM>  
 A/Cross-references: UNIPARC:UPI000011EDE2; GB:S66911; NID:g440935; PIDN:AMB28655.1; PID:  
 C/Comment: This sequence is the chimeric product of a translocation mutation.  
 C/Genetics:  
 A/Gene: EMSR1/FLI1; EMS/FLI-1  
 A/Map position: 22q12/11q24  
 C/Keywords: fusion protein

Query Match 26.5%; Score 22; DB 4; Length 17;  
 Best Local Similarity 36.4%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQVMVDLS 11  
 Db 7 DEGPDLIDPS 17

## RESULT 4

coat protein VP1 - human poliovirus 1 (fragment)  
 C/Species: human poliovirus 1  
 C/Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
 C/Accession: S02473  
 R/Martin, A.; Mychowski, C.; Couderc, T.; Crainic, R.; Hogle, J.; Girard, M.  
 EMBO J. 7, 2839-2847, 1988  
 A/Title: Engineered a poliovirus type 2 antigenic site on a type 1 capsid results in a  
 A/Reference number: S02473; PMID:89030650; PMID:2460345  
 A/Accession: S02473  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-16 <MAR>  
 A/Cross-references: UNIPROT:Q8QNT2; UNIPROT:Q84871; UNIPROT:Q84866; UNIPROT:Q84865; UNIF

Query Match 25.9%; Score 21.5; DB 2; Length 16;  
 Best Local Similarity 63.6%; Pred. No. 2.1e+03;  
 Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 MDVDLSTASTT 16  
 Db 1 MTVD-NPASTT 10

## RESULT 5

Ig kappa chain V-I region (BLA) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
 C/Accession: B61458  
 R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
 J. Exp. Med. 170, 1551-1558, 1989  
 A/Title: Expression of a public idotype by human monoclonal Igm directed to myelin-assoc  
 A/Reference number: A61458; PMID:90039128; PMID:2478651  
 A/Accession: B61458  
 A/Status: preliminary  
 A/Molecule type: protein

A/Residues: 1-13 <BRO>  
 A/Cross-references: UNIPARC:UPI000017C25D  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 25.3%; Score 21; DB 2; Length 13;  
 Best Local Similarity 30.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTT 16  
 Db 1 DIQWTSPTT 10

## RESULT 6

Ig kappa chain V-I region (BOU) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
 C/Accession: A61458; PLO156  
 R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
 J. Exp. Med. 170, 1551-1558, 1989  
 A/Title: Expression of a public idotype by human monoclonal Igm directed to myelin-assoc  
 A/Reference number: A61458; PMID:90039128; PMID:2478651  
 A/Accession: A61458  
 A/Molecule type: protein  
 A/Residues: 1-13 <BRO>  
 A/Cross-references: UNIPARC:UPI000017C25E  
 C/Comment: This protein is one of monoclonal Igm reactive with myeloma-associated glycop  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 25.3%; Score 21; DB 2; Length 13;  
 Best Local Similarity 30.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTT 16  
 Db 1 DIQWTSPTT 10

## RESULT 7

protein kinase, 80K - pig (fragment)  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993  
 C/Accession: PLO137  
 R/Dechert, U.; Weber, M.; Weber-Schaeufelen, M.; Wolny, E.  
 J. Neurochem. 53, 1268-1275, 1989  
 A/Title: Isolation and partial characterization of an 80,000-dalton protein kinase from t  
 A/Reference number: PLO137; PMID:89361455; PMID:2769266  
 A/Accession: PLO137  
 A/Molecule type: protein  
 A/Residues: 1-16 <DEC>  
 A/Cross-references: UNIPARC:UPI0000177D3E  
 C/Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 25.3%; Score 21; DB 2; Length 16;  
 Best Local Similarity 57.1%; Pred. No. 2.6e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GQVMDVD 9  
 Db 1 GDEVVDV 7

## RESULT 8

48k bile/gallbladder stone protein - unidentified bacterium (fragment)  
 C/Species: unidentified bacterium  
 C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004  
 C/Accession: G58501  
 R/Binette, J.P.; Binette, M.B.  
 submitted to the Protein Sequence Database, October 1996  
 A/Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501  
A:Accession: G58501  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <BIN>  
A:Cross-references: UNIPROT:O7M1C8, UNIPARC:UPI000017ABD6  
A:Experimental source: human bile and gallbladder stones  
A>Note: 1-Ser and 4-Glu were also found

Query Match 24.1% Score 20; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDGQVM 6  
|||:  
Db 5 EDGKAL 10

## RESULT 9

PS0259  
39K protein 3225 - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C:Accession: PS0259  
R:Teugita, A.; Kamo, M.  
Submitted to JIPID, April 1993  
A:Reference number: PS0209  
A:Accession: PS0259  
A:Molecule type: protein  
A:Residues: 1-11 <TSU>  
A:Cross-references: UNIPARC:UPI000017B102  
A:Experimental source: callus  
C:Comment: molecular weight 39K, pI 5.7.

Query Match 24.1% Score 20; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDGQVM 6  
|||:  
Db 4 EDGPIV 9

## RESULT 10

S70719  
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Salmonella typhimurium (fr  
C:Species: Salmonella typhimurium  
C>Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 31-Dec-2004  
C:Accession: S70719  
R:Qi, S.Y.; Li, Y.; Szynski, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.  
Mol. Microbiol. 17, 523-531, 1995  
A>Title: Salmonella typhimurium responses to a bactericidal protein from human neutroph  
A:Reference number: S70719; MUID:96100451; PMID:8559071  
A:Accession: S70719  
A:Molecule type: protein  
A:Residues: 1-15 <OIS>  
A:Cross-references: UNIPROT:Q9RFJ3, UNIPROT:Q8XGK4, UNIPARC:UPI000017CD82  
A:Experimental source: strain SL1344  
C:Superfamily: H(+)-transporting ATP synthase  
C:Keywords: ATP binding; hydrogen ion transport; hydrolase

Query Match 24.1% Score 20; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 3.6e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GQVMDV 8  
|||:  
Db 10 GAVVDV 15

## RESULT 11

P00778  
NADH2 dehydrogenase (EC 1.6.99.3) 46K chain - fava bean mitochondrion (fragment)

N:Alternate names: complex I 46K chain; NADH-ubiquinone reductase 46K chain  
C:Species: mitochondrion Vicia faba (fava bean)  
C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 03-Jun-2002  
C:Accession: P00778  
R:Leberme, S.; Bontly, M.  
Plant Physiol. 102, 435-443, 1993

A>Title: Purification and preliminary characterization of mitochondrial complex I (NADH:  
A:Reference number: P00775; MUID:94151437; PMID:8108509  
A:Accession: P00778  
A:Molecule type: protein

A:Residues: 1-15 <LEF>  
A:Cross-references: UNIPARC:UPI000017CDAF  
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th  
ranging from 5K to 75K.  
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by

C:Genetics:  
A:Genome: mitochondrion  
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 24.1% Score 20; DB 2; Length 15;  
Best Local Similarity 37.5%; Pred. No. 3.6e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EDGQVMDV 8  
|||:  
Db 3 DNGDVTDV 10

## RESULT 12

A42291  
tail fiber protein I - phage P2 (fragment)  
C:Species: phage P2  
C>Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: A42291  
R:Haggard-Jungquist, E.; Halling, C.; Calendar, R.  
J. Bacteriol. 174, 1462-1477, 1992  
A>Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon  
A:Reference number: A42291; MUID:92165720; PMID:1531648  
A:Accession: A42291  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-16 <HAG>  
A:Cross-references: UNIPROT:P26701, UNIPARC:UPI000017A829; GB:M64677

Query Match 24.1% Score 20; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 3.9e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 DQGVMDV 8  
|||:  
Db 7 DGDVITV 13

## RESULT 13

GXHU1  
gastric juice peptide - human  
C:Species: Homo sapiens (man)  
C>Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
C:Accession: A01628  
R:Heathcote, J.G.; Washington, R.J.  
Int. J. Protein Res. 2, 117-126, 1970  
A>Title: Peptides of normal human gastric juice.  
A:Reference number: A01628; MUID:75150968; PMID:5538385  
A:Accession: A01628  
A:Molecule type: protein  
A:Residues: 1-10 <HEA>  
A:Cross-references: UNIPROT:P01358, UNIPARC:UPI000012B049  
A>Note: a second peptide lacking 1-Leu, but otherwise identical in composition with the  
C:Keywords: stomach

Query Match 22.9% Score 19; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 3.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GQVMDVD 9  
|:| |  
Db 4 GKVEDSD 10

## RESULT 14

PN0160  
ribosomal protein S16 - fungus (*Fusarium sporotrichioides*) (fragment)  
C/Species: *Fusarium sporotrichioides*  
C/Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 09-Jul-2004  
C/Accession: PN0160  
R/Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.  
Submitted to JIPID, May 1994  
A/Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
A/Reference number: PN0160  
A/Accession: PN0160  
A/Molecule type: protein  
A/Residues: 1-12 <FUK>  
A/Cross-references: UNIPROT:Q7M4Y0, UNIPARC:UPI000017B41C  
C/Keywords: protein biosynthesis; ribosome

Query Match 22.9%; Score 19; DB 2; Length 12;  
Best Local Similarity 80.0%; Pred. No. 4.1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VMDVD 9  
| | | |  
Db 6 VRDVD 10

## RESULT 15

PQ0491  
self-incompatibility locus glycoprotein delta - wild cabbage (fragment)  
C/Species: *Brassica oleracea* (wild cabbage)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Dec-2004  
C/Accession: PQ0491  
R/Gaude, T.; Frilly, A.; Heilmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.  
Plant Cell 5, 75-86, 1993  
A/Title: Expression of a self-incompatibility gene in a self-compatible line of *Brassica oleracea*  
A/Reference number: JQ1733; MUID:93177215; PMID:8439745  
A/Accession: PQ0491  
A/Molecule type: protein  
A/Residues: 1-13 <GAU>  
A/Cross-references: UNIPROT:Q9SXH5, UNIPROT:Q9SXH7, UNIPROT:Q23846, UNIPROT:Q23837, UNIPROT:Q9SXH4, UNIPROT:Q23833, UNIPROT:Q8S9B2, UNIPROT:Q9SXH6, UNIPROT:Q23834, UNIPROT:Q8W  
A/Experimental source: stigma, var. *acephala* P5751  
C/Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-specific  
C/Keywords: glycoprotein

Query Match 22.9%; Score 19; DB 2; Length 13;  
Best Local Similarity 37.5%; Pred. No. 4.5e+03;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 LSTASTQ 17  
::| | | |  
Db 1 INTLSTE 8

Search completed: December 12, 2005, 22:15:08  
Job time : 38 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 12, 2005, 22:02:21 ; Search time 229 Seconds  
(without alignments)  
52.375 Million cell updates/sec

Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDGQVMDVLDLASTATTQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 10169

Minimum DB seq length: 0  
Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	30.1	10	Q70G06_PRYKA	Q70G06 pseudorabies
2	25	30.1	15	Q9UWH9_9EURY	Q9UWH9 thermococcus
3	25	30.1	15	Q69FJ1_9PLEO	Q69FJ1 stemphylium
4	24	28.9	14	Q69FHS_9PLEO	Q69FHS stemphylium
5	24	28.9	15	1 DNAK_COMAC	P83709 comamonas a
6	24	28.9	15	Q69FJ3_9PLEO	Q69FJ3 stemphylium
7	24	28.9	15	Q69GDI_9PLEO	Q69GDI stemphylium
8	24	28.9	16	Q69G98_9PLEO	Q69G98 pleospora s
9	24	28.9	16	Q69G80_9PLEO	Q69G80 pleospora s
10	24	28.9	16	Q69GCS_9PLEO	Q69GCS stemphylium
11	24	28.9	16	Q69G8_9PLEO	Q69G8 stemphylium
12	24	28.9	17	Q69G47_9PLEO	Q69G47 pleospora p
13	23	27.7	16	Q85HM7_9PAS	Q85HM7 motacilla f
14	23	27.7	15	Q9CTB2_MOUSE	Q9CTB2 mus musculus
15	23	27.7	17	Q71IF7_LACDL	Q71IF7 lactobacill
16	23	27.7	17	Q9QV75_9MURI	Q9QV75 rattus sp.
17	23	27.7	17	Q9QVK3_9MURI	Q9QVK3 rattus sp.
18	22	26.5	13	Q7TE19_9CLOS	Q7TE19 citrus tris
19	22	26.5	13	Q7TE20_9CLOS	Q7TE20 citrus tris
20	22	26.5	13	Q7TE23_9CLOS	Q7TE23 citrus tris
21	22	26.5	13	Q7TE24_9CLOS	Q7TE24 citrus tris
22	22	26.5	14	1 GRF75_CANPA	P99502 canis fami
23	22	26.5	15	Q9T2K8_SPIOI	Q9T2K8 spinacia o
24	22	26.5	16	Q69F17_9PLEO	Q69F17 stemphylium
25	22	26.5	17	Q9HDO6_CANRU	Q9HDO6 candida rug
26	21	25.3	10	Q9LSW6_LIBAC	Q9LSW6 liberibace
27	21	25.3	11	Q9RIN6_MOUSE	Q9RIN6 mus musculu
28	21	25.3	13	Q7TE26_9CLOS	Q7TE26 citrus tris
29	21	25.3	13	Q7TE28_9CLOS	Q7TE28 citrus tris
30	21	25.3	13	Q7TE30_9CLOS	Q7TE30 citrus tris
31	21	25.3	13	Q7TE32_9CLOS	Q7TE32 citrus tris

32	21	25.3	13	2	Q7TE34_9CLOS	Q7TE34 citrus tris
33	21	25.3	13	2	Q7TE36_9CLOS	Q7TE36 citrus tris
34	21	25.3	13	2	Q7TE38_9CLOS	Q7TE38 citrus tris
35	21	25.3	13	2	Q7TE40_9CLOS	Q7TE40 citrus tris
36	21	25.3	13	2	Q7TE42_9CLOS	Q7TE42 citrus tris
37	21	25.3	13	2	Q7TE44_9CLOS	Q7TE44 citrus tris
38	21	25.3	13	2	Q7TE46_9CLOS	Q7TE46 citrus tris
39	21	25.3	13	2	Q7TE48_9CLOS	Q7TE48 citrus tris
40	21	25.3	13	2	Q7TE50_9CLOS	Q7TE50 citrus tris
41	21	25.3	13	2	Q7TE52_9CLOS	Q7TE52 citrus tris
42	21	25.3	13	2	Q7TE54_9CLOS	Q7TE54 citrus tris
43	21	25.3	13	2	Q7TE56_9CLOS	Q7TE56 citrus tris
44	21	25.3	13	2	Q7TE58_9CLOS	Q7TE58 citrus tris
45	21	25.3	13	2	Q7TE60_9CLOS	Q7TE60 citrus tris

## ALIGNMENTS

## RESULT 1

Q70G06\_PRYKA PRELIMINARY; PRT; 10 AA.  
ID Q70G06\_PRYKA  
AC Q70G06;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE ORF1.2 protein (Fragment).  
OS Pseudorabies virus (strain Kaplan) (PRV).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
RN NCBI\_TaxID=33703;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Kaplan;  
RX PubMed=14671123; DOI=10.1128/JVI.78.1.424-440.2004;  
RA Klupp B.G., Hengartner C.J., Mettenleiter T.C., Enquist L.W.;  
RT "Complete, annotated sequence of the pseudorabies virus genome.";  
RL J. Virol. 78:424-440(2004).  
DR EMBL; AJ581560; CAB6335.1; -; Genomic\_DNA.  
FT NON\_TER  
SQ SEQUENCE 10 AA; 1006 MW; D276B4C1A8640B02 CRC64;

Query Match 30.1%; Score 25; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 3.1e+03;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MDVLISTAS 14  
Db 1 MDVERTAA 9

## RESULT 2

Q9UWH9\_9EURY PRELIMINARY; PRT; 15 AA.  
ID Q9UWH9\_9EURY  
AC Q9UWH9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Aldhyde ferredoxin oxidoreductase (Fragment).  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=35749;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC STRAIN=ES-1;  
RX MEDLINE=95370155; PubMed=7642503;  
RA Heider J., Ma K., Adams M.W.;  
RT "Purification, characterization, and metabolic function of tungsten-containing aldehyde ferredoxin oxidoreductase from the RT hyperthermophilic and proteolytic archaeon Thermococcus strain ES-1.";  
RL J. Bacteriol. 177:4757-4764(1995).  
SQ SEQUENCE 15 AA; 1750 MW; 0441670278198619 CRC64;

Query Match 30.1%; Score 25; DB 2; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQVMDVDLST 12  
 DB 6 GKLRVNLTT 15

RESULT 3  
 069FJ1\_9PLEO PRELIMINARY; PRT; 15 AA.  
 ID 069FJ1\_9PLEO PRELIMINARY; PRT; 15 AA.  
 AC 069FJ1\_9PLEO PRELIMINARY; PRT; 15 AA.  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Stenphylium solani.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.  
 NCBI\_TaxID=110364;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=EGS41-135;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of  
 RT Stenphylium."  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY339855; AARP0451.1; -, Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1547 MW; 84F7BEBAD16DF45 CRC64;

Query Match 30.1%; Score 25; DB 2; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 4.7e+03;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTTQ 17  
 DB 3 DIBPTINGTQ 13

RESULT 4  
 069FH5\_9PLEO PRELIMINARY; PRT; 14 AA.  
 ID 069FH5\_9PLEO PRELIMINARY; PRT; 14 AA.  
 AC 069FH5\_9PLEO PRELIMINARY; PRT; 14 AA.  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Stenphylium callisteph.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.  
 NCBI\_TaxID=119932;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NO 0536;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of  
 RT Stenphylium."  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY339863; AARP0467.1; -, Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 14 AA; 1401 MW; CSF7BFCD166F5D CRC64;

Query Match 28.9%; Score 24; DB 2; Length 14;  
 Best Local Similarity 36.4%; Pred. No. 6.5e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 DVDLSTASTTQ 17  
 DB 3 DIBPTINGTQ 13

DB 2 DIBPTINGTQ 12

RESULT 5  
 DNAX COMAC STANDARD; PRT; 15 AA.  
 ID 069FJ1\_9PLEO PRELIMINARY; PRT; 15 AA.  
 AC 069FJ1\_9PLEO PRELIMINARY; PRT; 15 AA.  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Chaperone protein dnax (Heat shock protein 70) (Heat shock 70 kDa  
 DE protein) (HSP70) (Fragment).  
 GN Name-dnax;  
 OS Comamonas acidovorans (Pseudomonas acidovorans).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Delftia.  
 NCBI\_TaxID=80866;  
 RN [1]  
 RP PROTEIN SEQUENCE, AND INDUCTION.  
 RC STRAIN=MCI;  
 RA PubMed=15073309; DOI=10.1099/mic.0.26774-0;  
 RA Benndorf D., Davidson I., Babel W.;  
 RT "Regulation of catabolic enzymes during long-term exposure of Delftia  
 RT acidovorans MCI to chlorophenox herbicides";  
 RL Microbiology 150:1005-1014(2004).  
 CC -1- FUNCTION: Acts as a chaperone. (By similarity).  
 CC -1- INDUCTION: By stress conditions e.g. heat shock, and by the  
 CC herbicide dichloroprop [(R)-2-(2,4-dichlorophenoxy)propionate].  
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC HAMAP\_MF\_00332; -; 1.  
 DR InterPro: IPR001023; HSP70.  
 DR Pfam: PF00012; HSP70; 1.  
 DR PROSITE: PS00297; HSP70\_1; 1.  
 DR PROSITE: PS00329; HSP70\_2; PARTIAL.  
 DR PROSITE: PS01036; HSP70\_3; PARTIAL.  
 KW ATP-binding; Chaperone; Direct protein sequencing; Heat shock;  
 KW Nucleotide-binding.  
 FT NON TER 15  
 SQ SEQUENCE 15 AA; 1513 MW; 28EAD48F7526C40F CRC64;

Query Match 28.9%; Score 24; DB 1; Length 15;  
 Best Local Similarity 25.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 QVMDVDLST 15  
 DB 1 KIICIDIGTINS 12

RESULT 6  
 069FJ3\_9PLEO PRELIMINARY; PRT; 15 AA.  
 ID 069FJ3\_9PLEO PRELIMINARY; PRT; 15 AA.  
 AC 069FJ3\_9PLEO PRELIMINARY; PRT; 15 AA.  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Stenphylium sarciniforme.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.  
 NCBI\_TaxID=119934;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=EGS38-121;  
 RA Inderbitzin P., Berbee M.L.;  
 RT "Mating type gene evolution in Pleospora, the sexual state of



```

RT   Stenphylium."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY339854; AAR04449.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER
SQ   SEQUENCE 15 AA; 1533 MW; 84EF1D8AD166DF45 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      3 DIEVPTINGTQ 13

Db

RESULT 7
Q69GDI_9PLEO PRELIMINARY; PRT; 15 AA.
AC   Q69GDI;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE   Hypothetical protein (Fragment).
OS   Stenphylium sp. EGS08-174.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.
OX   NCBI_TaxId=234989;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EGS 08-174;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphylium."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335169; AAR00951.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER
SQ   SEQUENCE 15 AA; 1533 MW; 84EF1D8AD166DF45 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      3 DIEVPTINGTQ 13

Db

RESULT 8
Q69G98_9PLEO PRELIMINARY; PRT; 16 AA.
AC   Q69G98;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Pleospora sp. P327.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; Pleospora.
OX   NCBI_TaxId=234982;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=P327;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphylium."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335180; AAR00984.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER
SQ   SEQUENCE 16 AA; 1662 MW; 54D36D8AD166DF07 CRC64;

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Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 16;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      4 DIEVPTINGTQ 14

Db

RESULT 9
Q69GB0_9PLEO PRELIMINARY; PRT; 16 AA.
AC   Q69GB0;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Pleospora etumina.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; Pleospora.
OX   NCBI_TaxId=235069;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EGS 29-099;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphylium."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335176; AAR00972.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER
SQ   SEQUENCE 16 AA; 1632 MW; 54CF1D8AD166DF07 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 16;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      4 DIEVPTINGTQ 14

Db

RESULT 10
Q69GCS_9PLEO PRELIMINARY; PRT; 16 AA.
AC   Q69GCS;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Stenphylium sp. EGS48-089.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.
OX   NCBI_TaxId=235021;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EGS 48-089;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphylium."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335171; AAR00957.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER
SQ   SEQUENCE 16 AA; 1632 MW; 54CF1D8AD166DF07 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 16;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      4 DIEVPTINGTQ 14

Db

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RESULT 11
ID 069GC8_9PLEO PRELIMINARY; PRT; 16 AA.
AC 069GC8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Stenphylium sp. EG548-074.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.
OX NCBI_TaxID=235018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGS 48-074;
RA Inderbitzin P., Berbee M.L.;
RT "Matrig type gene evolution in Pleospora, the sexual state of
RT Stenphylium.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY35170; AAR0954.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD16DF07 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 7.5e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTQ 17
DB 4 DIEVPTINGTQ 14

RESULT 12
ID 069GA7_9PLEO PRELIMINARY; PRT; 17 AA.
AC 069GA7;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pleospora paludiscitri.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxID=235070;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGS 31-016;
RA Inderbitzin P., Berbee M.L.;
RT "Matrig type gene evolution in Pleospora, the sexual state of
RT Stenphylium.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY35177; AAR0975.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 17 AA; 1733 MW; 38C9DD8AD16DF07 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 17;
Best Local Similarity 36.4%; Pred. No. 7.9e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTQ 17
DB 5 DIEVPTINGTQ 15

RESULT 13
ID 085HM7_9PASS PRELIMINARY; PRT; 15 AA.
AC 085HM7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)

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DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE ATPase subunit 8 (Fragment).
OS Name=ATP8;
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Motacillidae; Motacilla.
OX NCBI_TaxID=228286;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=22745498; PubMed=12859633;
RX DOI=10.1046/j.1365-294X.2003.01883.x;
RA Odeen A., Bjorklund M.;
RT "Dynamics in the evolution of sexual traits: losses and gains,";
RT radiation and convergence in yellow wagtails (Motacilla flava).";
RL Mol. Ecol. 12:2113-2130(2003).
DR EMBL; AY259472; AAR20723.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER 1
SQ SEQUENCE 15 AA; 1768 MW; 85F1FD2323295861 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 LSTASTT 16
DB 2 LTPSTT 8

RESULT 14
ID 09CTB2_MOUSE PRELIMINARY; PRT; 16 AA.
AC 09CTB2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:110033N23 product:nitrogen fixation gene 1 (S.
DE cerevisiae), full insert sequence. (Fragment).
GN Name=Nfsl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai U., Shinagawa A., Shibata K., Yoshino W., Itoh M., Iehi Y.,
RX Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
RX Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RX Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RX Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RX Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RX Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RX Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RX Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RX Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RX Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RX Lyons P., Marchionni L., Mashima J., Mazzaelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitteker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RA The FANTOM Consortium,
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kikunishi T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsui M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Aizawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK004077; BAB3157.1; -; mRNA.
DR MGI; MGI:1316706; Nfsl.
DR GO; GO:0005615; C:extracellular space; TRS.
DR GO; GO:0005759; C:mitochondrial matrix; IDA.
FT NON TER 1
SO SEQUENCE 16 AA; 1881 MW; 029ECF9BC205263 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 16;
Best Local Similarity 35.3%; Pred. No. 1.1e+04;
Matches 6; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

OY 1 EDGQVMDVLDSTASTTQ 17
Db :|||:|:|
3 ODG---IDLKSIKWTQ 15

RESULT 15
O71IF7_LACDL
ID O71IF7_LACDL PRELIMINARY; PRT; 17 AA.
AC O71IF7;

```

```

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glycyl kinase (EC 2.7.1.30) (Fragment).
OC Lactobacillus delbrueckii (subsp. lactis).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 4797;
RA Langenhein J.F., Ulrich R.L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496306; AAQ06980.1; -; Genomic DNA.
DR GO; GO:0004370; F:glycerol kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Kinase; Transferase.
FT NON TER 17
SQ SEQUENCE 17 AA; 1878 MW; 424DDE87D29A0C64 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 17;
Best Local Similarity 36.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 VMDVLDSTAST 15
Db :|||:|:|
6 ILAIDEGTTST 16

Search completed: December 12, 2005, 22:14:25
Job time : 230 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 92.181 Seconds  
(without alignments)  
81.030 Million cell updates/sec

Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDGQVMDVLDLSTASTTQ 17

Scoring table: BLASTUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	17	ADR10616	AdR10616 Human IGE
2	83	100.0	98	AAR85587	Aar85587 FC(epsilo
3	83	100.0	106	AAR85587	Aar85587 FC(epsilo
4	83	100.0	128	ABG74778	Abg74778 Human mod
5	83	100.0	236	ABG74780	Abg74780 Human mod
6	83	100.0	255	AAP50305	Aap50305 Fused ant
7	83	100.0	315	AAR85582	Aar85582 FC(epsilo
8	83	100.0	320	AAO19667	Aao19667 Human IGE
9	83	100.0	323	AAU80286	Aau80286 Human IGE
10	83	100.0	323	AAU80285	Aau80285 Human IGE
11	83	100.0	323	AAU80284	Aau80284 Human IGE
12	83	100.0	324	AAR83559	Aar83559 FC(epsilo
13	83	100.0	325	AAR77241	Aar77241 Human IGE
14	83	100.0	325	AAR77241	Aar77241 Human IGE
15	83	100.0	325	AAR83582	Aar83582 CH2 to CH
16	83	100.0	325	AAV79994	Aav79994 Human imm
17	83	100.0	327	ADY21849	Ady21849 Human IGE
18	83	100.0	330	AAU80289	Aau80289 Human IGE
19	83	100.0	331	AAAB0362	Aaab0362 Human IGE
20	83	100.0	331	ADP25768	Adp25768 Binding d
21	83	100.0	331	ADY21799	Ady21799 Human IGE
22	83	100.0	331	ADY21722	Ady21722 Human IGE
23	83	100.0	336	AAU80288	Aau80288 Human IGE
24	83	100.0	346	ABG74781	Abg74781 Human IGE

25	83	100.0	346	6	ABG74785	Abg74785 Human CH2
26	83	100.0	347	6	ABG74784	Abg74784 Human CH2
27	83	100.0	347	6	ABG74783	Abg74783 Human CH2
28	83	100.0	348	6	ABG74782	Abg74782 Human CH2
29	83	100.0	367	1	AAP80291	Aap80291 Interleuk
30	83	100.0	425	6	AAE35114	Aae35114 Human imm
31	83	100.0	427	6	AAO19666	Aao19666 Human IGE
32	83	100.0	428	2	AAAR42950	Aaar42950 Human IGE
33	83	100.0	428	5	AAU47863	Aau47863 Human Ig-
34	83	100.0	428	5	AAU80283	Aau80283 Human IGE
35	83	100.0	428	5	AAAM50940	Aam50940 Human IGE
36	83	100.0	428	6	AAE35113	Aae35113 Human imm
37	83	100.0	428	7	ADD48440	Add48440 Human Pro
38	83	100.0	428	7	ADE97382	Ade97382 Human IGE
39	83	100.0	441	5	AAU80287	Aau80287 Human IGE
40	83	100.0	493	1	AAP40065	Aap40065 Sequence
41	83	100.0	497	9	ADW24784	Adw24784 Human var
42	83	100.0	497	9	ADW24742	Adw24742 Human var
43	83	100.0	497	9	ADZ08809	Adz08809 Mammalian
44	83	100.0	497	9	ADZ08940	Adz08940 Mammalian
45	83	100.0	497	9	ADZ44466	Adz44466 Human imm

## ALIGNMENTS

RESULT 1  
ID ADR10616 standard; peptide, 17 AA.  
XX  
AC ADR10616;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Human IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 16.  
XX  
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
(UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
HAMMERBERG B;  
XX  
WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian IGE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC human IgE 3.76 recognition site.

XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 83; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17  
 DB 1 EDGQVMDVDLSTASTTQ 17

# RESULT 2

AA85588 standard; peptide; 98 AA.

XX  
 AC AAR85588;

XX  
 DT 06-MAR-1996 (first entry)

XX  
 DE Fc(epsilon) CH2'-CH4 amino acids 234-330.

XX Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;  
 KM constant heavy region; E.coli; glycosylation; antigenic; immunogenic;  
 KM histamine; anti-allergenic; vaccine; immune response.

XX  
 OS Synthetic.

XX  
 PN FR2715304-A1.

XX  
 PD 28-JUL-1995.

XX  
 PF 26-JAN-1994; 94FR-00000846.

XX  
 PR 26-JAN-1994; 94FR-00000846.

XX  
 PA (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.

XX  
 PI Hurpin CM, Panero MJM;

XX  
 DR WPI; 1995-265243/35.

XX  
 PT Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has  
 PT epitope(s) not present in native IgE, also derived antibodies for  
 PT treating or preventing allergies, inflammatory immune disease, etc.

XX  
 PS Claim 7; Page 32-33; 44pp; French.

XX Peptides AAR85582-9 are fragments of the Fc(epsilon) CH2'-CH4 fragment  
 CC (AAR85589). This sequence covers amino acids 234-330 of the Fc(epsilon)  
 CC constant heavy chain. The subfragments were derived from the sequence of  
 CC the Fc(epsilon) CH2'-CH4 coding sequence (AAT01865) by recombinant  
 CC methods from the plasmid pE2-4(7). When expressed in E.coli, the peptides  
 CC produced are non-glycosylated Fc(epsilon) fragments. Altering the pattern  
 CC of glycosylation unmasks new antigenic sites thus rendering the Fc  
 CC fragment immunogenic and able to induce antibodies that recognise native  
 CC IgE but do not form histamine-releasing complexes. The Fc fragments can  
 CC be used in anti-allergic vaccines to modulate the intensity of immune  
 CC responses mediated by IgE

XX  
 SQ Sequence 98 AA;

Query Match 100.0%; Score 83; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17  
 ||||||||||||||||

DB 38 EDGQVMDVDLSTASTTQ 54

# RESULT 3

AA85587 standard; peptide; 106 AA.

XX  
 AC AAR85587;

XX  
 DT 06-MAR-1996 (first entry)

XX  
 DE Fc(epsilon) CH2'-CH4 amino acids 226-330.

XX Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;  
 KM constant heavy region; E.coli; glycosylation; antigenic; immunogenic;  
 KM histamine; anti-allergenic; vaccine; immune response.

XX  
 OS Synthetic.

XX  
 PN FR2715304-A1.

XX  
 PD 28-JUL-1995.

XX  
 PF 26-JAN-1994; 94FR-00000846.

XX  
 PR 26-JAN-1994; 94FR-00000846.

XX  
 PA (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.

XX  
 PI Hurpin CM, Panero MJM;

XX  
 DR WPI; 1995-265243/35.

XX  
 PT Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has  
 PT epitope(s) not present in native IgE, also derived antibodies for  
 PT treating or preventing allergies, inflammatory immune disease, etc.

XX  
 PS Claim 7; Page 32-33; 44pp; French.

XX Peptides AAR85582-9 are fragments of the Fc(epsilon) CH2'-CH4 fragment  
 CC (AAR85589). This sequence covers amino acids 226-330 of the Fc(epsilon)  
 CC constant heavy chain. The subfragments were derived from the sequence of  
 CC the Fc(epsilon) CH2'-CH4 coding sequence (AAT01865) by recombinant  
 CC methods from the plasmid pE2-4(7). When expressed in E.coli, the peptides  
 CC produced are non-glycosylated Fc(epsilon) fragments. Altering the pattern  
 CC of glycosylation unmasks new antigenic sites thus rendering the Fc  
 CC fragment immunogenic and able to induce antibodies that recognise native  
 CC IgE but do not form histamine-releasing complexes. The Fc fragments can  
 CC be used in anti-allergic vaccines to modulate the intensity of immune  
 CC responses mediated by IgE

XX  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 83; DB 2; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17  
 DB 46 EDGQVMDVDLSTASTTQ 62

# RESULT 4

ABG74778 standard; protein; 128 AA.

XX  
 AC ABG74778;

XX  
 DT 05-JUN-2003 (first entry)

XX  
 DE Human modified IgE CH2 domain.

XX  
 KM CH3 domain; IgE; antigen; non-anaphylactic; anti-IgE; fusion protein;

KM	dermatologic rhinitis; anti-inflammatory; ophthalmologically; allergy; asthma;
KM	allergic rhinitis; gastroenteric allergy; food allergy; eosinophilia;
KM	conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;
KM	gene therapy; human.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	EP1262491-A2.
XX	
XX	04-DEC-2002.
PD	
XX	
PF	22-MAY-2002; 2002EP-00253606.
XX	
FR	22-MAY-2001; 2001US-0292638P.
XX	
PA	(PF12 ) PFIZER PROD INC.
XX	
PI	Brown TM, Morsey MA;
XX	
XX	WPI; 2003-122561/12.
DR	N-PSDS; ACAA55176.
PT	
PT	Novel isolated antigenic peptide comprising amino acid residues of CH3
PT	domain of IGE molecule from first species and a second unrelated species,
PT	induces non-anaphylactic anti-IGE immune response in animal.
XX	
PS	Claim 15; Page 32; 50pp; English.
XX	
CC	This invention describes a novel antigenic peptide comprising amino acid
CC	residues of an IGE CH3 domain from a first species (ADE1) and amino acid
CC	residues of an IGE CH3 domain of a second unrelated species (ADE2), where
CC	AD1 is conserved in the IGE CH3 domain of the second species and ADE2 is
CC	not conserved in the IGE CH3 domain of the first species. The novel
CC	antigenic peptide induces a non-anaphylactic anti-IGE immune response in
CC	an animal. The invention also discloses the polynucleotide sequence in
CC	encoding the antigenic peptide and an antigenic fusion protein comprising
CC	the antigenic peptide of the invention and a heterologous protein
CC	carrier, where the fusion protein induces an anti-IGE immune response
CC	that does not cause anaphylaxis when administered to an animal. The
CC	products of the invention have dermatological, anti-inflammatory and
CC	ophthalmological activity. The antigenic peptide described is capable of
CC	preventing IGE from binding to high affinity receptors on mast cells and
CC	basophils. The products of the invention are useful in the manufacture of
CC	a medicament for treating or preventing IGE-mediated allergic disorders
CC	including asthma, allergic rhinitis, gastroenteric allergies such as
CC	food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea
CC	allergies or atopic dermatitis, in an animal, e.g. human or dog. The
CC	polynucleotide products are useful for treating IGE-mediated allergic
CC	disorders, by gene therapy. Antigenic peptides comprising conserved amino
CC	acid residues of the CH3 domain of an IGE molecule from one species
CC	flanked by variable amino acid residues of the CH3 domain of an IGE
CC	molecule from a second unrelated species are capable of inducing a high
CC	titre of anti-IGE antibodies when administered to an animal without
CC	causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
CC	used in designing the constructs described in the disclosure of the
CC	invention
XX	
XX	
XX	Sequence 128 AA;
XX	
XX	Query Match 100.0%; Score 83; DB 6; Length 128;
XX	Best Local Similarity 100.0%; Pred. No. 2.5e-06;
XX	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 EDGQVMDVLDLSTASTTQ 17
DB	
DB	70 EDGQVMDVLDLSTASTTQ 86
XX	
XX	RESULT 5
XX	ABG74780
XX	ID ABG74780 standard; protein; 236 AA.

XX ABG74780  
 DT 05-JUN-2003 (first entry)  
 XX  
 DE Human modified IGE CH2-CH4 carrier protein.  
 XX  
 KW CH3 domain; IGE; antigen; non-anaphylactic; anti-IGE; fusion protein;  
 KW dermatological; antinflammatory; ophthalmological; allergy; asthma;  
 KW allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;  
 KW conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;  
 KW gene therapy; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN EPI262491-A2.  
 XX  
 PD 04-DEC-2002.  
 XX  
 PF 22-MAY-2002; 2002EP-00253566.  
 XX  
 PR 22-MAY-2001; 2001US-0292638P.  
 PA  
 PI (PIFZ ) PFIZER PROD INC.  
 XX  
 FI Brown TM, Morse MA;  
 XX  
 DR WPI; 2003-122561/12.  
 DR N-PSDB; ACAS5178.  
 XX  
 PT Novel isolated antigenic peptide comprising amino acid residues of CH3  
 PT domain of IGE molecule from first species and a second unrelated species,  
 PT induces non-anaphylactic anti-IGE immune response in animal.  
 PS  
 PS Claim 15; Page 33-34; 50pp; English.  
 CC This invention describes a novel antigenic peptide comprising amino acid  
 CC residues of an IGE CH3 domain from a first species (ADE1) and amino acid  
 CC residues of an IGE CH3 domain of a second unrelated species (ADE2), where  
 CC ADE1 is conserved in the IGE CH3 domain of the second species and ADE2 is  
 CC not conserved in the IGE CH3 domain of the first species. The novel  
 CC antigenic peptide induces a non-anaphylactic anti-IGE immune response in  
 CC an animal. The invention also discloses the polynucleotide sequence  
 CC encoding the antigenic peptide and an antigenic fusion protein comprising  
 CC the antigenic peptide of the invention and a heterologous protein  
 CC carrier, where the fusion protein induces an anti-IGE immune response  
 CC that does not cause anaphylaxis when administered to an animal. The  
 CC products of the invention have dermatological, antinflammatory and  
 CC ophthalmological activity. The antigenic peptide described is capable of  
 CC preventing IGE from binding to high affinity receptors on mast cells and  
 CC basophils. The products of the invention are useful in the manufacture of  
 CC a medicament for treating or preventing IGE-mediated allergic disorders  
 CC including asthma, allergic rhinitis, gastrointestinal allergies such as  
 CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea  
 CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The  
 CC polynucleotide products are useful for treating IGE-mediated allergic  
 CC disorders, by gene therapy. Antigenic peptides comprising conserved amino  
 CC acid residues of the CH3 domain of an IGE molecule from one species  
 CC flanked by variable amino acid residues of the CH3 domain of an IGE  
 CC molecule from a second unrelated species are capable of inducing a high  
 CC titre of anti-IGE antibodies when administered to an animal without  
 CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences  
 CC used in designing the constructs described in the disclosure of the  
 CC invention  
 CC  
 SQ Sequence 236 AA;  
 XX  
 Query Match 100.0%; Score 83; DB 6; Length 236;  
 - Best Local Similarity 100.0%; Prid. No. 5,1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 0Y 1 EDGQVMDVISTASTTQ 17

Db		70	EDGQVMDVDLSTASTTQ	86
RESULT 6				
AAFP50305				
ID	AAFP50305	standard; protein;	255 AA.	
AC	AAP50305;			
XX				
DT	25-MAR-2003	(revised)		
DT	15-JAN-1992	(first entry)		
XX				
DE	Fused antibody recognition site and interleukin-2 fragment.			
KW	IgE; hIL-2.			
XX				
OS	Homo sapiens.			
XX				
FT	Key	Location/Qualifiers		
FT	Protein	3..118		
FT	Protein	/label= IgE Ab recognition site		
FT	Protein	123..255		
XX		/label= IL-2 structural protein		
FN	WO9504673-A.			
XX				
PD	24-OCT-1985.			
XX				
PF	10-APR-1984;	84WO-JP000181.		
XX				
PR	10-APR-1984;	84WO-JP000181.		
XX				
PA	(TAKE ) TAKEDA CHEM IND LTD.			
XX				
PI	Seno M, Onda H, Igarashi K;			
XX				
DR	WPI; 1985-276145/44.			
DR	N-PSDB; AAN50356.			
XX				
PT	Novel DNA contg. DNA with structural gene coding peptide - contg.			
PT	antibody recognition site and DNA contg. structural gene coding human			
PT	interleukin 2 peptide.			
XX				
PS	Disclosure; Fig 2; 36pp; Japanese.			
CC	The fused Igs-II-2 product may be used in refining the human interleukin			
CC	-2 antibody. The product may be expressed by an E.coli host under the			
CC	control of the trp promoter in plasmid pGEL 1028. (Updated on 25-MAR-2003			
CC	to correct PA field.)			
XX				
SQ	Sequence 255 AA;			
Query Match	100.0%; Score 83; DB 1; Length 255;			
Best Local Similarity	100.0%; Pred. NO. 5.6e-06;			
Matches 17; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 EDGQVMDVDLSTASTTQ 17			
Db	56 EDGQVMDVDLSTASTTQ 72			
RESULT 7				
AA85582				
ID	AA85582	standard; peptide;	315 AA.	
XX				
AC	AA85582;			
XX				
DT	06-MAR-1996	(first entry)		
XX				
DE	Fc(epsilon) CH2'-CH4 amino acids 234-547.			
XX				
FC	(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;			
KW	constant heavy region; E.coli; glycosylation; antigenic; immunogenic;			

KW	hiscamine; anti-allergenic; vaccine; immune response.
OS	Synthetic.
XX	
PN	FR2715304-A1.
XX	
PD	28-JUL-1995.
XX	
PF	26-JAN-1994; 94FR-00000846.
XX	
PR	26-JAN-1994; 94FR-00000846.
XX	
PA	(INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
XX	
PI	Hurpin CM, Panero MJM;
XX	
DR	WPI; 1995-26543/35.
XX	
PT	Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has
XX	epitope(s) not present in native IgE, also derived antibodies for
PT	treating or preventing allergies, inflammatory immune disease, etc.
XX	
PS	Claim 4; Page 32-33; 44pp; French.
XX	
CC	Peptides AAR85582-9 are fragments of the Fc(epsilon) CH2'-CH4 fragment
CC	(AAR83559). This sequence covers amino acids 234-547 of the Fc(epsilon)
CC	constant heavy chain. The subfragments were derived from the sequence of
CC	the Fc(epsilon) CH2'-CH4 coding sequence (AAT01865) by recombinant
CC	methods from the plasmid pE2-4(17). When expressed in E.coli, the peptides
CC	produced are non-glycosylated Fc(epsilon) fragments. Altering the pattern
CC	of glycosylation unmasks new antigenic sites thus rendering the Fc
CC	fragment immunogenic and able to induce antibodies that recognise native
CC	IgE but do not form histamine-releasing complexes. The Fc fragments can
CC	be used in anti-allergenic vaccines to modulate the intensity of immune
CC	responses mediated by IgE
XX	
SQ	Sequence 315 AA;
Query Match	100.0%; Score 83; DB 2; Length 315;
Best Local Similarity	100.0%; Pred. No. 7,2e-06;
Matches 17; conservative 0; mismatches 0; indels 0; gaps 0;	
QY	1 EDGQVMDVLDLSTASTTQ 17 
DB	38 EDGQVMDVLDLSTASTTQ 54
RESULT 8	
AAO19667	
ID	AAO19667 standard; protein; 320 AA.
XX	
AC	AAO19667;
XX	
DT	28-MAR-2003 (first entry)
XX	
DE	Human IgE heavy chain constant region CH2-CH3-CH4 portion.
XX	
KW	Human; IgE; immunoglobulin E; immunotherapy; immune disease;
KW	Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
KW	antihistaminic; antiallergic; antiinflammatory; dermatological;
KW	antiarthritic; antirheumatic; antidiabetic; neuroprotective;
XX	CH2-CH3-CH4 region.
OS	Homo sapiens.
XX	
PN	WO200288317-A2.
XX	
PD	07-NOV-2002.
XX	
PF	01-MAY-2002; 2002WO-US013527.
XX	
PR	01-MAY-2001; 2001US-00847208.
XX	
PR	24-OCT-2001; 2001US-00000439.
XX	



XX (REGC ) UNIV CALIFORNIA.  
PA Saxon A, Zhang K, Zhu D;  
PI WPI; 2003-103456/09.  
XX  
XX  
XX New fusion molecules comprising polypeptide sequences that bind to IgG  
PT inhibitory receptor and native IGE receptor, useful for treating IGE-  
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
PT autoimmune diseases.  
XX  
XX Claim 21; Fig 6; 116pp; English.  
XX  
XX The present invention relates to a fusion molecule comprising a first  
CC polypeptide sequence capable of specific binding to a native IGE  
CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IGE receptor  
CC (FcεRI). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC treating an IGE-mediated biological response, preferably an IGE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IGE  
CC heavy chain constant region CH2-CH3-CH4 portion  
XX  
XX Sequence 320 AA;  
SQ  
Query Match 100.0%; Score 83; DB 6; Length 320;  
Best Local Similarity 100.0%; Pred. No. 7.3e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVDLSTASTTQ 17  
Db 43 EDGQVMDVDLSTASTTQ 59  
RESULT 9  
AAU80286  
ID AAU80286 standard; protein; 323 AA.  
XX  
XX AAU80286;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX Human IGE C2-C3-C4 domains for E.Coli expression.  
XX  
XX IGE; allergy; human; antiallergic; immunosuppressive; anti-anaphylactic;  
XX antiaesthetic; dermatological; anti-inflammatory; immunoglobulin E; IGE;  
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
XX heavy chain C domain.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200220038-A2.  
XX  
XX 14-MAR-2002.  
XX  
XX 06-SEP-2001; 2001WO-DK000579.  
XX  
XX 06-SEP-2000; 2000DK-00001326.  
XX  
XX 15-SEP-2000; 2000US-0232831P.  
XX  
XX (PHAR-) PHARMEXA AS.  
XX  
XX Klyener S, Von Hoegen P, Voldborg B, Gautam A;  
XX

DR WPI; 2002-383033/41.  
DR N-PSDB; ABKS1134.  
XX  
XX Inducing immune response against autologous immunoglobulin E in an  
PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
PT epitope an/or B-cell epitope derived from the immunoglobulin.  
XX  
XX Disclosure; Page 112-113; 151pp; English.  
XX  
XX This invention relates to a novel method for inducing an immune response  
CC against autologous immunoglobulin E (IGE) in an animal. The method  
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
CC (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell  
CC epitope (TH epitope) which is foreign to the animal, by antigen  
CC presenting cells (APCs) of the animal's immune system. The epitopes of  
CC the invention may be used as a vaccine against allergic diseases. The  
CC method of the invention is useful for inducing an immune response against  
CC autologous IGE in an animal, which is useful for downregulating  
CC autologous IGE in the animal. This method is useful in the prevention and  
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
CC asthma and atopic dermatitis. The present sequence represents the human  
CC IGE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli  
CC system, this sequence was used to create the epitopes of the invention  
XX  
XX Sequence 323 AA;  
SQ  
Query Match 100.0%; Score 83; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVDLSTASTTQ 17  
Db 46 EDGQVMDVDLSTASTTQ 62  
RESULT 10  
AAU80285  
ID AAU80285 standard; protein; 323 AA.  
XX  
XX AAU80285;  
XX  
XX 30-JUL-2002 (first entry)  
XX  
XX Human IGE C2-C3-C4 domains for mammalian expression.  
XX  
XX IGE; allergy; human; antiallergic; immunosuppressive; anti-anaphylactic;  
XX antiaesthetic; dermatological; anti-inflammatory; immunoglobulin E; IGE;  
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
XX heavy chain C domain.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200220038-A2.  
XX  
XX 14-MAR-2002.  
XX  
XX 06-SEP-2001; 2001WO-DK000579.  
XX  
XX 06-SEP-2000; 2000DK-00001326.  
XX  
XX 15-SEP-2000; 2000US-0232831P.  
XX  
XX (PHAR-) PHARMEXA AS.  
XX  
XX Klyener S, Von Hoegen P, Voldborg B, Gautam A;  
XX  
XX WPI; 2002-383033/41.  
XX  
XX N-PSDB; ABKS1133.  
XX  
XX Inducing immune response against autologous immunoglobulin E in an  
PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
PT epitope an/or B-cell epitope derived from the immunoglobulin.  
XX

PS Disclosure; Page 108-110; 151pp; English.  
XX  
CC This invention relates to a novel method for inducing an immune response  
CC against autologous immunoglobulin E (IgE) in an animal. The method  
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell  
CC epitope (TH epitope) which is foreign to the animal, by antigen  
CC presenting cells (APCs) of the animal's immune system. The epitopes of  
CC the invention may be used as a vaccine against allergic diseases. The  
CC method of the invention is useful for inducing an immune response against  
CC autologous IgE in an animal, which is useful for downregulating  
CC autologous IgE in the animal. This method is useful for preventing and  
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
CC asthma and atopic dermatitis. The present sequence represents the human  
CC IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian  
CC system, this sequence was used to create the epitopes of the invention  
XX  
SQ Sequence 323 AA;  
  
Query Match 100.0%; Score 83; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EDGQVMDVLDSTASTQ 17  
Db 46 EDGQVMDVLDSTASTQ 62  
|||||  
  
RESULT 11  
ID AAU80284 standard; protein; 323 AA.  
XX  
AC AAU80284;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE Human IgE heavy chain C2-C3-C4 domains.  
XX  
XX IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
XX antiaesthetic; dermatological; antiinflammatory; immunoglobulin E; IgE;  
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
XX heavy chain C domain.  
XX  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX  
XX Domain 8..103  
XX /note= "IgE heavy chain C2 domain"  
XX  
XX Region 100..114  
XX /note= "Epitope including C2C3 linker"  
XX  
XX Region 104..111  
XX /note= "Linker between domains C2 and C3"  
XX  
XX Domain 112..211  
XX /label= "IgE heavy chain C3 domain"  
XX  
XX Region 139..145  
XX /note= "Epitope in BC loop"  
XX  
XX Region 167..175  
XX /note= "Epitope in DB loop"  
XX  
XX Domain 196..206  
XX /note= "Epitope in FG loop"  
XX  
XX Region 210..218  
XX /note= "Epitope including C3C4 linker"  
XX  
XX Region 212..215  
XX /note= "Linker between domains C3 and C4"  
XX  
XX Domain 216..317  
XX /note= "IgE heavy chain C4 domain"  
XX  
XX  
XX W0200220038-A2.  
XX  
XX 14-MAR-2002.  
XX  
XX 06-SEP-2001; 2001WO-DK000579.  
XX

PR 06-SEP-2000; 2000DK-00001326.  
PR 15-SEP-2000; 2000US-0232831P.  
XX  
XX  
XX (PHAR-) PHARMEXA AS.  
XX  
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;  
XX WPI: 2002-383033/41.  
XX  
XX  
XX Inducing immune response against autologous immunoglobulin E in an  
XX animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
XX epitope an/or B-cell epitope derived from the immunoglobulin.  
XX  
XX Disclosure; Page 105-106; 151pp; English.  
XX  
XX  
XX This invention relates to a novel method for inducing an immune response  
XX against autologous immunoglobulin E (IgE) in an animal. The method  
XX comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
XX (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell  
XX epitope (TH epitope) which is foreign to the animal, by antigen  
XX presenting cells (APCs) of the animal's immune system. The epitopes of  
XX the invention may be used as a vaccine against allergic diseases. The  
XX method of the invention is useful for inducing an immune response against  
XX autologous IgE in an animal, which is useful for downregulating  
XX autologous IgE in the animal. This method is useful in the prevention and  
XX treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
XX asthma and atopic dermatitis. The present sequence represents the human  
XX IgE heavy chain C2-C3-C4 domains used to create the epitopes of the  
XX invention  
XX  
XX  
SQ Sequence 323 AA;  
  
Query Match 100.0%; Score 83; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EDGQVMDVLDSTASTQ 17  
Db 46 EDGQVMDVLDSTASTQ 62  
|||||  
  
RESULT 12  
ID AAR83559 standard; protein; 324 AA.  
XX  
XX AAR83559;  
XX  
XX 06-MAR-1996 (first entry)  
XX  
XX DE Fc(epsilon) CH2'-CH4 protein sequence.  
XX  
XX Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;  
XX constant heavy region; E.coli; glycosylation; antigenic; immunogenic;  
XX histamine; anti-allergenic; vaccine; immune response.  
XX  
XX Synthetic.  
XX  
XX OS FR2715304-A1.  
XX  
XX PN FR2715304-A1.  
XX  
XX PD 28-JUL-1995.  
XX  
XX 26-JAN-1994; 94FR-00000846.  
XX  
XX 26-JAN-1994; 94FR-00000846.  
XX  
XX (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.  
XX  
XX Hurpin CM, Panero MM;  
XX WPI: 1995-265243/35.  
XX  
XX N-PSDB; AAT01865.  
XX  
XX Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has  
XX

PT epitope(s) not present in native IGE, also derived antibodies for  
 PT treating or preventing allergies, inflammatory immune disease, etc.

PS Claim 3; Page 32-33; 44pp; French.

XX The amino acid sequence of the Fc(epsilon) CH2-CH4 fragment covering  
 CC amino acids 226-547. The DNA sequence was isolated from a human myeloma  
 CC 266BL CDNA library screened with a probe corres. to the N-terminus of  
 CC IGE. The region encoding amino acids 218-547 was cloned into the vector  
 CC pMT211 under control of the tryptophan promoter. The resultant protein  
 CC produced contains some non-Fc amino acids. These were removed by  
 CC replacing their coding sequence with a bicistronic linker. The resultant  
 CC construct encodes the Fc(epsilon) constant heavy region from amino acids  
 CC 226-547. When it is expressed in E.coli, the protein produced is a non-  
 CC glycosylated Fc(epsilon) fragment. Altering the pattern of glycosylation  
 CC unblocks new antigenic sites thus rendering the Fc fragment immunogenic  
 CC and able to induce antibodies that recognise native IGE but do not form  
 CC histamine-releasing complexes. The Fc fragments can be used in anti-  
 CC allergic vaccines to modulate the intensity of immune responses  
 CC mediated by IGE

XX Sequence 324 AA;

Query Match 100.0%; Score 83; DB 2; Length 324;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDVLDLSTASTTQ 17  
 |||||  
 DB 47 EDGQVMDVLDLSTASTTQ 63

#### RESULT 13

ID AAR75225 standard; protein; 325 AA.

XX AAR75225;

XX 25-MAR-2003 (revised)

DT 10-NOV-1995 (first entry)

XX Human IGE Fc chain (amino acids 224-547) mutant sequence.

XX IGE Fc fragment; antiallergic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= Val1224

FT Misc-difference 2 /note= "any AA or deletion"

FT Misc-difference 3 /label= Cys225 /note= "Ala, any other AA, or deletion"

FT Misc-difference 4 /label= Ser226 /note= "any AA or deletion"

FT Misc-difference 5 /label= Arg227 /note= "any AA or deletion"

FT Misc-difference 149 /label= "any AA or deletion"

FT Misc-difference 172 /label= Asn371 /note= "glycosylation site"

FT Misc-difference 172 /label= Asn394 /note= "glycosylation site"

FT W09514779-A1.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-GB002561.

XX 22-NOV-1993; 93GB-00024013.

XX (THRE-) 31 RES EXPL LTD.

XX (CLLT ) CELLTech THERAPEUTICS LTD.

XX Gould HU, Young RJ, Sutton BJ, Owens RJ;

XX WPI, 1995-206936/27.

XX N-PSDB; AAQ87474.

XX Mutated glycosylated polypeptide(s) contg. parts of human IGE-Fc - useful

XX to study and treat allergy.

XX Disclosure; Page 6; 55pp; English.

XX The sequence represents a mutant sequence of a human IGE-Fc chain (amino

XX acids 224-547) which is of sufficient length to bind Fc-epsilon RI and/or

XX Fc-epsilon FII IGE receptor sites on human cells. The protein is useful

XX in the study and treatment of allergy. (Updated on 25-MAR-2003 to correct

XX PN field.)

OY 1 EDGQVMDVLDLSTASTTQ 17  
 |||||  
 DB 48 EDGQVMDVLDLSTASTTQ 64

#### RESULT 14

ID AAR77241 standard; protein; 325 AA.

XX AAR77241;

XX 25-MAR-2003 (revised)

DT 10-NOV-1995 (first entry)

XX Human IGE Fc chain (amino acids 224-547) wild-type sequence.

XX IGE Fc fragment; antiallergic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 149 /label= Asn371 /note= "glycosylation site"

FT Misc-difference 172 /label= Asn394 /note= "glycosylation site"

FT W09514779-A1.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-GB002561.

XX 22-NOV-1993; 93GB-00024013.

XX (THRE-) 31 RES EXPL LTD.

XX (CLLT ) CELLTech THERAPEUTICS LTD.

XX Gould HU, Young RJ, Sutton BJ, Owens RJ;

XX WPI, 1995-206936/27.

XX N-PSDB; AAQ91170.

XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc - useful  
PT to study and treat allergy.  
XX  
XX  
PS Disclosure; Page 35-36; 55pp; English.  
XX  
CC The sequence represents the wild-type sequence of a human IgE-Fc chain  
CC (amino acids 224-547) which is of sufficient length to bind Fc-epsilon RI  
CC and/or Fc-epsilon RI IgE receptor sites on human cells. The sequence is  
CC preferably mutated (see AAR75325) to represent a protein encoding a  
CC protein where Cys225 is mutated, optionally together with Val224, Ser226  
CC and Arg227. The protein is useful in the study and treatment of allergy.  
CC (Updated on 25-MAR-2003 to correct PW field.)  
XX  
SQ Sequence 325 AA;  
  
Query Match 100.0%; Score 83; DB 2; Length 325;  
Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EDGQVMDVDLSTASTTQ 17  
Db 48 EDGQVMDVDLSTASTTQ 64

SQ Sequence 325 AA;  
  
Query Match 100.0%; Score 83; DB 2; Length 325;  
Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 EDGQVMDVDLSTASTTQ 17  
Db 48 EDGQVMDVDLSTASTTQ 64  
  
Search completed: December 12, 2005, 20:30:34  
Job time : 94.181 secs

RESULT 15  
AAR83582  
ID AAR83582 standard; protein; 325 AA.  
XX  
AC AAR83582;  
XX  
DT 13-JUN-1996 (first entry)  
XX  
DE CH2 to CH4 of human IgE epsilon chain.  
XX  
KM IGE; CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope;  
KM vaccine; allergy; antibody; constant heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN WO9526365-A1.  
XX  
PD 05-OCT-1995.  
XX  
PF 24-MAR-1995; 95WO-US003741.  
XX  
PR 28-MAR-1994; 94US-00218461.  
PR 25-OCT-1994; 94US-00328912.  
XX  
PA (UNBI-) UNITED BIOMEDICAL INC.  
XX  
PI Wang CY;  
XX  
PI WPI; 1995-351297/45.  
XX  
DR  
XX  
PT Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper T  
PT cell epitope - useful for eliciting antibody prodn. for allergy  
PT treatment.  
XX  
PS Disclosure; Page 55; 87pp; English.  
XX  
CC AAR83582 represents the human IgE epsilon chain from the CH2 to the CH4.  
CC Human IgE CH4 region peptides can be derived from this sequence and used  
CC in the preparation of a peptide immunogen that is useful in vaccines for  
CC treating allergic reactions. In the immunogen the IgE CH4 peptide is  
CC attached C-terminally to a series of amino acids including a helper T  
CC cell epitope. The immunogen may also opt. contain a fatty acid or fatty  
CC acid derivative, an invasin domain or alpha-NH2. The immunogen produces  
CC high titres of antibodies to the effector site in human IgE heavy chain  
CC (the CH4 domain peptide) which inhibit mast cell activation and reduce  
CC allergen-induced IgE prodn. The immunogens may be used in either a  
CC radially branching multimeric form or a linearly arranged monomeric form  
XX

GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: December 12, 2005, 19:23:41 ; Search time 23.1552 Seconds  
(without alignments)  
60.699 Million cell updates/sec

Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDGQVMDVLDLSTASTTQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a perfect greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	325	US-09-701-623C-1	Sequence 1, Appli
2	83	100.0	331	US-09-401-636-1	Sequence 1, Appli
3	42	50.6	337	US-09-605-703B-136	Sequence 136, App
4	42	50.6	404	US-09-605-703B-134	Sequence 134, App
5	41	49.4	303	US-09-107-532A-6113	Sequence 6113, Ap
6	40	48.2	105	US-09-902-540-16521	Sequence 16521, A
7	40	48.2	160	US-08-441-629-7	Sequence 7, Appli
8	40	48.2	160	US-08-776-207-7	Sequence 7, Appli
9	40	48.2	160	US-09-507-773-7	Sequence 7, Appli
10	40	48.2	160	US-10-016-447-7	Sequence 7, Appli
11	40	48.2	160	PCT-US95-09172-7	Sequence 7, Appli
12	40	48.2	211	US-09-252-991A-29508	Sequence 29508, A
13	40	48.2	531	US-08-687-590-29	Sequence 29, Appli
14	39	47.0	176	US-09-605-703B-388	Sequence 388, App
15	39	47.0	176	US-09-605-703B-390	Sequence 390, App
16	39	47.0	268	US-09-543-681A-4704	Sequence 4704, Ap
17	39	47.0	361	US-08-483-926A-9	Sequence 9, Appli
18	39	47.0	361	US-08-737-045-13	Sequence 13, Appli
19	38.5	46.4	90	US-09-227-357-635	Sequence 635, App
20	38.5	46.4	90	US-09-973-278-408	Sequence 408, App
21	38.5	46.4	199	US-09-949-016-8343	Sequence 8343, Ap
22	38.5	46.4	232	US-08-773-910-1	Sequence 1, Appli
23	38.5	46.4	232	US-09-199-892-1	Sequence 1, Appli
24	38	45.8	119	US-10-104-047-2322	Sequence 2322, Ap
25	38	45.8	138	US-09-621-976-5032	Sequence 5032, Ap
26	38	45.8	197	US-09-248-796A-27136	Sequence 27136, A
27	38	45.8	255	US-09-902-540-12488	Sequence 12488, A

28	38	45.8	340	2	US-10-155-947-6	Sequence 6, Appli
29	38	45.8	359	1	US-08-483-926A-8	Sequence 8, Appli
30	38	45.8	359	1	US-08-737-045-11	Sequence 11, Appli
31	38	45.8	359	2	US-08-932-871B-1	Sequence 1, Appli
32	38	45.8	359	2	US-09-476-919-1	Sequence 1, Appli
33	38	45.8	359	2	US-08-780-311A-1	Sequence 1, Appli
34	38	45.8	364	1	US-08-483-926A-10	Sequence 10, Appli
35	38	45.8	364	1	US-08-737-045-10	Sequence 10, Appli
36	38	45.8	431	2	US-09-252-991A-32589	Sequence 32589, A
37	38	45.8	951	2	US-09-252-991A-23338	Sequence 23338, A
38	38	45.8	971	1	US-08-446-010B-19	Sequence 19, Appli
39	38	45.8	971	1	US-08-446-010B-19	Sequence 19, Appli
40	38	45.8	971	1	US-08-805-445-19	Sequence 19, Appli
41	38	45.8	971	1	US-08-064-067D-19	Sequence 19, Appli
42	38	45.8	971	1	US-09-066-208-19	Sequence 19, Appli
43	37	44.6	170	2	US-09-248-796A-26360	Sequence 26360, A
44	37	44.6	170	2	US-09-107-532A-5092	Sequence 5092, Ap
45	37	44.6	207	2	US-09-270-767-32889	Sequence 32889, A

## ALIGNMENTS

```

RESULT 1
US-09-701-623C-1
; Sequence 1, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 325
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: CH2CH3 of human Ige
; PUBLICATION INFORMATION:
; AUTHORS: Dorrington,
; JOURNAL: Immunology
; VOLUME: 41
; PAGES: 3-25
; DATE: 1978
; US-09-701-623C-1

Query Match          100.0%: Score 83; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVLDLSTASTTQ 17
Db      48 EDGQVMDVLDLSTASTTQ 64

RESULT 2
US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636

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; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1

Query Match      100.0%; Score 83; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDLSTASTTQ 17
Db      54 EDGQVMDVLDLSTASTTQ 70

RESULT 3
US-09-605-703B-136
; Sequence 136, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schröder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 136
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-136

Query Match      50.6%; Score 42; DB 2; Length 337;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2 DGOVMDVLDLSTASTTQ 17
Db      205 EGTLPDVLQVAVSTR 220

RESULT 4
US-09-605-703B-134
; Sequence 134, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schröder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
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; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 134
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-134

Query Match      50.6%; Score 42; DB 2; Length 404;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2 DGOVMDVLDLSTASTTQ 17
Db      205 EGTLPDVLQVAVSTR 220

RESULT 5
US-09-107-532A-6113
; Sequence 613, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...303
; SEQUENCE DESCRIPTION: SEQ ID NO: 6113:
US-09-107-532A-6113

Query Match      49.4%; Score 41; DB 2; Length 303;
Best Local Similarity 56.2%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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QY 1 EDGQVMDVLDSTAST 16  
:|||||:|:|  
Db 209 KDGVSDVITSTMAST 224

RESULT 6  
US-09-902-540-16521

; Sequence 16521, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Mlegend, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 16521  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-16521

Query Match 48.2%; Score 40; DB 2; Length 105;  
Best Local Similarity 64.3%; Pred. No. 17;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQVMDVLDSTAST 16  
:|||||:|:|  
Db 57 GRPHVDVLDSTADRT 70

## RESULT 7

US-08-441-629-7  
; Sequence 7, Application US/08441629  
; Patent No. 5766923  
; GENERAL INFORMATION:  
; APPLICANT: Kirschner, Marc W.  
; APPLICANT: Kinoshita, No. 5766923iyuki  
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,629  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/279,217  
; FILING DATE: 22-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: HU95-01A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 160 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-441-629-7

Query Match 48.2%; Score 40; DB 1; Length 160;  
Best Local Similarity 57.1%; Pred. No. 29;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGQVMDVLDSTAST 15  
:|||||:|:|  
Db 134 DGHVMDQDLKASRT 147

## RESULT 8

US-08-776-207-7  
; Sequence 7, Application US/08776207A  
; Patent No. 6080718  
; GENERAL INFORMATION:  
; APPLICANT: Kirschner, Marc W.  
; APPLICANT: Kinoshita, No. 6080718iyuki  
; TITLE OF INVENTION: Receptor-Ligand Assay  
; FILE REFERENCE: HU95-01A2  
; CURRENT APPLICATION NUMBER: US/08/776,207A  
; EARLIER FILING DATE: 1997-06-23  
; EARLIER APPLICATION NUMBER: PCT/US95/09172  
; EARLIER FILING DATE: 1995-07-19  
; EARLIER APPLICATION NUMBER: 08/441,629  
; EARLIER FILING DATE: 1995-05-15  
; EARLIER APPLICATION NUMBER: 08/279,217  
; EARLIER FILING DATE: 1994-07-22  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-776-207-7

Query Match 48.2%; Score 40; DB 2; Length 160;  
Best Local Similarity 57.1%; Pred. No. 29;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGQVMDVLDSTAST 15  
:|||||:|:|  
Db 134 DGHVMDQDLKASRT 147

## RESULT 9

US-09-507-773-7  
; Sequence 7, Application US/09507773  
; Patent No. 6399386  
; GENERAL INFORMATION:  
; APPLICANT: Kirschner, Marc W.  
; APPLICANT: Kinoshita, No. 6399386iyuki  
; TITLE OF INVENTION: Receptor-Ligand Assay  
; FILE REFERENCE: HU95-01A2  
; CURRENT APPLICATION NUMBER: US/09/507,773  
; CURRENT FILING DATE: 2000-02-18  
; PRIOR APPLICATION NUMBER: 08/776,207  
; PRIOR FILING DATE: 1997-06-23  
; PRIOR APPLICATION NUMBER: 08/441,629  
; PRIOR FILING DATE: 1995-05-15  
; PRIOR APPLICATION NUMBER: 08/279,217  
; PRIOR FILING DATE: 1994-07-22  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 160  
; TYPE: PRT

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; ORGANISM: Mus musculus
; US-09-507-773-7
Query Match      48.2%; Score 40; DB 2; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGVMDVDLSTAST 15
Db      134 DGHVMDDLKASRT 147

RESULT 10
US-10-016-447-7
; Sequence 7, Application US/10016447
; Patent No. 6844193
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: H095-01A2
; CURRENT APPLICATION NUMBER: US/10/016,447
; PRIORITY FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/776,207
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/441,629
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/279,217
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-016-447-7

Query Match      48.2%; Score 40; DB 2; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGVMDVDLSTAST 15
Db      134 DGHVMDDLKASRT 147

RESULT 11
PCT-US95-09172-7
; Sequence 7, Application PC/TUS9509172
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, Noriyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09172
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/279,217
; FILING DATE: 22-JUL-1994
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,629
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09172-7

Query Match      48.2%; Score 40; DB 4; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGVMDVDLSTAST 15
Db      134 DGHVMDDLKASRT 147

RESULT 12
US-09-252-991A-29508
; Sequence 29508, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIORITY FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29508
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29508

Query Match      48.2%; Score 40; DB 2; Length 211;
Best Local Similarity 57.1%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 EDGQVMDVISTAS 14
Db      108 EDGQVLAHELYTAS 121

RESULT 13
US-08-687-590-29
; Sequence 29, Application US/08687590
; Patent No. 6255070
; GENERAL INFORMATION:
; APPLICANT: Willison, Keith Robert
; APPLICANT: Kubota, Hiroyshi
; APPLICANT: Ashworth, Alan
; TITLE OF INVENTION: Folding Proteins
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```



```

STATE: California
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,590
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00192
FILING DATE: 31-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401791.0
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9418234.2
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Baetian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 084619-000000US
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 531 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
OS-08-687-590-29

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Query Match	48.2%	Score 40;	DB 2;	Length 531;
Best Local Similarity	66.7%	Pred. No. 1,2e+02;		
Matches	8;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;
OY	1	EDGQMDVDLST	12	
Db	472	ESGQLVGDVLT	483	

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RESULT 14
US-09-605-703B-388
; Sequence 388, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habershauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/605.703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 388
; LENGTH: 176
; TYPE: PRP
; ORGANISM: Corynebacterium glutamicum
; US-09-605-703B-388

```

Query Match	47.0%;	Score 39;	DB 2;	Length 176;
Best Local Similarity	66.7%;	Pred. No. 48;		
Matches	8;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;

QY 1 EDGQVMDVDLST 12

Db 30 ENGQVPEVDAST 41

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RESULT 15
US-09-605-703B-390
Sequence 390, Application US/09605703B
Patent No. 6962989
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauser, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
FILE REFERENCE: BGI-139C
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 390
LENGTH: 176
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-605-703B-390

```

Query Match	47.0%;	Score 39;	DB 2;	Length 176;
Best Local Similarity	66.7%;	Pred. No. 48;		
Matches	8;	Conservative	2;	Mismatches
			2;	Indels
				Gaps
				0;
QY	1	EDGQVMDVDIST	12	
		: : : : :		
Db	30	ENGQVPEVDAST	41	

Search completed: December 12, 2005, 19:37:08  
Job time : 24.1552 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 75.9138 Seconds  
(without alignments)  
93.568 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83  
Sequence: 1 EDGQVMDVLDSTASTTQ 17

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBSCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBSCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBSCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBSCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBSCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBSCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	US-10-758-165-16	Sequence 16, Appl
2	83	100.0	128	US-10-152-190-7	Sequence 7, Appl
3	83	100.0	236	US-10-152-190-9	Sequence 9, Appl
4	83	100.0	320	US-09-847-208-6	Sequence 6, Appl
5	83	100.0	320	US-10-000-439-6	Sequence 6, Appl
6	83	100.0	323	US-09-949-375A-2	Sequence 2, Appl
7	83	100.0	323	US-09-949-375A-4	Sequence 4, Appl
8	83	100.0	323	US-09-949-375A-6	Sequence 6, Appl
9	83	100.0	323	US-10-363-954A-2	Sequence 4, Appl
10	83	100.0	323	US-10-363-954A-4	Sequence 4, Appl
11	83	100.0	323	US-10-363-954A-6	Sequence 6, Appl
12	83	100.0	327	US-10-627-556-224	Sequence 224, App
13	83	100.0	330	US-09-949-375A-10	Sequence 10, Appl
14	83	100.0	330	US-10-363-954A-10	Sequence 10, Appl
15	83	100.0	331	US-09-401-636-1	Sequence 1, Appl
16	83	100.0	331	US-10-176-664-1	Sequence 1, Appl
17	83	100.0	331	US-10-207-655-329	Sequence 329, App
18	83	100.0	331	US-10-673-594-1	Sequence 1, Appl
19	83	100.0	331	US-10-627-556-97	Sequence 97, Appl
20	83	100.0	331	US-10-627-556-174	Sequence 174, App
21	83	100.0	336	US-09-949-375A-8	Sequence 8, Appl
22	83	100.0	336	US-10-363-954A-8	Sequence 10, Appl
23	83	100.0	346	US-10-152-190-10	Sequence 10, Appl
24	83	100.0	346	US-10-152-190-14	Sequence 14, Appl
25	83	100.0	347	US-10-152-190-12	Sequence 12, Appl
26	83	100.0	347	US-10-152-190-13	Sequence 13, Appl
27	83	100.0	348	US-10-152-190-11	Sequence 11, Appl

28	83	100.0	427	US-09-847-208-5	Sequence 5, Appl
29	83	100.0	427	US-10-000-439-5	Sequence 5, Appl
30	83	100.0	428	US-09-916-230-1	Sequence 1, Appl
31	83	100.0	428	US-09-949-375A-1	Sequence 1, Appl
32	83	100.0	428	US-10-047-542-60	Sequence 60, Appl
33	83	100.0	428	US-10-363-954A-1	Sequence 1, Appl
34	83	100.0	441	US-09-949-375A-7	Sequence 7, Appl
35	83	100.0	441	US-10-363-954A-7	Sequence 7, Appl
36	83	100.0	497	US-10-872-932A-35	Sequence 35, Appl
37	83	100.0	497	US-10-810-881A-34	Sequence 34, Appl
38	83	100.0	497	US-10-981-936-34	Sequence 34, Appl
39	83	100.0	569	US-09-847-208-7	Sequence 7, Appl
40	83	100.0	569	US-10-000-439-7	Sequence 7, Appl
41	83	100.0	574	US-10-047-542-45	Sequence 45, Appl
42	83	100.0	574	US-10-214-524-37	Sequence 37, Appl
43	83	100.0	574	US-10-050-902-176	Sequence 176, App
44	83	100.0	574	US-10-050-898-176	Sequence 176, App
45	83	100.0	586	US-10-627-556-384	Sequence 384, App

## ALIGNMENTS

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RESULT 1
US-10-758-165-16
; Sequence 16, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-758-165-16

Query Match      100.0%; Score 83; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3,9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVLDSTASTTQ 17
      |||||
DB      1 EDGQVMDVLDSTASTTQ 17

RESULT 2
US-10-152-190-7
; Sequence 7, Application US/10152190
; Publication No. US20030096369A1
; GENERAL INFORMATION:
; APPLICANT: Moresey, Mohamed A.
; TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
; FILE REFERENCE: PCI11011A
; CURRENT APPLICATION NUMBER: US/10/152,190
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Modified Human CH2 domain
US-10-152-190-7

Query Match      100.0%; Score 83; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 4,2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 EDGQVMDVLDSTASTQ 17
      |||||
Db      70 EDGQVMDVLDSTASTQ 86

RESULT 3
US-10-152-190-9
; Sequence 9, Application US/10152190
; Publication No. US20030096369A1
; GENERAL INFORMATION:
; APPLICANT: Morse, Mohamed A.
; TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic Ige vaccines
; FILE REFERENCE: PC11011A
; CURRENT APPLICATION NUMBER: US/10/152.190
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Modified Human CH2-CH4 carrier protein
US-10-152-190-9

Query Match      100.0%; Score 83; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 EDGQVMDVLDSTASTQ 17
      |||||
Db      70 EDGQVMDVLDSTASTQ 86

RESULT 4
US-09-847-208-6
; Sequence 6, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-6

Query Match      100.0%; Score 83; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 EDGQVMDVLDSTASTQ 17
      |||||
Db      43 EDGQVMDVLDSTASTQ 59

RESULT 5
US-10-000-439-6
; Sequence 6, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000.439
```

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; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-6

Query Match      100.0%; Score 83; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 EDGQVMDVLDSTASTQ 17
      |||||
Db      43 EDGQVMDVLDSTASTQ 59

RESULT 6
US-09-949-375A-2
; Sequence 2, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949.375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human Ige heavy chain C2 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)
; OTHER INFORMATION: Human Ige heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human Ige heavy chain C4 domain
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (210)..(218)
; OTHER INFORMATION: Epitope including C3C4 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
```

NAME/KEY: MISC FEATURE  
LOCATION: (196)..(206)  
OTHER INFORMATION: Epitope in FG loop  
US-09-949-375A-2

Query Match 100.0%; Score 83; DB 3; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVDLSTASTTQ 17  
DB 46 EDGQVMDVDLSTASTTQ 62

RESULT 7  
US-09-949-375A-4  
Sequence 4, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE  
FILE REFERENCE: 3631-0111P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.  
US-09-949-375A-4

Query Match 100.0%; Score 83; DB 3; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVDLSTASTTQ 17  
DB 46 EDGQVMDVDLSTASTTQ 62

RESULT 8  
US-09-949-375A-6  
Sequence 6, Application US/09949375A  
Patent No. US20020172673A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE  
FILE REFERENCE: 3631-0111P  
CURRENT APPLICATION NUMBER: US/09/949,375A  
CURRENT FILING DATE: 2002-01-18  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.  
US-09-949-375A-6

Query Match 100.0%; Score 83; DB 3; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVDLSTASTTQ 17  
DB 46 EDGQVMDVDLSTASTTQ 62

RESULT 9

US-10-363-954A-2  
Sequence 2, Application US/10363954A  
Publication No. US20040156638A1  
GENERAL INFORMATION:  
APPLICANT: KLYSNER, Steen et al.  
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE  
FILE REFERENCE: 4614-0115P  
CURRENT APPLICATION NUMBER: US/10/363,954A  
CURRENT FILING DATE: 2003-03-06  
PRIOR APPLICATION NUMBER: US 60/232,831  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: DK PA 2000 01326  
PRIOR FILING DATE: 2000-09-06  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (8)..(103)  
OTHER INFORMATION: Human IGE heavy chain C2 domain  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (112)..(211)  
OTHER INFORMATION: Human IGE heavy chain C3 domain  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (216)..(317)  
OTHER INFORMATION: Human IGE heavy chain C4 domain  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (104)..(111)  
OTHER INFORMATION: Linker between domains C2 and C3  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (212)..(215)  
OTHER INFORMATION: Linker between domains C3 and C4  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (100)..(114)  
OTHER INFORMATION: Epitope including C2C3 linker  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (210)..(218)  
OTHER INFORMATION: Epitope including C3C4 linker  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (139)..(145)  
OTHER INFORMATION: Epitope in BC loop  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (167)..(175)  
OTHER INFORMATION: Epitope in DE loop  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (196)..(206)  
OTHER INFORMATION: Epitope in FG loop  
US-10-363-954A-2

Query Match 100.0%; Score 83; DB 4; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 EDGQVMDVDLSTASTTQ 17  
DB 46 EDGQVMDVDLSTASTTQ 62

RESULT 10  
US-10-363-954A-4  
Sequence 4, Application US/10363954A

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; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial protein sequence optimized for expression in mammalian
; OTHER INFORMATION: cells of human IGE heavy chain fragment spanning C2, C3, and C4.
; NAME/KEY: DOMAIN
; LOCATION: (11)..(116)
; OTHER INFORMATION: Human IGE heavy chain C1 domain
US-10-363-954A-4
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Query Match      100.0%; Score 83; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 EDGQVMDVDLSTASTQ 17
Db      46 EDGQVMDVDLSTASTQ 62
```

```
RESULT 11
US-10-363-954A-6
; Sequence 6, Application US/10363954A
; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial protein sequence optimized for expression in
; OTHER INFORMATION: E. coli of human IGE heavy chain fragment spanning C2,
; OTHER INFORMATION: C3, and C4
US-10-363-954A-6
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```
Query Match      100.0%; Score 83; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 EDGQVMDVDLSTASTQ 17
Db      46 EDGQVMDVDLSTASTQ 62
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RESULT 12
US-10-627-556-224
; Sequence 224, Application US/10627556
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; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.C1P2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 224
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-10-627-556-224
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```
Query Match      100.0%; Score 83; DB 5; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 EDGQVMDVDLSTASTQ 17
Db      50 EDGQVMDVDLSTASTQ 66
```

```
RESULT 13
US-09-949-375A-10
; Sequence 10, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 9.
US-09-949-375A-10
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Query Match      100.0%; Score 83; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EDGQVMDVDLSTASTQ 17
Db      46 EDGQVMDVDLSTASTQ 62
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RESULT 14
US-10-363-954A-10
; Sequence 10, Application US/10363954A
; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
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; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial protein sequence optimised for expression in
; OTHER INFORMATION: mammalian cells of human Ige fragment spanning C2, C3, C4
; US-10-363-954A-10

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Query Match          100.0%; Score 83; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EDGQVMDVLDLSTASTTQ 17
        |||||
Db      46 EDGQVMDVLDLSTASTTQ 62

```

```

RESULT 15
US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-1

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```

Query Match          100.0%; Score 83; DB 3; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EDGQVMDVLDLSTASTTQ 17
        |||||
Db      54 EDGQVMDVLDLSTASTTQ 70

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Search completed: December 12, 2005, 20:19:26
Job time : 76.9136 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.78448 Seconds  
(without alignments)  
34.094 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83

Sequence: 1 EDGQVMDVLDSTASTTQ 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US09\_NEM\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEM\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEM\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEM\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_NEM\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEM\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEM\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	325	6	US-10-723-207-1
2	83	100.0	497	6	US-10-999-866-34
3	83	100.0	497	7	US-11-061-821-34
4	38	45.8	317	7	US-11-055-822-320
5	38	45.8	340	7	US-11-100-352-6
6	38	45.8	359	6	US-10-888-962-5
7	37	44.6	340	7	US-11-100-352-2
8	37	44.6	340	7	US-11-100-352-5
9	37	44.6	1049	7	US-11-137-462-42
10	36	43.4	742	6	US-10-658-986-2
11	36	43.4	777	6	US-10-658-986-4
12	35	42.2	112	6	US-10-467-657-6306
13	35	42.2	193	7	US-11-055-822-568
14	35	42.2	352	6	US-10-888-962-8
15	35	42.2	612	6	US-10-518-018-1
16	35	42.2	895	6	US-10-485-517-129
17	34	41.0	263	6	US-10-467-657-6102
18	34	41.0	319	6	US-10-878-556A-159
19	34	41.0	753	6	US-10-467-657-6852
20	34	41.0	2516	6	US-10-647-956A-2
21	34	41.0	2828	7	US-11-080-991-54
22	34	41.0	2828	7	US-11-186-284-49
23	33	39.8	226	6	US-10-467-657-6482
24	33	39.8	279	6	US-10-467-657-996
25	33	39.8	339	6	US-10-821-234-1507

26	33	39.8	382	7	US-11-055-822-302	Sequence 302, App
27	33	39.8	382	7	US-11-055-822-344	Sequence 344, App
28	33	39.8	710	7	US-11-045-802-22	Sequence 22, Appl
29	33	39.8	710	7	US-11-045-802-23	Sequence 23, Appl
30	33	39.8	3717	6	US-10-821-234-1076	Sequence 1076, Ap
31	32	38.6	169	7	US-11-110-082-22	Sequence 22, Appl
32	32	38.6	219	6	US-10-793-626-32	Sequence 21, Appl
33	32	38.6	250	6	US-10-821-234-1297	Sequence 1297, Ap
34	32	38.6	257	6	US-10-467-657-120	Sequence 720, App
35	32	38.6	293	6	US-10-821-234-1374	Sequence 1374, Ap
36	32	38.6	306	6	US-10-878-556A-56	Sequence 56, Appl
37	32	38.6	317	6	US-10-821-234-1529	Sequence 1529, Ap
38	32	38.6	333	7	US-11-074-176-32	Sequence 32, Appl
39	32	38.6	334	7	US-11-129-143-103	Sequence 103, App
40	32	38.6	367	6	US-10-888-962-6	Sequence 6, Appli
41	32	38.6	384	6	US-10-858-730-216	Sequence 216, App
42	32	38.6	393	7	US-11-055-822-356	Sequence 356, App
43	32	38.6	393	7	US-11-055-822-974	Sequence 974, App
44	32	38.6	493	6	US-10-878-556A-65	Sequence 65, Appl
45	32	38.6	581	6	US-10-793-626-28	Sequence 28, Appl

## ALIGNMENTS

RESULT 1  
US-10-723-207-1  
Sequence 1, Application US/10723207  
Publication No. US20050250934A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Yi  
INVENTOR: Walfield, Alan M.  
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
FILE REFERENCE: 1151-4153US2  
CURRENT FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: 09/701,623  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US99/13959  
PRIOR FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: 09/100,287  
PRIOR FILING DATE: 1998-06-20  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 325  
TYPE: PRT  
ORGANISM: HUMAN  
FEATURE:  
OTHER INFORMATION: CH2CH3 of human Igt  
PUBLICATION INFORMATION:  
AUTHORS: Dorrington,  
JOURNAL: Immunology  
VOLUME: 41  
PAGES: 3-25  
DATE: 1978  
US-10-723-207-1  
Query Match  
Best Local Similarity 100.0%; Pred. No. 8.3e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EDGQVMDVLDSTASTTQ 17  
|||||  
Db 48 EDGQVMDVLDSTASTTQ 64  
RESULT 2  
US-10-999-866-34  
Sequence 34, Application US/10999866  
Publication No. US20050266004A1

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; GENERAL INFORMATION:
; APPLICANT: GILES-ROMAR, Jill; SCALLION, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AN
; FILE REFERENCE: CEN5042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 60/527,794
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(497)
; OTHER INFORMATION: Ige heavy chain constant region
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(210)
; OTHER INFORMATION: CH1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(210)
; OTHER INFORMATION: CH2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (211)..(318)
; OTHER INFORMATION: CH3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(497)
; OTHER INFORMATION: CH4
; OTHER INFORMATION: CH4
US-10-999-866-34

Query Match      100.0%; Score 83; DB 6; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTASTQ 17
Db      151 EDGQVMDVLDSTASTQ 167

RESULT 3
US-11-061-821-34
; Sequence 34, Application US/11061821
; Publication No. US2005026605A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George; Li, Li; Oneil, Karyn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES
; FILE REFERENCE: CEN5048 NP
; CURRENT APPLICATION NUMBER: US/11/061,821
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/548,648
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver 3.3
; SEQ ID NO 34
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(497)
; OTHER INFORMATION: Ige heavy chain constant region
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(103)
; OTHER INFORMATION: CH1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(210)
; OTHER INFORMATION: CH2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (211)..(318)
; OTHER INFORMATION: CH3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(497)
; OTHER INFORMATION: CH4
; OTHER INFORMATION: CH4
US-11-061-821-34

Query Match      100.0%; Score 83; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTASTQ 17
Db      151 EDGQVMDVLDSTASTQ 167

RESULT 4
US-11-055-822-320
; Sequence 320, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 320
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-320

Query Match      45.8%; Score 38; DB 7; Length 317;
Best Local Similarity 42.9%; Pred. No. 6.6;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTAS 14
Db      185 EDGQVMDVLDSTAS 198
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; LOCATION: (104)..(210)
; OTHER INFORMATION: CH2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (211)..(318)
; OTHER INFORMATION: CH3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(497)
; OTHER INFORMATION: CH4
; OTHER INFORMATION: CH4
US-11-061-821-34

Query Match      100.0%; Score 83; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTASTQ 17
Db      151 EDGQVMDVLDSTASTQ 167

RESULT 4
US-11-055-822-320
; Sequence 320, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 320
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-320

Query Match      45.8%; Score 38; DB 7; Length 317;
Best Local Similarity 42.9%; Pred. No. 6.6;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTAS 14
Db      185 EDGQVMDVLDSTAS 198
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RESULT 5
US-11-100-352-6
; Sequence 6, Application US/11100352
; Publication No. US20050266016A1
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard S.
; APPLICANT: Kubo, Aya
; TITLE OF INVENTION: Porinb (porb) as a Therapeutic Target
; FILE REFERENCE: BERK-006
; CURRENT APPLICATION NUMBER: US/11/100,352
; CURRENT FILING DATE: 2005-04-05
; PRIOR APPLICATION NUMBER: US/10/155,947
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/09/775,195
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 340
; TYPE: PRT
; ORGANISM: C. trachomatis (C)
US-11-100-352-6

Query Match          45.8%; Score 38; DB 7; Length 340;
Best Local Similarity 50.0%; Pred. No. 7.4;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 EDGQMDVDLSTASTT 16
Db      78 BEAQKDVPVVTSMTT 93

RESULT 6
US-10-888-962-5
; Sequence 5, Application US/1088962
; Publication No. US20050266531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Basu, Arnab
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-888-962-5

Query Match          45.8%; Score 38; DB 6; Length 359;
Best Local Similarity 42.9%; Pred. No. 7.9;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 GQWMDVDLSTASTT 16
Db      75 GSVYDIEIDTLETT 88

RESULT 7
US-11-100-352-2
; Sequence 2, Application US/11100352
; Publication No. US20050266016A1
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard S.
```

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; APPLICANT: Kubo, Aya
; TITLE OF INVENTION: Porinb (porb) as a Therapeutic Target
; FILE REFERENCE: BERK-006
; CURRENT APPLICATION NUMBER: US/11/100,352
; CURRENT FILING DATE: 2005-04-05
; PRIOR APPLICATION NUMBER: US/10/155,947
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/09/775,195
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: C. trachomatis
US-11-100-352-2

Query Match          44.6%; Score 37; DB 7; Length 340;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 EDGQMDVDLSTASTT 16
Db      78 BEAQKDVPVVTSVTT 93

RESULT 8
US-11-100-352-5
; Sequence 5, Application US/11100352
; Publication No. US20050266016A1
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard S.
; APPLICANT: Kubo, Aya
; TITLE OF INVENTION: Porinb (porb) as a Therapeutic Target
; FILE REFERENCE: BERK-006
; CURRENT APPLICATION NUMBER: US/11/100,352
; CURRENT FILING DATE: 2005-04-05
; PRIOR APPLICATION NUMBER: US/10/155,947
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/09/775,195
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 340
; TYPE: PRT
; ORGANISM: C. trachomatis (L2)
US-11-100-352-5

Query Match          44.6%; Score 37; DB 7; Length 340;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 EDGQMDVDLSTASTT 16
Db      78 BEAQKDVPVVTSVTT 93

RESULT 9
US-11-137-465-42
; Sequence 42, Application US/11137465
; Publication No. US20050255558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahnlick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
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; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-42
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Query Match          44.6%; Score 37; DB 7; Length 1049;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      1 EDGQVMDVD 9
Db      119 EDGQVQCID 127
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RESULT 10
US-10-658-986-2
; Sequence 2, Application US/10658986
; Publication No. US20050255476A1
; GENERAL INFORMATION:
; APPLICANT: Wordinger, Robert J.
; TITLE OF INVENTION: Methods for Diagnosing Glaucoma and Discovering Anti-Glaucoma Dru
; FILE REFERENCE: 1581 US P
; CURRENT APPLICATION NUMBER: US/10/658,986
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/21054
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: USSN 60/033,227
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 742
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-658-986-2

Query Match          43.4%; Score 36; DB 6; Length 742;
Best Local Similarity 46.7%; Pred. No. 43;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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QY      3 GQWVDVLTASTTQ 17
Db      329 GQWVHYDMNTASLSQ 343
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RESULT 11
US-10-658-986-4
; Sequence 4, Application US/10658986
; Publication No. US20050255476A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Abbot F.
; APPLICANT: Wordinger, Robert J.
; TITLE OF INVENTION: Methods for Diagnosing Glaucoma and Discovering Anti-Glaucoma Dru
; FILE REFERENCE: 1581 US P
; CURRENT APPLICATION NUMBER: US/10/658,986
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/21054
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; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: USSN 60/033,227
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 777
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-658-986-4
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Query Match          43.4%; Score 36; DB 6; Length 777;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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QY      3 GQWVDVLTASTTQ 17
Db      329 GQWVHYDMNTASLSQ 343
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RESULT 12
US-10-467-657-6306
; Sequence 6306, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqW1n9, version 1.04
; SEQ ID NO 6306
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6306
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Query Match          42.2%; Score 35; DB 6; Length 112;
Best Local Similarity 50.0%; Pred. No. 6.5;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY      1 EDGQVMDVLTASTS 14
Db      4 EDGQVREVSAGAAA 17
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RESULT 13
US-11-055-822-568
; Sequence 568, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
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; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 568
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-568

Query Match      42.2%; Score 35; DB 7; Length 193;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      3 GQVMDVDLSTASTT 16
Db      77 GAVVDVDTGAAVT 90

RESULT 14
US-10-888-962-8
; Sequence 8, Application US/10888962
; Publication No. US20050266531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Baau, Arnab
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-888-962-8

Query Match      42.2%; Score 35; DB 6; Length 352;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      3 GQVMDVDLSTASTT 16
Db      75 GQVVELIDTLETT 88

RESULT 15
US-10-518-018-1
; Sequence 1, Application US/10518018
; Publication No. US20050249715A1
; GENERAL INFORMATION:
; APPLICANT: Shitaki, Kimiyasu
; APPLICANT: Kurokawa, Masahiko
```

```

; APPLICANT: Tamura, Yoshitaka
; APPLICANT: Yamauchi, Koji
; APPLICANT: Wakabayashi, Hiroyuki
; APPLICANT: Shin, Kouichirou
; TITLE OF INVENTION: Inhibitor of Interleukin-6 Production
; FILE REFERENCE: TOYA108.008APC
; CURRENT APPLICATION NUMBER: US/10/518,018
; PRIOR FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/JP2003/015009
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2003-45509
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-518-018-1

Query Match      42.2%; Score 35; DB 6; Length 612;
Best Local Similarity 46.7%; Pred. No. 51;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      3 GQVMDVDLSTASTTQ 17
Db      121 GQIVDHDIDFAPETE 135
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Search completed: December 12, 2005, 20:19:50  
Job time : 3.78448 secs

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## OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 14.3621 Seconds  
(without alignments)  
113.889 Million cell updates/sec

Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDGQVMDVLDLASTATTQ 17

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	83	100.0	428	1	EHNU
2	78	99.0	426	2	I36948
3	44	53.0	118	2	G84322
4	44	53.0	578	2	H65006
5	44	53.0	757	2	T05688
6	42	50.6	361	2	E86692
7	41	49.4	225	1	J03040
8	41	49.4	374	2	H91251
9	41	49.4	694	2	J02041
10	41	49.4	375	2	H69200
11	41	49.4	677	2	A69210
12	41	49.4	879	2	F85875
13	41	49.4	879	2	E91031
14	41	49.4	1155	2	B96761
15	40	48.2	146	2	H85545
16	40	48.2	171	2	H43612
17	40	48.2	531	2	S43063
18	39	47.0	112	2	F70954
19	39	47.0	150	2	T24956
20	39	47.0	257	2	A10935
21	39	47.0	362	2	S22395
22	39	47.0	445	2	B40590
23	39	47.0	1459	2	T30196
24	39	47.0	1847	2	T28969
25	38.5	46.4	219	2	T34523
26	38	45.8	111	2	T36386
27	38	45.8	120	1	R5H524
28	38	45.8	145	2	AH2102
29	38	45.8	203	2	C95882

30	38	45.8	205	2	T08272	probable thioredox
31	38	45.8	255	2	AB0986	conserved hypothet
32	38	45.8	347	2	H84270	geranylgeranyl dip
33	38	45.8	359	2	A35714	fetuin precursor -
34	38	45.8	364	2	S22394	fetuin precursor -
35	38	45.8	537	1	Q0BE30	BRP2 protein - hu
36	38	45.8	552	2	AB0496	probable membrane
37	38	45.8	568	2	T34522	hypothetical prote
38	38	45.8	720	2	F85572	probable outer mem
39	38	45.8	723	2	G90721	probable outer mem
40	38	45.8	730	2	B83592	hypothetical prote
41	38	45.8	818	1	E64807	outer membrane ush
42	38	45.8	1237	2	T37529	hypothetical prote
43	38	45.8	1502	2	T48309	hypothetical prote
44	38	45.8	1630	2	A53577	ascites sialoglyco
45	38	45.8	3856	2	T51174	ataxia-telangiecta

## ALIGNMENTS

## RESULT 1

Ig epsilon chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 09-Jul-2004  
C/Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46  
R/Flanagan, J.G.; Rabbits, T.H.  
EMBO J. 1, 655-660, 1982  
A/Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene  
A/Reference number: A22771; MUID:84236029; PMID:6234164  
A/Accession: A22771  
A/Molecule type: DNA  
A/Residues: 1-428 <FLA>  
A/Cross-references: UNIPROT:P01854; UNIPARC:UPI000004B848; GB:L00022; GB:J00227; GB:V005  
R/Ueda, S.; Nakai, S.; Nishida, Y.; Hiseajima, H.; Honjo, T.  
EMBO J. 1, 1539-1544, 1982  
A/Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog  
A/Reference number: A23195; MUID:84207910; PMID:6327276  
A/Accession: A23195  
A/Molecule type: DNA  
A/Residues: 2-428 <UED>  
A/Cross-references: UNIPARC:UPI0000173783; GB:J00222; NID:G184755  
R/Zhang, K.; Saxon, A.; Max, E.E.  
J. Exp. Med. 176, 233-243, 1992  
A/Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing  
A/Reference number: PH1214; MUID:92308839; PMID:1613458  
A/Accession: PH1214  
A/Molecule type: DNA  
A/Residues: 320-428 <ZHA>  
A/Cross-references: UNIPARC:UPI000014452D; EMBL:X63693; GB:S36668; NID:G32987  
R/Seno, M.; Kurokawa, T.; Ono, Y.; Ono, H.; Saesda, R.; Igataehi, K.; Kikuchi, M.; Sugi  
Nucleic Acids Res. 11, 719-726, 1983  
A/Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha  
A/Reference number: A93491; MUID:83168897; PMID:6300763  
A/Accession: A93491  
A/Molecule type: mRNA  
A/Residues: 1-428 <SEN>  
A/Cross-references: UNIPARC:UPI000004B848; GB:L00022; GB:J00227; GB:V00555; NID:G185035  
R/Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.  
Cell 29, 691-699, 1982  
A/Title: Duplication and deletion in the human immunoglobulin epsilon genes.  
A/Reference number: A90824; MUID:83001945; PMID:6288268  
A/Accession: A90824  
A/Molecule type: DNA  
A/Residues: 1-358, 'L', 360-428 <MAX>  
A/Cross-references: UNIPARC:UPI0000173784; GB:J00222; NID:G184755  
A/Note: this sequence difference may be due to polymorphism  
R/Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.  
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3  
A/Reference number: A94418  
A/Accession: A94418  
A/Molecule type: protein





C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: H65006  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: H65006  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-578 <BLAT>  
A:Cross-references: UNIPARC:UPI000016ED73; GB:AE000322; GB:U00096; NID:G1788672; PIDN:AA  
A:Experimental source: strain K-12, substrain MG1655

Query Match 53.0%; Score 44; DB 2; Length 578;  
Best Local Similarity 57.1%; Pred. No. 18;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQMDVDLSTAS 14  
:::|::|::|::|  
Db 346 QNGQVEYDISTAS 359

RESULT 5  
T05688  
hypothetical protein F20M13.160 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1998 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T05688  
R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15420  
A:Accession: T05688  
A:Molecule type: DNA  
A:Residues: 1-757 <BEV>  
A:Cross-references: UNIPROT:Q9S2N9; UNIPARC:UPI000004AFAC; EMBL:AL035540  
A:Experimental source: cultivar Columbia; BAC clone F20M13  
C:Genetics:  
A:Map position: 4  
A:Introns: 6/2; 235/1; 496/3; 571/3; 606/3; 633/3; 663/1; 696/3; 736/3  
A:Note: F20M13.160

Query Match 53.0%; Score 44; DB 2; Length 757;  
Best Local Similarity 61.5%; Pred. No. 24;  
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQMDVDLSTAS 13  
:::|::|::|  
Db 476 QDGRLDVPLSTAS 488

RESULT 6  
E86692  
N-acetylglucosyl-L-alanine amidase (EC 3.5.1.28) [imported] - Lactococcus lactis subsp.  
N:Alternate names: N-acetylglucosylamidase  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E86692  
R:Boletín, A.; Wincker, P.; Mauge, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se  
A:Reference number: A6625; MUID:21235186; PMID:11337471  
A:Accession: E86692  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-361 <STO>  
A:Cross-references: UNIPROT:Q9C125; UNIPARC:UPI000006859; GB:AE005176; PID:G12723426; F  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: acmd  
C:Keywords: hydrolase

Query Match 50.6%; Score 42; DB 2; Length 361;  
Best Local Similarity 57.1%; Pred. No. 23;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GQWMDVDLSTAST 16  
:::|::|::|::|  
Db 297 GQWMDVDLSTAST 310

RESULT 7  
J02040  
nonstructural protein V - simian paramyxovirus SV41  
C:Species: simian paramyxovirus SV41  
C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: J02040  
R:Kawano, M.; Tsurudome, M.; Okai, N.; Nishio, M.; Komada, H.; Matsumura, H.; Kusagawa, S.  
J. Gen. Virol. 74, 911-916, 1993  
A:Title: Sequence determination of the P gene of simian virus 41: presence of irregular  
A:Reference number: J02040; MUID:93260408; PMID:8492098  
A:Accession: J02040  
A:Molecule type: genomic RNA  
A:Residues: 1-225 <KAW>  
A:Cross-references: UNIPROT:P36315; UNIPARC:UPI0000138E96; GB:S60811; NID:G385516; PIDN:  
A:Genetics:  
C:Superfamily: simian paramyxovirus nonstructural protein V; V/P protein homology  
C:Keywords: alternative splicing; nonstructural protein  
F.1-163/Domain: V/P protein homology <VPN>

Query Match 49.4%; Score 41; DB 1; Length 225;  
Best Local Similarity 46.7%; Pred. No. 20;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 GQWMDVDLSTAST 17  
:::|::|::|::|  
Db 109 GRMDDLATGTVTQ 123

RESULT 8  
H91251  
Probable tail protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: H91251  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gsawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno  
A:Reference number: A9629; MUID:21156231; PMID:11258796  
A:Accession: H91251  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-374 <HAY>  
A:Cross-references: UNIPROT:Q8X2Y0; UNIPARC:UPI000002A42; GB:BA000007; PIDN:BA038407.1;  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: EC64984  
C:Superfamily: phage Mu gene P protein

Query Match 49.4%; Score 41; DB 2; Length 374;  
Best Local Similarity 53.3%; Pred. No. 35;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQMDVDLSTAST 15  
:::|::|::|::|  
Db 287 ENGQMDINDLTLAVT 301

RESULT 9  
J02041  
polymerase-associated nucleocapsid phosphoprotein - simian paramyxovirus SV41  
N:Alternate names: P protein  
C:Species: simian paramyxovirus SV41

C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: JQ2041  
R/Kawano, M.; Tsurudome, M.; Oki, N.; Nishio, M.; Komada, H.; Matsumura, H.; Kusagawa, S  
J. Gen. Virol. 74, 911-916, 1993  
A/Title: Sequence determination of the P gene of simian virus 41: presence of irregular  
A/Reference number: JQ2040; MUID:93260408; PMID:8492098  
A/Accession: JQ2041  
A/Molecule type: mRNA  
A/Residues: 1-394 <KAW>  
A/Cross-references: UNIPROT:Q86606; UNIPARC:UPI0000178672  
C/Genetics:  
A/Genes: P  
C/Superfamily: simian paramyxovirus P protein; V/P protein homology  
C/Keywords: nucleocapsid; phosphoprotein; RNA editing  
F:1-163/Domain: V/P protein homology <VPN>  
  
Query Match 49.4%; Score 41; DB 2; Length 394;  
Best Local Similarity 46.7%; Pred. No. 37;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
  
QY 3 GQVMDVLDLSTASTQ 17  
:::||||:|  
109 GRMTDLPLATGTVTQ 123  
  
RESULT 10  
H69200  
heavy-metal transporting CPX-type ATPase - Methanobacterium thermoautotrophicum (strain  
C/Species: Methanobacterium thermoautotrophicum  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: H69200  
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
A/Reference number: A69000; MUID:98037514; PMID:9371463  
A/Accession: H69200  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Residues: 1-675 <MTH>  
A/Molecule type: DNA  
A/Cross-references: UNIPROT:Q26849; UNIPARC:UPI0000066732; GB:AE000854; GB:AE000666; NIT  
C/Genetics:  
A/Experimental source: strain Delta H  
C/Genetics:  
A/Genes: MTH755  
C/Superfamily: Enterococcus copper-transporting ATPase cobB; ATPase nucleotide-binding d  
F:76-413/Domain: ATPase transduction domain homology <ATT>  
F:484-626/Domain: ATPase nucleotide-binding domain homology <ATN>  
  
Query Match 49.4%; Score 41; DB 2; Length 675;  
Best Local Similarity 72.7%; Pred. No. 68;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 DGOVMDVDLST 12  
||:||||:  
Db 176 DGKVEDVDVST 186  
  
RESULT 11  
A69210  
sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Del  
C/Species: Methanobacterium thermoautotrophicum  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: A69210  
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
A/Reference number: A69000; MUID:98037514; PMID:9371463  
A/Accession: A69210  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA

A/Residues: 1-677 <MTH>  
A/Cross-references: UNIPROT:Q26913; UNIPARC:UPI0000066738; GB:AE000859; GB:AE000666; NIT  
A/Experimental source: strain Delta H  
C/Genetics:  
A/Genes: MTH823  
A/Start codon: TTG  
  
Query Match 49.4%; Score 41; DB 2; Length 677;  
Best Local Similarity 46.7%; Pred. No. 68;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 EDGOVMDVDLSTAST 15  
|||:||||:  
Db 395 EDGRILDVNSTLAGT 409  
  
RESULT 12  
F85875  
probable fimbrial usher Z3600 [imported] - Escherichia coli (strain O157:H7, substrain E  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
C/Accession: F85875  
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
Hiller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: F85875  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-879 <STO>  
A/Cross-references: UNIPROT:Q8XCP4; UNIPARC:UPI000016589B; GB:AE005174; NID:q12516702; P  
A/Experimental source: strain O157:H7, substrain EDL933  
C/Genetics:  
A/Genes: Z3600  
C/Superfamily: outer membrane usher protein find  
  
Query Match 49.4%; Score 41; DB 2; Length 879;  
Best Local Similarity 50.0%; Pred. No. 92;  
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EDGOVMDVDLSTAS 14  
:::||||:  
Db 345 QNGQVDEYDINTAS 358  
  
RESULT 13  
E91031  
probable outer membrane protein Ecs3221 [imported] - Escherichia coli (strain O157:H7, s  
C/Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004  
C/Accession: E91031  
R/Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom  
A/Reference number: A99629; MUID:21156231; PMID:11258796  
A/Accession: E91031  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-879 <HAY>  
A/Cross-references: UNIPROT:Q8XCP4; UNIPARC:UPI0000004053; GB:BA000007; PIDN:BA036644.1;  
A/Experimental source: strain O157:H7, substrain RIMD 0509952  
C/Genetics:  
A/Genes: Ecs3221  
C/Superfamily: outer membrane usher protein find  
  
Query Match 49.4%; Score 41; DB 2; Length 879;  
Best Local Similarity 50.0%; Pred. No. 92;  
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 EDGOVMDVDLSTAS 14  
:::||||:  
Db 345 QNGQVDEYDINTAS 358

Db 345 QNGOVQEXYDINTAS 358

# RESULT 14

B96761 Probable protein kinase T9L24.36 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: B96761

R/Theologian: A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A6141; MUID:21016719; PMID:11130712

A/Accession: B96761

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1155 <STO>

A/Cross-references: UNIPROT:Q9FX38; UNIPARC:UPI000009FSD2; GB:AE005173; NID:G11120796; F

C/Genetics:

A/Gene: T9L24.36

A/Map position: 1

Query Match 49.4%; Score 41; DB 2; Length 1155;

Best Local Similarity 50.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGOVMDVLDLSTAQ 17

Db 520 DGOVMDVLDLSTAQ 535

# RESULT 15

H83545

hypothetical protein PA0803 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C/Accession: H83545

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warener, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10964043

A/Accession: H83545

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-146 <STO>

A/Cross-references: UNIPROT:Q91SD5; UNIPARC:UPI00000C5160; GB:AE004515; GB:AE004091; NID

C/Genetics:

A/Experimental source: strain PA01

A/Gene: PA0803

Query Match 48.2%; Score 40; DB 2; Length 146;

Best Local Similarity 57.1%; Pred. No. 18;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGOVMDVLDLSTAS 14

Db 43 EDGOVMDVLDLSTAS 56

Search completed: December 12, 2005, 20:42:55  
Job time : 16.3621 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 92.3276 Seconds  
(without alignments)  
129.907 Million cell updates/sec

Title: US-10-758-165A-16  
Perfect score: 83  
Sequence: 1 EDGQVMDVLDLSTASTTQ 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	428	1	IGHH_HUMAN
2	47	56.6	247	2	OPUY3_MOUSE
3	46	55.4	203	2	OSIX57_SILPO
4	46	55.4	977	2	P91775_PACLE
5	45	54.2	475	2	Q454N1_TETNG
6	45	54.2	632	2	Q7VHC8_HELHP
7	45	54.2	797	2	Q4KMD7_BRARE
8	44	53.0	118	1	RL24_HALSA
9	44	53.0	574	2	Q72PFB_LEPIC
10	44	53.0	574	2	Q8F6B9_LEPIN
11	44	53.0	632	2	Q8G7N6_BIFLO
12	44	53.0	757	2	Q9SZN9_ARATH
13	44	53.0	773	2	Q7NGR5_GLOVI
14	44	53.0	812	2	Q5V826_HALMA
15	44	53.0	881	1	YFCU_ECOLI
16	44	53.0	1888	2	Q6WWM4_ARATH
17	43	51.8	132	2	Q69XU5_ORYSA
18	43	51.8	330	2	Q873P6_RHOTO
19	43	51.8	393	2	Q7S2C7_NEUCR
20	43	51.8	704	2	Q52F86_MAGR
21	43	51.8	798	2	Q7PTM4_ANOGA
22	43	51.8	1250	2	Q9W595_CABEL
23	42	50.6	105	2	Q71181_LACDL
24	42	50.6	129	2	Q4UPG1_XANCP
25	42	50.6	129	2	Q8B3Y3_XANCP
26	42	50.6	226	2	Q67E28_9PERC
27	42	50.6	234	2	Q67E27_9PERC
28	42	50.6	360	2	Q9PUV5_9PERC
29	42	50.6	371	2	Q9C125_LACLA
30	42	50.6	393	2	Q68383_PSEFL
31	42	50.6	404	2	Q8NP11_CORGL

32	42	50.6	820	2	Q6CRB9_KLULA	Q6CRB9_KLULOMYC
33	42	50.6	885	2	Q57T59_SALCH	Q57T59_SALMOMELIA
34	42	50.6	885	2	Q87658_SALTY	Q87658_SALMOMELIA
35	42	50.6	1420	2	Q4PH85_USDMA	Q4PH85_USLILIGO_MA
36	42	50.6	3004	2	Q54C20_DICDI	Q54C20_DICYOSELI
37	41.5	50.0	291	2	Q7MZH1_PRODL	Q7MZH1_PHOTOCHABD
38	41	49.4	96	2	Q98F99_RHILIO	Q98F99_RHIZOBIIUM_I
39	41	49.4	171	2	Q7T006_MOUSE	Q7T006_MOUSE_MUSCULU
40	41	49.4	214	2	Q67E22_9SMEG	Q67E22_SYNGNATHUS
41	41	49.4	225	1	VY_SVALI	P36315_SILMIAN_VIRU
42	41	49.4	225	2	Q67E20_9PERC	Q67E20_PAMPUS_ARGE
43	41	49.4	238	2	Q67E16_9TELE	Q67E16_HOPILOTECHU
44	41	49.4	248	2	Q64AB8_9ARCH	Q64AB8_UNCULTURED
45	41	49.4	273	2	Q9PUV6_9PERC	Q9PUV6_STROMATEUS

## ALIGNMENTS

```

RESULT 1
ID_IGHE_HUMAN          STANDARD;          PRT;          428 AA.
AC   P01854;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig epsilon chain C region.
GN   Name=IGHE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=8316897; PubMed=630763;
RA   Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
RA   Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
RA   "Molecular cloning and nucleotide sequencing of human immunoglobulin
RT   epsilon chain cDNA.";
RL   Nucleic Acids Res. 11:719-726(1983).
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND VARIANT LEU-359.
RX   MEDLINE=83001945; PubMed=6288268; DOI=10.1016/0092-8674(82)90185-4;
RA   Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
RA   "Duplication and deletion in the human immunoglobulin epsilon genes.";
RL   Cell 29:691-699(1982).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84236029; PubMed=6234164;
RA   Flanagan J.G., Rabbitts T.H.;
RA   "The sequence of a human immunoglobulin epsilon heavy chain constant
RT   region gene, and evidence for three non-allelic genes.";
RL   EMBO J. 1:655-660(1982).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84207910; PubMed=6327276;
RA   Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
RA   "Long terminal repeat-like elements flank a human immunoglobulin
RT   epsilon pseudogene that lacks introns.";
RL   EMBO J. 1:1539-1544(1982).
RN   [5]
RP   PRELIMINARY PROTEIN SEQUENCE (MYELOMA PROTEIN ND).
RA   Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RA   (in) Bach M.K. (eds.);
RA   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 1-40; 68-114 AND 427-428.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Moggaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RA   "Cloning and sequence determination of the gene for the human

```

RT immunoglobulin epsilon chain expressed in a myeloma cell line.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).  
 RN [7]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=87089848; PubMed=3796618; DOI=10.1016/0161-5890(86)90005-2;  
 RA Padlan E.A., Davies D.R.;  
 RL "A model of the Fc of immunoglobulin E.";  
 CC -1- SIMILARITY: Contains 4 Ig-like (immunoglobulin-like) domains.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: L00022; AAB59424.1; ALT\_INIT; Genomic\_DNA.  
 DR PIR; A22771; EHHU.  
 DR PDB; 1F6A; X-ray; B/D=211-428.  
 DR PDB; 1FP5; X-ray; A=211-428.  
 DR PDB; 1G84; NMR; A=106-208.  
 DR PDB; 1IGE; Model; A/B=107-428.  
 DR PDB; 1OOV; X-ray; A/B=106-427.  
 DR Ensemble; ENSG0000017154; Homo sapiens.  
 DR HGNC; HGNC:5522; IGHE.  
 DR MIM; 147180; -.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; Pf07654; C1-set; 3.  
 DR Pfam; Pf00047; Ig; 1.  
 DR SMART; SM00407; IGcl; 4.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KM 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW Immunoglobulin C region; Immunoglobulin domain; Repeat.  
 FT DOMAIN 6 103  
 FT DOMAIN 112 210  
 FT DOMAIN 214 318  
 FT DOMAIN 324 423  
 FT CARBOHYD 21 21  
 FT CARBOHYD 49 49  
 FT CARBOHYD 99 99  
 FT CARBOHYD 146 146  
 FT CARBOHYD 252 252  
 FT CARBOHYD 275 275  
 FT DISULFID 14 14  
 FT DISULFID 15 105  
 FT DISULFID 29 85  
 FT DISULFID 121 121  
 FT DISULFID 135 193  
 FT DISULFID 209 209  
 FT DISULFID 239 299  
 FT DISULFID 345 405  
 FT VARIANT 359 359  
 FT NON\_TER 1 1  
 FT STRAND 113 119  
 FT STRAND 130 138  
 FT STRAND 148 151  
 FT TURN 152 153  
 FT STRAND 154 156  
 FT HELIX 158 160  
 FT STRAND 163 165  
 FT STRAND 173 181  
 FT STRAND 182 186  
 FT TURN 187 188  
 FT STRAND 191 196  
 FT STRAND 201 206  
 FT STRAND 218 221  
 FT HELIX 226 230

W -> L (possible polymorphism).  
 /Frtid=VAR\_003885.

FT TURN 231 232  
 FT STRAND 236 244  
 FT STRAND 252 257  
 FT TURN 258 259  
 FT STRAND 267 272  
 FT TURN 274 275  
 FT STRAND 278 285  
 FT HELIX 288 292  
 FT TURN 293 294  
 FT STRAND 297 302  
 FT TURN 304 305  
 FT STRAND 310 314  
 FT STRAND 322 322  
 FT STRAND 325 330  
 FT STRAND 334 334  
 FT TURN 335 336  
 FT STRAND 337 337  
 FT STRAND 340 351  
 FT STRAND 356 361  
 FT TURN 362 363  
 FT STRAND 364 365  
 FT HELIX 368 370  
 FT STRAND 371 373  
 FT STRAND 377 378  
 FT STRAND 384 393  
 FT STRAND 394 399  
 FT HELIX 403 408  
 FT STRAND 410 411  
 FT TURN 413 415  
 FT STRAND 417 422  
 SQ SEQUENCE 428 AA; 47019 MW; 25C4CA072AAS58A0 CRC64;

Query Match 100.0%; Score 83; DB 1; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGQWMDVDDISTASTQ 17  
 Db 151 EDGQWMDVDDISTASTQ 167

RESULT 2  
 O9PUY3 9TELE PRELIMINARY; PRT; 247 AA.  
 AC O9PUY3;  
 DT 01-MAY-2000 (TEMBUREL. 13, Created)  
 DT 01-MAY-2000 (TEMBUREL. 13, Last sequence update)  
 DT 01-DEC-2001 (TEMBUREL. 19, Last annotation update)  
 DE Mixed lineage leukemia-like protein (Fragment).  
 GN Name=M11;  
 OS Barbus tetrazona.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Barbus.  
 OC NCBITaxID=94221;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=9938697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate  
 evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF137224; AAD53447.1; -; Genomic\_DNA.  
 FT NON\_TER 1 1  
 FT STRAND 247 247  
 SQ SEQUENCE 247 AA; 26620 MW; B9160D133798C71F CRC64;

Query Match 56.6%; Score 47; DB 2; Length 247;  
 Best Local Similarity 56.2%; Pred. No. 15;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EDGQWMDVDDISTASTT 16  
 :||| ||:|:|

Db 145 DDGSSDVSI8TSTT 160

RESULT 3

OSLX57\_SILPO PRELIMINARY; PRT; 203 AA.

AC OSLX57;

DT 01-FEB-2005 (TREMBlrel. 29, Created)

DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)

DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)

DE Glutathione S-transferase family protein.

OS OrderedLocustNames=SP00270;

GN Silicibacter pomeroyi.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;

OC Rhodobacteraceae; Silicibacter.

NCBI\_TaxId=89184;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=DS-3 / ATCC 70808 / DSM 15171;

RC PubMed=15602564; DOI=10.1038/nature03170;

RA Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B., Kiene R.P., Henriksen J.R., King G.M., Belas R., Fugua C., Brinkac L.M., Lewis M., John S., Weaver B., Pai G., Eichen J.A., Rame E., Sheldon W.M., Ye W., Miller T.R., Carlton J., Raeko D.A., Paulsen I.T., Ren Q., Daugherty S.C., DeBoy R.T., Dodson R.J., RA Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J., RA Haft D.H., Selengut J., Ward N.;

RT "Genome sequence of *Silicibacter pomeroyi* reveals adaptations to the marine environment."

RL Nature 433:910-913(2004).

CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione. -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

DR EMBL: CP000031; AAV93590.1; -: Genomic DNA.

DR GO: GO:0016740; F:transferase activity; IEA.

DR InterPro: IPR004045; GST\_Nterm.

DR InterPro: IPR012335; Thioiodoxin-like.

DR Pfam: PF02798; GST\_N; 1.

KW Complete proteome; Transferase.

SO SEQUENCE 203 AA; 22285 MW; 5D33E1A87C546E06 CRC64;

Query Match 55.4%; Score 46; DB 2; Length 203;

Best Local Similarity 62.5%; Pred. No. 18;

Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 1 EDGQVMDVLDLSTASTT 16

Db 21 ESGQLDDVDLDTAGGT 36

RESULT 4

P91775\_PACLE PRELIMINARY; PRT; 977 AA.

AC P91775;

DT 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Pacificatin heavy chain precursor.

OS Pacificastacus leniusculus (Signal crayfish).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Plecymetata; Astacidae;

OC Astacoidae; Astacidae; Pacificastacus.

NCBI\_TaxId=6720;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=97338078; PubMed=9192625; DOI=10.1073/pnas.94.13.6682;

RA Liang Z., Sottrup-Jensen L., Asapan A., Hall M., Soderhall K.;

RT "Pacificatin, a novel 155-kDa heterodimeric proteinase inhibitor containing a unique transferrin chain."

RT Proc. Natl. Acad. Sci. U.S.A. 94:6682-6687(1997).

RL EMBL: U81824; AAC64660.1; -: mRNA.

DR HSP; P56410; IAOV.

DR GO: GO:0005576; C:extracellular region; IEA.

DR GO: GO:0008199; F:ferric iron binding; IEA.

DR GO: GO:0006879; P:iron ion homeostasis; IEA.

DR GO: GO:0006825; P:iron ion transport; IEA.

DR GO: GO:0006810; P:transport; IEA.

DR InterPro: IPR001156; Peptidase\_S60.

DR Pfam: PF00405; Transferin; 2.

DR PRINTS: PR00422; TRANSFERIN.

DR SMART: SM00094; TR\_FER; 2.

DR PROSITE: PS00206; TRANSFERRIN\_2; 1.

KW Signal.

FT SIGNAL 1 22 Potential.

FT CHAIN 23 977 Pacificatin heavy chain.

SO SEQUENCE 977 AA; 106866 MW; SEF1706133350E99 CRC64;

Query Match 55.4%; Score 46; DB 2; Length 977;

Best Local Similarity 57.1%; Pred. No. 97;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 EDGQVMDVLDLSTASTT 14

Db 935 EDGHLVDLSSVMS 948

RESULT 5

O4S4N1\_TETNG PRELIMINARY; PRT; 475 AA.

ID O4S4N1\_TETNG

AC O4S4N1\_TETNG

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Chromosome 2 SCAP14738, whole genome shotgun sequence. (Fragment).

GN ORFNames=GSTENG00024108001;

OS Tetradodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

NCBI\_TaxId=99883;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S., RA Anthouard V., Uudin C., Castelli V., Kacinka M., Vacherie B., RA Blemont C., Skaili Z., Catolico L., Poullain J., De Bernardinis V., RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J., RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J., RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., RA Wincker P., Lander E.S., Weissbach J., Roest Croliius H.;

RT "Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals the early vertebrate proto-karyotype."

RL Nature 431:946-957(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL: CA801014738; CAG04401.1; -: Genomic DNA.

DR EMBL; CA801014738; CAG04401.1; -: Genomic DNA.

DR NON\_TER 1 475

FT NON\_TER 1 475

SO SEQUENCE 475 AA; 53728 MW; FFB80CB714EF095 CRC64;

Query Match 54.2%; Score 45; DB 2; Length 475;

Best Local Similarity 47.1%; Pred. No. 67;

Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 EDGQVMDVLDLSTASTTQ 17

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Db      180 EDSMLSDIDISTASTAPAR 196

RESULT 6
O7VHC8 HELHP
ID O7VHC8_HELHP PRELIMINARY; PRT; 632 AA.
AC O7VHC8;
DT 01-OCT-2003 (TREMBlurel. 25, Created)
DT 01-OCT-2003 (TREMBlurel. 25, Last sequence update)
DE 01-OCT-2003 (TREMBlurel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=HH1039;
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxId=32025;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 51449 / 3B1;
RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
Suerbaum S., Josephans C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fattmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauder D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"the complete genome sequence of the carcinogenic bacterium
RT Helicobacter hepaticus."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
DR EMBL: AE017147; AAF7656.1; -, Genomic_DNA.
KM Complete proteome.
SQ SEQUENCE 632 AA; 73803 MW; 45396869ACA33BBB CRC64;

Query Match 54.2%; Score 45; DB 2; Length 632;
Best Local Similarity 64.3%; Pred. No. 91;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 DQVMDVDLSTAST 15
Db 473 EGKILVLDLSTAST 486

RESULT 7
O4KMD7_BRAPE PRELIMINARY; PRT; 797 AA.
ID O4KMD7;
AC O4KMD7;
DT 13-SEP-2005 (TREMBlurel. 31, Created)
DT 13-SEP-2005 (TREMBlurel. 31, Last sequence update)
DE 13-SEP-2005 (TREMBlurel. 31, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeebber B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hodkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.J.,
Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullan S.J.,
Boesak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shcherbina Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RG NIH MGC Project;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC098614; AAH98614.1; -, mRNA.
KM Hypothetical protein.
SQ SEQUENCE 797 AA; 89937 MW; C1F915CC7CCA221 CRC64;

Query Match 54.2%; Score 45; DB 2; Length 797;
Best Local Similarity 52.9%; Pred. No. 1,2e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 EDQVMDVDLSTASTQ 17
Db 250 EDSILSDIDISTASTAPAR 266

RESULT 8
RL24 HALSA STANDARD; PRT; 118 AA.
ID RL24_HALSA
AC O9HPC3;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 50S ribosomal protein L24p.
GN Name=rpL24p; OrderedLocustNames=VNG1702G;
OS Halobacterium salinarum (Halobacterium halobium).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxId=2242;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
NG W.V., Kennedy S.P., Mahatras G.G., Berquist B., Pan M.,
Shukla H.D., Laaky S.R., Baliga N.S., Thorson V., Shrogen J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danon M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenberger T.A., Peck R.F., Pohlshocher M., Spudich J.L., Jung K.-H.,
Alam M., Freltas T., Hou S., Daniels C.J., Dennis P.P., Omar A.D.,
Ehardt H., Lowe T.W., Liang P., Riley M., Hood L., Dasarma S.;
"Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
CC -1- FUNCTION: One of two assembly initiator proteins, it binds
CC directly to the 5' end of the 23S rRNA, where it nucleates
CC assembly of the 50S subunit (By similarity).
CC -1- FUNCTION: Located at the polypeptide exit tunnel on the outside of
CC the subunit (By similarity).
CC -1- SUBUNIT: Part of the 50S ribosomal subunit.
CC -1- SIMILARITY: Belongs to the ribosomal protein L24p family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL: AB005077; AAG19947.1; -, Genomic_DNA.
DR PIR: G84322; G84322.
DR HAMAP: MF_01326; -; 1.
DR InterPro: IPR005824; KOW.
DR InterPro: IPR006646; KOW sub.
DR InterPro: IPR005825; Ribosomal_L24_26.
DR Pfam: PF00467; KOW; 1.
DR SMART: SM00739; KOW; 1.
DR PROSITE: PS01108; RIBOSOMAL_L24; 1.

```



KW Complete proteome; Ribonucleoprotein; Ribosomal protein; RNA-binding;  
KW rRNA-binding.  
SQ SEQUENCE 118 AA; 13369 MW; 90C2F1C4577190A8 CRC64;

Query Match 53.0%; Score 44; DB 1; Length 118;  
Best Local Similarity 69.2%; Pred. No. 23;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DGOVMDVDLSTAS 13  
|||:|||||  
DB 59 DGEVVDVLDLRA 71

RESULT 9  
O72PM8\_LEPIC PRELIMINARY; PRT; 574 AA.  
AC O72PM8;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
GN OrderedLocustNames=LIC12349;  
OS Lepospiira interrogans (serogroup Icterohaemorrhagiae / serovar  
OS Copenhagensi).  
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=44275;  
RN [1]

NUCLEOTIDE SEQUENCE.  
RC STRAIN=fiocruz LI-130;  
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;  
RA Nascimmento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,  
Ho P.L., Haake D.A., Verjovsky-Almeida S., Hartkearl R.A.,  
Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carer H.,  
Coutinho L.L., Degraive W.M., Dellagostin O.A., El-Dorri H.,  
Ferreto E.S., Ferro M.I.T., Furian L.R., Gamberini M., Gigliotti E.A.,  
Goes-Melo A., Goldman G.H., Goldman M.H.S., Harakava R.,  
Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,  
Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,  
de Oliveira R.C., Pereira G.G., Reis M.S., Schiefer A.,  
Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,  
Camarago L.E.A., Kitajima J.P., Secubal J.C., Van Sluys M.A.;  
RT "Comparative genomics of two Leptospira interrogans serovars reveals  
novel insights into physiology and pathogenesis.";  
RL J. Bacteriol. 186:2164-2172(2004).  
DR EMBL; AF017296; AAS70918.1; --; Genomic\_DNA.  
DR InterPro; IPR000585; Hemopexin.  
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN\_1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 574 AA; 65826 MW; 1F5E2B1C8183306C CRC64;

Query Match 53.0%; Score 44; DB 2; Length 574;  
Best Local Similarity 69.2%; Pred. No. 1.2e+02;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DGOVMDVDLSTAS 14  
|||:|||||  
DB 497 DGEVVDVLDLRA 509

RESULT 10  
O8F6B9\_LEPIN PRELIMINARY; PRT; 574 AA.  
AC O8F6B9;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DE Hypothetical protein.  
GN OrderedLocustNames=IA1389;  
OS Leptospira interrogans.  
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
OX NCBI\_TaxID=173;  
RN [1]

NUCLEOTIDE SEQUENCE.  
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;  
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,  
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,  
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,  
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,  
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,  
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,  
Xu J.-G., Zhao G.-P.;  
RT "Unique physiological and pathogenic features of Leptospira  
interrogans revealed by whole-genome sequencing.";  
RL Nature 422:888-893(2003).  
DR EMBL; AE011318; AAN48588.1; --; Genomic\_DNA.  
DR InterPro; IPR000585; Hemopexin.  
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 574 AA; 65826 MW; 1F5E2B1C8183306C CRC64;

Query Match 53.0%; Score 44; DB 2; Length 574;  
Best Local Similarity 69.2%; Pred. No. 1.2e+02;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DGOVMDVDLSTAS 14  
|||:|||||  
DB 497 DGEVVDVLDLRA 509

RESULT 11  
O8G7N6\_BIFLO PRELIMINARY; PRT; 632 AA.  
AC O8G7N6;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DE Hypothetical protein.  
GN OrderedLocustNames=BL0213;  
OS Bifidobacterium longum.  
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
OC Bifidobacteriaceae; Bifidobacterium.  
OX NCBI\_TaxID=216816;  
RN [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=NCC 2705;  
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;  
RA Schell M.A., Karimantzou M., Snel B., Vilanova D., Berger B.,  
Peebi G., Zwanen M.-C., Desiere F., Bork P., Delley M.,  
RT "The genome sequence of Bifidobacterium longum reflects its adaptation  
to the human gastrointestinal tract.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
DR EMBL; AE014295; AAN24065.1; --; Genomic\_DNA.  
DR InterPro; IPR001173; Glyco\_trans\_2.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 632 AA; 72156 MW; 31F5A3ADCCF3A7D CRC64;

Query Match 53.0%; Score 44; DB 2; Length 632;  
Best Local Similarity 46.7%; Pred. No. 1.3e+02;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 2 DGOVMDVDLSTASTT 16  
|||:|||||  
DB 150 DGEVVDLSTASTT 164

RESULT 12  
O9S2N9\_ARATH PRELIMINARY; PRT; 757 AA.  
AC O9S2N9;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE Hypothetical protein F20M13.160 (Hypothetical protein ATg38600).  
GN Name=F20M13.160; Synonyms=ATg38600;

NUCLEOTIDE SEQUENCE.  
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;  
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;  
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,  
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,  
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,  
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,  
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,  
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,  
Xu J.-G., Zhao G.-P.;  
RT "Unique physiological and pathogenic features of Leptospira  
interrogans revealed by whole-genome sequencing.";  
RL Nature 422:888-893(2003).  
DR EMBL; AE011318; AAN48588.1; --; Genomic\_DNA.  
DR InterPro; IPR000585; Hemopexin.  
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 574 AA; 65826 MW; 1F5E2B1C8183306C CRC64;

```
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Weiler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Schueller C.,
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Weiler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL035540; CAB37516.1; -; Genomic DNA.
DR EMBL: AL161593; CAB80524.1; -; Genomic DNA.
DR PIR: T05688; T05688.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0006512; F:ubiquitin cycle; IEA.
DR InterPro: IPR000569; HECT.
DR Pfam: PF00637; HECT_1.
DR SMART: SM00119; HECTc; 1.
DR PROSITE: PS50237; HECT_1.
DR Hypothetical protein.
SQ SEQUENCE 757 AA; 82683 MW; 9F7E225EC65C0656 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 757;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 1 EDGQVMDVLDSTA 13
Db 476 QDGRLLDVPVLSA 488

RESULT 13
ID Q7NGR5_GLOVI PRELIMINARY; PRT; 773 AA.
AC Q7NGR5_
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G113103 protein.
GN OrderedLocustNames=g113103;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxId=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145 (2003).
DR EMBL: BA000045; BAC91044.1; -; Genomic DNA.
DR HSSP; P06129; IJWJ.
DR GO: GO:0019867; C:outer membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
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DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000531; TonB_receptor.
DR Pfam: PF00593; TonB_dep_Rec; 1.
KW Complete proteome; Membrane; Outer membrane; TonB box.
SQ SEQUENCE 773 AA; 83958 MW; F129A553B6DAB48 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 773;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Cy 1 EDGQVMDVLDSTA 14
Db 347 EDGRIMNADMYTAS 360

RESULT 14
ID Q5V826_HALMA PRELIMINARY; PRT; 812 AA.
AC Q5V826_
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ATP-dependant helicase.
GN Name=yrcJ1; OrderedLocustNames=png2034;
OS Haloarcula marismortui (Halobacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxId=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciolo M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
the Dead Sea.";
RL Genome Res. 14:2221-2234 (2004).
DR EMBL: AY596291; AAY44326.1; -; Genomic DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR011545; DEAD/DEAH_N.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD_1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELICc; 1.
KW ATP-binding; Complete proteome; DNA-binding; Helicase; Hydrolase;
KW Plasmid.
SQ SEQUENCE 812 AA; 89620 MW; B1BDA603A8216CF CRC64;

Query Match 53.0%; Score 44; DB 2; Length 812;
Best Local Similarity 58.8%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 1 EDGQVMDVLDSTA 17
Db 276 EDDSTADVDEDTASTQ 292

RESULT 15
ID YFCU_ECOCI STANDARD; PRT; 881 AA.
AC P77196; P77532;
DT 01-NOV-1997 (Ref. 35, Created)
DT 15-DEC-1998 (Ref. 37, Last sequence update)
DT 13-SEP-2005 (Ref. 48, Last annotation update)
DE Hypothetical outer membrane usher protein yfcU precursor.
GN Name=yfcU; OrderedLocustNames=b23337/b2338;
```

```

OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayaishi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-Kb sequence of the Escherichia coli-
RT K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -1- FUNCTION: Involved in the export and assembly of a fimbrial
CC subunit across the outer membrane (By similarity).
CC -1- INTERACTION:
CC P60240:YAP; NbExp=1; IntAct=EBI-551635; EBI-551542;
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (by similarity).
CC -1- SIMILARITY: Belongs to the fimbrial export usher family.
CC -1- CAUTION: This is a conceptual translation.
CC -1- CAUTION: Ref.1 and Ref.2 sequences differ from that shown due to a
CC stop codon in position 579.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U00096; AAC75398.1; ALT_SEQ; Genomic DNA.
DR EMBL; U00096; AAC75397.1; ALT_INIT; Genomic DNA.
DR EMBL; D90864; BAA16191.1; ALT_INIT; Genomic DNA.
DR EMBL; D90864; BAA16192.1; ALT_SEQ; Genomic DNA.
DR IntAct; P77196; -.
DR EcoBASE; EB3876; -.
DR EcoGene; EG14124; yfcU.
DR InterPro; IPR000015; Fimb_usher.
DR Pfam; PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
KW Complete proteome; Fimbria; Hypothetical protein; Membrane;
KW Outer membrane; Signal; Transmembrane; Transport.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 881 Hypothetical outer membrane usher protein
FT yfcU.
SQ SEQUENCE 881 AA; 97439 MW; 23DE53B67541E041 CRC64;

Query Match 53.0%; Score 44; DB 1; Length 881;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1 EDGQVMDVLDSTAS 14  
 :|||:|:|  
 Db 346 QNGQVQVEYDISTS 359

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GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: December 12, 2005, 19:37:19 ; Search time 81.3362 Seconds  
(without alignments)  
81.030 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSP1QTDYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*
9:	Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	ADRI0601	Dog IGE e
2	81	100.0	312	AAV79995	Dog immun
3	81	100.0	417	AAW23067	Canine Ig
4	81	100.0	426	AAW7753	Canine Ig
5	81	100.0	426	ABP96583	Dog IGE h
6	53	65.4	15	ADRI0607	Pig IGE e
7	53	65.4	567	ABP96588	Pig IGE h
8	48	59.3	15	ADRI0602	Cat IGE e
9	48	59.3	431	ADG73237	Cat immun
10	48	59.3	496	ABP96580	Cat IGE h
11	48	59.3	496	ABU09338	Feline Ig
12	48	59.3	496	ABU09336	Feline Ig
13	48	59.3	496	ADG73251	Cat parti
14	48	59.3	496	ADG73255	Cat parti
15	43	53.1	1633	ABU42513	Protein e
16	42	51.9	1067	ABE91309	Herbicida
17	41	50.6	15	ADRI0603	Horse IGE
18	41	50.6	151	AAU57418	Propionib
19	41	50.6	151	ABW53937	Propionib
20	41	50.6	424	AAW50103	Equine Ig
21	41	50.6	424	AAW50104	Equine Ig
22	41	50.6	533	ABP39208	Staphyloc
23	41	50.6	533	ADSO5754	Staphyloc
24	41	50.6	569	ABP96585	Horse IGE

25	40	49.4	356	4	ABB64299	Drosophila
26	40	49.4	488	8	ADY09532	Plant full
27	40	49.4	555	6	ADA24243	Pseudomon
28	40	49.4	632	7	ABM90457	Rice abio
29	40	49.4	632	7	ABM85909	Rice abio
30	40	49.4	667	6	ADA33007	Acinetoba
31	40	49.4	1180	3	AAW01845	Haemophil
32	40	49.4	1188	3	AAW01844	Haemophil
33	40	49.4	2349	6	AAO16359	Human tra
34	40	49.4	2400	4	ABG20278	Novel hum
35	40	49.4	2415	4	ABG20279	Novel hum
36	39	48.1	226	8	ADR44996	SNSAG3 an
37	39	48.1	276	3	AAW08697	Arabidops
38	39	48.1	276	3	AAW42639	Arabidops
39	39	48.1	281	8	AD128921	Sarcocyst
40	39	48.1	281	8	ADR44989	Sarcocyst
41	39	48.1	294	3	AAW08696	Arabidops
42	39	48.1	294	3	AAW42638	Arabidops
43	39	48.1	294	8	ADW61841	Transcrip
44	39	48.1	295	3	AAW42637	Arabidops
45	39	48.1	295	3	AAW08695	Arabidops

## ALIGNMENTS

RESULT 1  
ADRI0601  
ID ADRI0601 standard; peptide, 15 AA.  
XX  
XX  
AC ADRI0601;  
XX  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.  
XX  
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; aetna;  
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
OS Canis familiaris.  
XX  
XX WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
XX 15-JAN-2004; 2004WO-US003566.  
XX  
XX 16-JAN-2003; 2003US-0440472P.  
XX  
XX (UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hammerberg B;  
XX  
XX WPI, 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
XX Example 6; Page 9; 14pp; English.  
XX  
XX The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine IGE corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.  
 XX

SO Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPITDQYTTTG 15  
 |||||  
 Db 1 RNDSPITDQYTTTG 15

RESULT 2  
 AAY79995  
 ID AAY79995 standard; protein; 312 AA.

AC AAY79995;  
 XX  
 DT 15-MAY-2000 (first entry)  
 XX

DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E, IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Canis sp.

PN WO967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US013959.

PR 20-JUN-1998; 98US-00100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

PS Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX Sequence 312 AA;

Query Match 100.0%; Score 81; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSPITDQYTTTG 15  
 |||||  
 Db 255 RNDSPITDQYTTTG 269

RESULT 3  
 AAW23067  
 ID AAW23067 standard; protein; 417 AA.

AC AAW23067;  
 XX  
 DT 30-JUN-2005 (revised)  
 DT 16-JUN-2005 (revised)  
 DT 19-FEB-1998 (first entry)  
 XX

DE Canine IgE heavy chain constant region (exon 1-4 product).

XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

OS Canis familiaris.

FN Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

PD 21-AUG-1997.

PF 14-FEB-1997; 97WO-US002322.

PR 14-FEB-1996; 96US-00601197.

PA (IDEX-) IDEXX LAB INC.

PI Mermer B, Harris RA, Siefiring AE;

XX WPI; 1997-425031/39.

DR N-PSDB; AAT79278.

XX Isolated canine IgE heavy chain constant region DNA - useful to develop  
 PT products for treatment of canine allergies and for immunomodulation in  
 PT dogs.

PS Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE  
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat Type I immediate hypersensitivity, and for immunomodulation

CC Revised record issued on 30-JUN-2005 : Typo in comments  
XX  
SQ Sequence 417 AA;

Query Match 100.0%; Score 81; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSP1QTDQYTTTG 15  
|||  
Db 352 RNDSP1QTDQYTTTG 366

## RESULT 4

AAR97753  
ID AAR97753 standard; protein; 426 AA.

AC AAR97753;

DT 28-AUG-1996 (first entry)

XX Canine IGE.

XX IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.

XX Canis familiaris.

XX WO9614867-A1.

XX 23-MAY-1996.

XX 03-NOV-1995; 95WO-US013795.

XX 09-NOV-1994; 94US-00336583.

PR 09-NOV-1994; 94US-00336891.

XX (MERI ) MERCK & CO INC.

XX Hollis GF, Patel MD;

XX WPI; 1996-277321/28.

DR N-PSDB; AAT29824.

XX New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense  
PT therapy, assays, drug screening, etc.

XX Claim 11; Page 29-30; 49pp; English.

XX The canine IGE amino acid sequence (AAR97753) was deduced from an  
CC isolated gene (AAT29824) obt'd. from a canine liver DNA library. The  
CC cloning of the IGE gene allows prodn. of large quantities of recombinant  
CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE  
CC can be used in drug development (e.g. small molecule screening, assay  
CC development and anti-IGE antibody generation). Fragments of IGE can be  
CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new  
CC sequence information permits targeted modulation of IGE-mediated immune  
CC responses

XX Sequence 426 AA;

Query Match 100.0%; Score 81; DB 2; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSP1QTDQYTTTG 15  
|||  
Db 357 RNDSP1QTDQYTTTG 371

## RESULT 5

ABP96583  
ID ABP96583 standard; protein; 426 AA.  
XX

AC ABP96583;  
XX  
DT 28-MAY-2003 (first entry)  
XX

Dog IGE heavy chain amino acid sequence SEQ ID NO:28.

XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
XX immune response; major histocompatibility complex; MHC; immunogenic;  
XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;  
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
XX urticaria hives.

XX Canis familiaris.

XX WO2003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
PT against IGE, by identifying peptide eliciting CTL response to IGE  
PT peptides naturally presented by major histocompatibility complex class I  
PT protein.

XX Example 7; Page 152-154; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides  
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
CC E (IGE), comprising providing a test peptide (T) suspected of being able  
CC to bind to major histocompatibility complex (MHC) class I molecule, and  
CC evaluating (T) for ability to elicit in a mammal a CTL response to  
CC naturally processed and presented IGE peptides, where a peptide that  
CC induces such a response is identified. Also described are compositions:  
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
CC (C2) comprising at least one isolated polynucleotide encoding (T); and  
CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
CC elicit in a mammal a CTL response to naturally processed and presented  
CC IGE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,  
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
CC and can be used as inducers of a CTL response against IGE, and in  
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
CC IGE-mediated atopic hypersensitivity condition. IGE-mediated non-atopic  
CC hypersensitivity condition. IGE myeloma in a mammal. Preferably, C1-3 are  
CC useful for treating atopic hypersensitivity conditions (such as allergic  
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
CC hives). The present sequence represents an IGE heavy chain amino acid  
CC sequence, which is given in an example from the present invention

XX Sequence 426 AA;

Query Match 100.0%; Score 81; DB 6; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSP1QTDQYTTTG 15  
|||  
Db 357 RNDSP1QTDQYTTTG 371

```

RESULT 6
ADRI0607
XX ADRI0607 standard; peptide; 15 AA.
XX
XX ADRI0607;
XX
XX 21-OCT-2004 (first entry)
XX
XX Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.
XX
XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX pig.
XX
XX Sus scrofa.
XX
XX WO2004065936-A2.
XX
XX 05-AUG-2004.
XX
XX 15-JAN-2004; 2004WO-US003566.
XX
XX 16-JAN-2003; 2003US-0440472P.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX of IGE from cat and horse, but did not exhibit cross-reactivity with
XX either pig or human epsilon-chains of IGE. The present sequence is the
XX pig IGE 5.91 recognition site.
XX
XX Sequence 15 AA;
XX
XX Query Match 65.4%; Score 53; DB 8; Length 15;
XX Best Local Similarity 57.1%; Pred. No. 0.042;
XX Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 RNDSPIQDYTTT 14
XX |||:|:|:|:|
XX Db 1 RNDAPVQADRHSTT 14
XX
XX RESULT 7
XX ABP96588
XX ABP96588 standard; protein; 567 AA.
XX
XX AC ABP96588;
XX
XX 28-MAY-2003 (first entry)
XX
XX Pig IGE heavy chain amino acid sequence SEQ ID NO:33.
XX

```

```

XX
XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.
XX
XX Sus scrofa.
XX
XX WO2003015716-A2.
XX
XX 27-FEB-2003.
XX
XX 08-AUG-2002; 2002WO-US026986.
XX
XX 13-AUG-2001; 2001US-0312120P.
XX
XX (IGET-) IGE THERAPEUTICS INC.
XX
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX
XX WPI; 2003-268242/26.
XX
XX Example 7; Page 164-167; 187pp; English.
XX
XX The present invention describes a method (M1) for identifying peptides
XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
XX B (IGB), comprising providing a test peptide (T) suspected of being able
XX to bind to major histocompatibility complex (MHC) class I molecule, and
XX evaluating (T) for ability to elicit in a mammal a CTL response to
XX naturally processed and presented IGE peptides, where a peptide that
XX induces such a response is identified. Also described are compositions:
XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);
XX (C2) comprising at least one isolated polynucleotide encoding (I); and
XX (C3) comprising antigen-presenting cells that recognise at least one (I).
XX where C1-3 are able to bind to at least one MHC class I molecule and to
XX elicit in a mammal a CTL response to naturally processed and presented
XX IGE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
XX vasotropic, dermatological, antiinflammatory and cytostatic activities,
XX and can be used as inducers of a CTL response against IGE, and in
XX vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
XX mammal. C1-3 are useful for modulating an IGE-mediated condition such as
XX IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
XX hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
XX useful for treating atopic hypersensitivity conditions (such as allergic
XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
XX hives). The present sequence represents an IGE heavy chain amino acid
XX sequence, which is given in an example from the present invention
XX
XX Sequence 567 AA;
XX
XX Query Match 65.4%; Score 53; DB 6; Length 567;
XX Best Local Similarity 57.1%; Pred. No. 2.1;
XX Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 RNDSPIQDYTTT 14
XX |||:|:|:|:|
XX Db 499 RNDAPVQADRHSTT 512
XX
XX RESULT 8
XX ADRI0602
XX ADRI0602 standard; peptide; 15 AA.
XX
XX AC ADRI0602;
XX

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XX 21-OCT-2004 (first entry)
XX
XX
DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.
XX
XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX cat.
XX
XX Felis catus.
XX
XX WO2004065936-A2.
XX
XX 05-AUG-2004.
XX
XX 15-JAN-2004; 2004WO-US003566.
XX
XX 16-JAN-2003; 2003US-0440472P.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX of IGE from cat and horse, but did not exhibit cross-reactivity with
XX either pig or human epsilon-chains of IGE. The present sequence is the
XX cat IGE 5.91 recognition site.
XX
XX Sequence 15 AA;
XX
XX Query Match 59.3%; Score 48; DB 8; Length 15;
XX Best Local Similarity 61.5%; Pred. No. 0.31;
XX Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 NDSPIQTDQYTTT 14
XX |||:::|:|
XX 2 NDSVPTREQATT 14
XX
XX
XX RESULT 9
XX ADG73237
XX ID ADG73237 standard; protein; 431 AA.
XX
XX AC ADG73237;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat immunoglobulin E (IGE) constant region.
XX
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
XX immune response; IGE-mediated response; allergy; cat; constant region.
XX
XX Felis catus.
XX

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XX US2003216565-A1.
XX
XX 20-NOV-2003.
XX
XX 07-APR-2003; 2003US-00409772.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX (MCCA/) MCCAUL C.
XX
XX (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2004-010802/01.
XX
XX N-PSDB; ADG73236.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IGE
XX heavy chain protein, useful for treating and/or eliciting feline immune
XX responses for IGE-mediated responses, such as allergies.
XX
XX Claim 12; SEQ ID NO 14; 44pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX portion of a feline IGE heavy chain protein. The methods and compositions
XX of the present invention are useful for eliciting feline immune responses
XX for and/or treating IGE-mediated responses, such as allergies. This is
XX the amino acid sequence of a cat immunoglobulin E (IGE) constant region.
XX
XX Sequence 431 AA;
XX
XX Query Match 59.3%; Score 48; DB 8; Length 431;
XX Best Local Similarity 61.5%; Pred. No. 11;
XX Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 NDSPIQTDQYTTT 14
XX |||:::|:|
XX 363 NDSVPTREQATT 375
XX
XX
XX RESULT 10
XX ABP96580
XX ID ABP96580 standard; protein; 496 AA.
XX
XX AC ABP96580;
XX
XX 28-MAY-2003 (first entry)
XX
XX Cat IGE heavy chain amino acid sequence SEQ ID NO:25.
XX
XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;
XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.
XX
XX Felis catus.
XX
XX WO2003015716-A2.
XX
XX 27-FEB-2003.
XX
XX 08-AUG-2002; 2002WO-US026986.
XX
XX 13-AUG-2001; 2001US-0312120P.
XX
XX (IGET-) IGE THERAPEUTICS INC.
XX
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX

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DR WPI; 2003-268242/26.  
XX  
XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
PT against IGE, by identifying peptide eliciting CTL response to IGE  
PT peptides naturally presented by major histocompatibility complex class I  
PT protein.  
XX  
XX Example 7, Page 145-147; 187pp; English.  
XX  
XX The present invention describes a method (M1) for identifying peptides  
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
CC E (IGE), comprising providing a test peptide (T) suspected of being able  
CC to bind to major histocompatibility complex (MHC) class I molecule, and  
CC evaluating (T) for ability to elicit in a mammal a CTL response to  
CC naturally processed and presented IGE peptides, where a peptide that  
CC induces such a response is identified. Also described are compositions:  
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
CC elicit in a mammal a CTL response to naturally processed and presented  
CC IGE peptides, C1-3 have antiallergic, antiasthmatic, immunosuppressive,  
CC vasotrophic, dermatological, antiinflammatory and cytostatic activities,  
CC and can be used as inducers of a CTL response against IGE, and in  
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
CC useful for treating atopic hypersensitivity conditions (such as allergic  
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
CC hives). The present sequence represents an IGE heavy chain amino acid  
CC sequence, which is given in an example from the present invention  
XX  
XX  
SQ Sequence 496 AA;  
XX  
XX  
Query Match 59.3%; Score 48; DB 6; Length 496;  
Best Local Similarity 61.5%; Pred. No. 13;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
XX  
Qy 2 NDSPIQTDQYTTT 14  
|||:::|  
Db 428 NDSPIQTDQYTTT 440  
XX  
XX  
RESULT 11  
ABU09338  
ID ABU09338 standard; protein; 496 AA.  
XX  
XX ABU09338;  
XX  
XX 27-JUN-2003 (first entry)  
XX  
XX Feline IGE epsilon heavy chain #2.  
XX  
XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
KM antibody technology; antiallergic; antiparasitic; cyostatic.  
XX  
XX Felis catus.  
XX  
XX US2003013183-A1.  
XX  
XX 16-JAN-2003.  
XX  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX  
XX (MCCA/) MCCA.L. C.  
PA (WEBE/) WEBER E.  
XX  
XX Mccall C, Weber E;  
PI

XX  
XX WPI; 2003-391997/37.  
DR N-PSDB; ABX95715.  
XX  
XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or  
PT light chain protein, useful for treating feline IGE-mediated responses  
PT e.g. allergies, parasitic infections or neoplasia.  
XX  
XX Claim 1; Page 37-39; 45pp; English.  
XX  
XX The present invention relates to the isolation of feline immunoglobulin E  
CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the  
CC polynucleotide sequences encoding them. The sequences of the invention  
CC are useful for treating feline IGE-mediated immune responses (e.g.  
CC allergies, parasitic infections or neoplasia), in vaccine technology,  
CC small molecule/antibody technology, molecular biology, and various  
CC immunological techniques related to feline IGE and its functions. The  
CC present sequence represents feline IGE epsilon heavy chain #2  
XX  
XX  
SQ Sequence 496 AA;  
XX  
XX  
Query Match 59.3%; Score 48; DB 6; Length 496;  
Best Local Similarity 61.5%; Pred. No. 13;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
XX  
Qy 2 NDSPIQTDQYTTT 14  
|||:::|  
Db 428 NDSPIQTDQYTTT 440  
XX  
XX  
RESULT 12  
ABU09336  
ID ABU09336 standard; protein; 496 AA.  
XX  
XX ABU09336;  
XX  
XX 27-JUN-2003 (first entry)  
XX  
XX Feline IGE epsilon heavy chain #1.  
XX  
XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
KM antibody technology; antiallergic; antiparasitic; cyostatic.  
XX  
XX Felis catus.  
XX  
XX OS  
XX  
XX Key  
FH Location/Qualifiers  
FT 66..496  
FT /note="This sequence is given as SEQ ID No:14 and is  
FT specifically claimed in Claim 12"  
FT 284..309  
FT /note="This sequence is given as SEQ ID No:11 and is  
FT specifically claimed in Claim 9"  
FT 288..305  
FT /note="This sequence is given as SEQ ID No:8 and is  
FT specifically claimed in Claim 10"  
FT 291..302  
FT /note="This sequence is given as SEQ ID No:5 and is  
FT specifically claimed in Claim 11"  
XX  
XX  
XX US2003013183-A1.  
XX  
XX 16-JAN-2003.  
XX  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX  
XX (MCCA/) MCCA.L. C.  
PA (WEBE/) WEBER E.  
XX  
XX Mccall C, Weber E;  
XX

DR WPI; 2003-39197/37.  
DR N-PSDB; ABX95713.  
PT New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or  
PT light chain protein, useful for treating feline IGE-mediated responses  
PT e.g. allergies, parasitic infections or neoplasia.  
XX  
XX Claim 1; Page 24-25; 45pp; English.  
XX  
CC The present invention relates to the isolation of feline immunoglobulin E  
CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the  
CC polynucleotide sequences encoding them. The sequences of the invention  
CC are useful for treating feline IGE-mediated immune responses (e.g.  
CC allergies, parasitic infections or neoplasia), in vaccine technology,  
CC small molecule/antibody technology, molecular biology, and various  
CC immunological techniques related to feline IGE and its functions. The  
CC present sequence represents feline IGE epsilon heavy chain #1  
XX  
SQ Sequence 496 AA;  
XX  
Query Match 59.3%; Score 48; DB 6; Length 496;  
Best Local Similarity 61.5%; Pred. No. 13;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 NDSP1QTDQYTTT 14  
Db 428 NDSPVTRTEQOATT 440  
XX  
RESULT 13  
ADG73251  
ID ADG73251 standard; protein; 496 AA.  
XX  
AC ADG73251;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
DE Cat partial immunoglobulin E (IGE) heavy chain #2.  
XX  
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;  
XX immune response; IGE-mediated response; allergy; cat; heavy chain.  
XX  
OS Felis catus.  
XX  
XX US2003216565-A1.  
XX  
XX 20-NOV-2003.  
XX  
XX 07-APR-2003; 2003US-00409772.  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX (MCCA/) MCCALL C.  
XX (WEBE/) WEBER E.  
XX  
XX McCall C, Weber E;  
XX  
XX WPI; 2004-010802/01.  
XX N-PSDB; ADG73250.  
DR  
XX  
PT New isolated nucleic acid molecule encoding a portion of a feline IGE  
PT heavy chain protein, useful for treating and/or eliciting feline immune  
PT responses for IGE-mediated responses, such as allergies.  
XX  
XX Claim 8; SEQ ID NO 29; 44pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
XX portion of a feline IGE heavy chain protein. The methods and compositions  
XX of the present invention are useful for eliciting feline immune responses  
XX for and/or treating IGE-mediated responses, such as allergies. This is  
XX the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy  
XX chain.

XX  
SQ Sequence 496 AA;  
XX  
Query Match 59.3%; Score 48; DB 8; Length 496;  
Best Local Similarity 61.5%; Pred. No. 13;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 NDSP1QTDQYTTT 14  
Db 428 NDSPVTRTEQOATT 440  
XX  
RESULT 14  
ADG73225  
ID ADG73225 standard; protein; 496 AA.  
XX  
AC ADG73225;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
XX Cat partial immunoglobulin E (IGE) heavy chain #1.  
XX  
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;  
XX immune response; IGE-mediated response; allergy; cat; heavy chain.  
XX  
XX Felis catus.  
XX  
XX US2003216565-A1.  
XX  
XX 20-NOV-2003.  
XX  
XX 07-APR-2003; 2003US-00409772.  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX (MCCA/) MCCALL C.  
XX (WEBE/) WEBER E.  
XX  
XX McCall C, Weber E;  
XX  
XX WPI; 2004-010802/01.  
XX N-PSDB; ADG73224.  
XX  
XX New isolated nucleic acid molecule encoding a portion of a feline IGE  
XX heavy chain protein, useful for treating and/or eliciting feline immune  
XX responses for IGE-mediated responses, such as allergies.  
XX  
XX Claim 8; SEQ ID NO 2; 44pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
XX portion of a feline IGE heavy chain protein. The methods and compositions  
XX of the present invention are useful for eliciting feline immune responses  
XX for and/or treating IGE-mediated responses, such as allergies. This is  
XX the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy  
XX chain.  
XX  
XX Sequence 496 AA;  
XX  
Query Match 59.3%; Score 48; DB 8; Length 496;  
Best Local Similarity 61.5%; Pred. No. 13;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 NDSP1QTDQYTTT 14  
Db 428 NDSPVTRTEQOATT 440  
XX  
RESULT 15  
ABU42513  
ID ABU42513 standard; protein; 1633 AA.  
XX  
XX ABU42513;

XX 19-JUN-2003 (first entry)  
XX Protein encoded by Prokaryotic essential gene #28040.  
DE Antisense: prokaryotic essential gene; cell proliferation; drug design.  
XX Staphylococcus epidermidis.  
XX W0200277183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
DR N-PSDB; ACA46383.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 70437; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 1633 AA:

Query March 53.1%; Score 43; DB 6; Length 1633;  
Best Local Similarity 61.5%; Pred. No. 3.6e+02;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NDSPIQTDOYTTT 14  
Db 242 NDEPTQDVEYTTT 254

Search completed: December 12, 2005, 20:30:25  
Job time : 84.3362 secs



REFERENCE/DOCKET NUMBER: 192111  
TELECOMMUNICATION INFORMATION:

TELEFAX: (908) 594-4720  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 426 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US95-13795-2

Query Match 100.0%; Score 81; DB 4; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDSPLOTDOYTTG 15  
 |||||  
 Db 357 NDSPLOTDOYTTG 371

RESULT 5  
 ; Sequence 14, Application US/09479614  
 ; Patent No. 6573372  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCall, Catherine  
 ; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
 ; FILE REFERENCE: P-1047  
 ; CURRENT FILING DATE: 2000-01-07  
 ; EARLIER FILING DATE: 1999-01-07  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 14  
 ; LENGTH: 431  
 ; TYPE: PRT  
 ; ORGANISM: Felis catus  
 ; US-09-479-614-14

Query Match 59.3%; Score 48; DB 2; Length 431;  
 Best Local Similarity 61.5%; Pred. No. 2.8;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 14  
 |||||  
 Db 363 NDSPRTREQAAT 375

RESULT 6  
 ; Sequence 2, Application US/09479614  
 ; Patent No. 6573372  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCall, Catherine  
 ; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
 ; FILE REFERENCE: P-1047  
 ; CURRENT FILING DATE: 2000-01-07  
 ; EARLIER FILING DATE: 1999-01-07  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 496  
 ; TYPE: PRT  
 ; ORGANISM: Felis catus  
 ; US-09-479-614-2

Query Match 59.3%; Score 48; DB 2; Length 496;  
 Best Local Similarity 61.5%; Pred. No. 3.3;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 14  
 |||||  
 Db 428 NDSPRTREQAAT 440

RESULT 7  
 ; Sequence 29, Application US/09479614  
 ; Patent No. 6573372  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCall, Catherine  
 ; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
 ; FILE REFERENCE: P-1047  
 ; CURRENT FILING DATE: 2000-01-07  
 ; EARLIER FILING DATE: 1999-01-07  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 29  
 ; LENGTH: 496  
 ; TYPE: PRT  
 ; ORGANISM: Felis catus  
 ; US-09-479-614-29

Query Match 59.3%; Score 48; DB 2; Length 496;  
 Best Local Similarity 61.5%; Pred. No. 3.3;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 14  
 |||||  
 Db 428 NDSPRTREQAAT 440

RESULT 8  
 ; Sequence 4053, Application US/09134001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucelte-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/064,964  
 ; PRIOR FILING DATE: 1997-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/055,779  
 ; PRIOR FILING DATE: 1997-08-14  
 ; NUMBER OF SEQ ID NOS: 5674  
 ; SEQ ID NO 4053  
 ; LENGTH: 533  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus epidermidis  
 ; US-09-134-001C-4053

Query Match 50.6%; Score 41; DB 2; Length 533;  
 Best Local Similarity 58.3%; Pred. No. 59;  
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 13  
 |||||  
 Db 466 NDAPLQSDQIYT 477

RESULT 9  
 ; Sequence 43446, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.

;; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
;; FILE REFERENCE: File Reference: 7326-094  
;; CURRENT APPLICATION NUMBER: US/09/270,767  
;; CURRENT FILING DATE: 1999-03-17  
;; NUMBER OF SEQ ID NOS: 62517  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 43446  
;; LENGTH: 163  
;; TYPE: PRT  
;; ORGANISM: *Drosophila melanogaster*  
;; FEATURE:  
;; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-43446

Query Match 49.4%; Score 40; DB 2; Length 163;  
Best Local Similarity 50.0%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNDSPLOTDOYTTT 14  
||:|:|:|:|:|  
Db 85 RNNEPLADNYIT 98

RESULT 10  
US-09-328-352-4294  
; Sequence 4294, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4294  
; LENGTH: 667  
; TYPE: PRT  
; ORGANISM: *Acinetobacter baumannii*  
US-09-328-352-4294

Query Match 49.4%; Score 40; DB 2; Length 667;  
Best Local Similarity 70.0%; Pred. No. 1,1e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIOTDOYTTT 14  
||:|:|:|:|:|  
Db 614 PLEADQYTTT 623

RESULT 11  
US-09-206-942-65  
; Sequence 65, Application US/09206942  
; Patent No. 6432669  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High  
; FILE REFERENCE: 1038-861 MIS:jb  
; CURRENT APPLICATION NUMBER: US/09/206,942  
; CURRENT FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: 09/167,568  
; EARLIER FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 65  
; LENGTH: 1180  
; TYPE: PRT  
; ORGANISM: *Haemophilus influenzae*  
US-09-206-942-65

Query Match 49.4%; Score 40; DB 2; Length 1180;  
Best Local Similarity 40.0%; Pred. No. 2,1e+02;  
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPLOTDOYTTTG 15  
||:|:|:|:|:|  
Db 13 RSDTNLENEYTG 27

RESULT 12  
US-10-193-764-61  
; Sequence 61, Application US/10193764  
; Patent No. 6849447  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH  
; FILE REFERENCE: 1038-1239MIS  
; CURRENT APPLICATION NUMBER: US/10/193,764  
; CURRENT FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: 09/167,568  
; PRIOR FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 61  
; LENGTH: 1180  
; TYPE: PRT  
; ORGANISM: *Haemophilus influenzae*  
US-10-193-764-61

Query Match 49.4%; Score 40; DB 2; Length 1180;  
Best Local Similarity 40.0%; Pred. No. 2,1e+02;  
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPLOTDOYTTTG 15  
||:|:|:|:|:|  
Db 13 RSDTNLENEYTG 27

RESULT 13  
US-09-206-942-63  
; Sequence 63, Application US/09206942  
; Patent No. 6432669  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High  
; FILE REFERENCE: 1038-861 MIS:jb  
; CURRENT APPLICATION NUMBER: US/09/206,942  
; CURRENT FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: 09/167,568  
; EARLIER FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 63  
; LENGTH: 1188  
; TYPE: PRT  
; ORGANISM: *Haemophilus influenzae*  
US-09-206-942-63

Query Match 49.4%; Score 40; DB 2; Length 1188;  
Best Local Similarity 40.0%; Pred. No. 2,2e+02;  
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPLOTDOYTTTG 15  
||:|:|:|:|:|  
Db 21 RSDTNLENEYTG 35



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RESULT 14
US-10-193-764-59
; Sequence 59, Application US/10193764
; Patent No. 6849447
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; FILE REFERENCE: 1038-1239WIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 59
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-59

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Query Match          49.4%; Score 40; DB 2; Length 1188;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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OY      1 RNDSPLOTDOYTTG 15
Db      21 RSDTNLENEYTG 35

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RESULT 15
US-09-949-016-10828
; Sequence 10828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10828
; LENGTH: 2186
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10828

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Query Match          49.4%; Score 40; DB 2; Length 2186;
Best Local Similarity 70.0%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY      5 PLOTDOYTTT 14
Db      1759 PLOSDOYTTT 1768

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Search completed: December 12, 2005, 19:37:03  
Job time : 21.431 secs

**RIGHT SIDE  
BLANK (OPTO)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 66.9828 Seconds  
(without alignments)  
93.568 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPIQDTQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBSCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBSCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBSCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBSCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBSCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBSCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	US-10-758-165-1	Sequence 1, Appli
2	81	100.0	426	US-10-214-524-28	Sequence 28, Appli
3	53	65.4	15	US-10-758-165-7	Sequence 7, Appli
4	53	65.4	567	US-10-214-524-33	Sequence 33, Appli
5	48	59.3	15	US-10-758-165-2	Sequence 2, Appli
6	48	59.3	431	US-09-479-614-14	Sequence 14, Appli
7	48	59.3	431	US-10-409-772-14	Sequence 14, Appli
8	48	59.3	496	US-09-479-614-2	Sequence 2, Appli
9	48	59.3	496	US-09-479-614-29	Sequence 29, Appli
10	48	59.3	496	US-10-214-524-25	Sequence 25, Appli
11	48	59.3	496	US-10-409-772-2	Sequence 2, Appli
12	48	59.3	496	US-10-409-772-29	Sequence 29, Appli
13	43	53.1	68	US-10-424-599-250413	Sequence 250413,
14	43	53.1	1633	US-10-282-122A-70437	Sequence 70437, A
15	42	51.9	123	US-10-437-963-169489	Sequence 169489,
16	42	51.9	161	US-10-425-115-238239	Sequence 238239,
17	41	50.6	15	US-10-758-165-3	Sequence 3, Appli
18	41	50.6	68	US-10-424-599-211575	Sequence 211575,
19	41	50.6	191	US-10-767-701-39191	Sequence 39191, A
20	41	50.6	424	US-10-451-078-2	Sequence 2, Appli
21	41	50.6	514	US-10-451-078-4	Sequence 4, Appli
22	41	50.6	533	US-10-424-599-177658	Sequence 177658,
23	41	50.6	533	US-10-724-972A-5049	Sequence 5049, Ap
24	40	49.4	356	US-11-097-143-19689	Sequence 19689, A
25	40	49.4	374	US-10-732-923-17586	Sequence 17586, A
26	40	49.4	374	US-10-732-923-17586	Sequence 17586, A
27	40	49.4	374	US-10-732-923-17624	Sequence 17624, A

28	40	49.4	433	4	US-10-425-115-355337	Sequence 355337,
29	40	49.4	438	4	US-10-425-114-65347	Sequence 65347, A
30	40	49.4	589	4	US-10-437-963-135296	Sequence 135296,
31	40	49.4	555	4	US-10-355-956-4	Sequence 4, Appli
32	40	49.4	555	5	US-10-504-048-4	Sequence 4, Appli
33	40	49.4	596	4	US-10-767-701-44580	Sequence 44580, A
34	40	49.4	1180	4	US-10-193-764-61	Sequence 61, Appli
35	40	49.4	1188	4	US-10-193-764-59	Sequence 59, Appli
36	40	49.4	2400	5	US-10-450-763-50637	Sequence 50637, A
37	40	49.4	2415	5	US-10-450-763-50638	Sequence 50638, A
38	39	48.1	51	4	US-10-425-115-26056	Sequence 26056,
39	39	48.1	170	4	US-10-424-599-148645	Sequence 148645,
40	39	48.1	281	4	US-10-369-430A-26	Sequence 26, Appli
41	39	48.1	446	5	US-10-450-763-56495	Sequence 56495, A
42	39	48.1	523	4	US-10-437-963-117513	Sequence 117513,
43	39	48.1	584	4	US-10-437-963-145953	Sequence 145953,
44	39	48.1	598	4	US-10-424-599-241468	Sequence 241468,
45	39	48.1	1589	4	US-10-425-115-303919	Sequence 303919,

ALIGNMENTS

RESULT 1  
US-10-758-165-1  
; Sequence 1, Application US/10758165  
; Publication No. US20050196616A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758.165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-758-165-1

Query Match 100.0%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.9e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNDSPIQDTQYTTTG 15  
|||||  
Db 1 RNDSPIQDTQYTTTG 15

RESULT 2  
US-10-214-524-28  
; Sequence 28, Application US/10214524  
; Publication No. US20030073142A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Swei-Shen Alex  
; APPLICANT: Yang, Yong-Min  
; APPLICANT: Barankiewicz, Theresa J.  
; APPLICANT: Chen, Zhong  
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
; FILE REFERENCE: IGB-00101.P.1.1  
; CURRENT APPLICATION NUMBER: US/10/214.524  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/312,120  
; PRIOR FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Dog (Canis familiaris)

US-10-214-524-28

Query Match 100.0%; Score 81; DB 4; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 15  
|||||:|:|:|:|:|:|  
Db 357 RNDSP1QTDQYTTT 371

RESULT 3

US-10-758-165-7  
; Sequence 7, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammetberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-7

Query Match 65.4%; Score 53; DB 5; Length 15;  
Best Local Similarity 57.1%; Pred. No. 0.035;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14  
|||:|:|:|:|:|  
Db 1 RNDAPVQADRHSTT 14

RESULT 4

US-10-214-524-33  
; Sequence 33, Application US/10214524  
; Publication No. US20030073142A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Yong-Min  
; APPLICANT: Barankiewicz, Theresa J.  
; APPLICANT: Chen, Zhong  
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
; FILE REFERENCE: IGE-00101.P.1.1  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US/10/214,524  
; PRIOR FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Pig (Sus scrofa)  
US-10-214-524-33

Query Match 65.4%; Score 53; DB 4; Length 567;  
Best Local Similarity 57.1%; Pred. No. 1.9;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14  
|||:|:|:|:|:|  
Db 499 RNDAPVQADRHSTT 512

RESULT 5

US-10-758-165-2

; Sequence 2, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammetberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-2

Query Match 59.3%; Score 48; DB 5; Length 15;  
Best Local Similarity 61.5%; Pred. No. 0.26;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14  
|||:|:|:|:|:|  
Db 2 NDSPIQTDQYTTT 14

RESULT 6

US-09-479-614-14  
; Sequence 14, Application US/09479614  
; Publication No. US20030013183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-14

Query Match 59.3%; Score 48; DB 3; Length 431;  
Best Local Similarity 61.5%; Pred. No. 10;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14  
|||:|:|:|:|:|  
Db 363 NDSPIQTDQYTTT 375

RESULT 7

US-10-409-772-14  
; Sequence 14, Application US/10409772  
; Publication No. US20030216565A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/479,614  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14  
LENGTH: 431  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-14

Query Match 59.3% Score 48; DB 4; Length 431;  
Best Local Similarity 61.5% Pred. No. 10;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
Db 363 NDSPVRTQOAT 375

RESULT 8  
US-09-479-614-2  
Sequence 2, Application US/09479614  
Publication No. US20030013183A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/09/479,614  
CURRENT FILING DATE: 2000-01-07  
EARLIER APPLICATION NUMBER: 60/115,033  
EARLIER FILING DATE: 1999-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-09-479-614-2

Query Match 59.3% Score 48; DB 3; Length 496;  
Best Local Similarity 61.5% Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
Db 428 NDSPVRTQOAT 440

RESULT 9  
US-09-479-614-29  
Sequence 29, Application US/09479614  
Publication No. US20030013183A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/09/479,614  
CURRENT FILING DATE: 2000-01-07  
EARLIER APPLICATION NUMBER: 60/115,033  
EARLIER FILING DATE: 1999-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-09-479-614-29

Query Match 59.3% Score 48; DB 3; Length 496;  
Best Local Similarity 61.5% Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
Db 428 NDSPVRTQOAT 440

RESULT 10  
US-10-214-524-25  
Sequence 25, Application US/10214524  
Publication No. US20030073142A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Swey-Shen Alex  
APPLICANT: Yang, Yong-Min  
APPLICANT: Barankiewicz, Theresa J.  
APPLICANT: Chen, Zhong  
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
FILE REFERENCE: IGE-00101.P.1.1  
CURRENT APPLICATION NUMBER: US/10/214,524  
CURRENT FILING DATE: 2002-08-08  
PRIOR APPLICATION NUMBER: 60/312,120  
PRIOR FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 25  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Cat (Felis catus)  
US-10-214-524-25

Query Match 59.3% Score 48; DB 4; Length 496;  
Best Local Similarity 61.5% Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
Db 428 NDSPVRTQOAT 440

RESULT 11  
US-10-409-772-2  
Sequence 2, Application US/10409772  
Publication No. US20030216565A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/10/409,772  
CURRENT FILING DATE: 2003-04-07  
PRIOR APPLICATION NUMBER: US/09/479,614  
PRIOR FILING DATE: 2000-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-2

Query Match 59.3% Score 48; DB 4; Length 496;  
Best Local Similarity 61.5% Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
Db 428 NDSPVRTQOAT 440

RESULT 12  
US-10-409-772-29  
Sequence 29, Application US/10409772  
Publication No. US20030216565A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047

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; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-10-409-772-29

Query Match      59.3%; Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 NDSPQTQDTT 14
DB      428 NDSPRTQQT 440

RESULT 13
US-10-424-599-250413
; Sequence 250413, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250413
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(68)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68150C.1.pep
; US-10-424-599-250413

Query Match      53.1%; Score 43; DB 4; Length 68;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4 SPIOTDQYTTG 15
DB      21 TPRTDQYTTIG 32

RESULT 14
US-10-282-122A-70437
; Sequence 70437, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Malone, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
```

```

; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 70437
; LENGTH: 1633
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-10-282-122A-70437

Query Match      53.1%; Score 43; DB 4; Length 1633;
Best Local Similarity 61.5%; Pred. No. 3.3e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 NDSPQTQDQYTTT 14
DB      242 NDERTQDQYTTT 254

RESULT 15
US-10-437-963-169489
; Sequence 169489, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169489
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67905C.1.pep
; US-10-437-963-169489

Query Match      51.9%; Score 42; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	RNDSPIC	8
Db	27	RNDSPIC	34

Search completed: December 12, 2005, 20:19:23  
Job time : 67.9828 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.4569 seconds  
(without alignments)  
34.094 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPICQDYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	312	6	US-10-723-207-2
2	38	46.9	1155	6	US-10-793-626-1780
3	36	44.4	543	6	US-10-689-742-78
4	35	43.2	128	6	US-10-467-657-5476
5	35	43.2	185	7	US-10-662-136
6	34	42.0	310	6	US-10-131-826A-538
7	34	42.0	310	7	US-11-025-834A-13
8	34	42.0	310	7	US-11-025-834A-15
9	34	42.0	354	6	US-10-467-657-5634
10	34	42.0	362	6	US-10-821-234-1148
11	34	42.0	428	6	US-10-821-234-997
12	34	42.0	790	6	US-10-763-712A-75
13	34	42.0	840	6	US-11-108-172-1102
14	33	40.7	180	7	US-11-098-662-114
15	33	40.7	181	7	US-11-098-662-32
16	33	40.7	181	7	US-11-098-662-42
17	33	40.7	181	7	US-11-098-662-46
18	33	40.7	181	7	US-11-098-662-50
19	33	40.7	181	7	US-11-098-662-70
20	33	40.7	181	7	US-11-098-662-74
21	33	40.7	181	7	US-11-098-662-78
22	33	40.7	181	7	US-11-098-662-82
23	33	40.7	181	7	US-11-098-662-110
24	33	40.7	182	7	US-11-098-662-34
25	33	40.7	182	7	US-11-098-662-38

26	33	40.7	182	7	US-11-098-662-44	Sequence 44, Appl
27	33	40.7	182	7	US-11-098-662-48	Sequence 48, Appl
28	33	40.7	182	7	US-11-098-662-52	Sequence 52, Appl
29	33	40.7	182	7	US-11-098-662-72	Sequence 72, Appl
30	33	40.7	182	7	US-11-098-662-76	Sequence 76, Appl
31	33	40.7	182	7	US-11-098-662-80	Sequence 80, Appl
32	33	40.7	182	7	US-11-098-662-84	Sequence 84, Appl
33	33	40.7	182	7	US-11-098-662-112	Sequence 112, Appl
34	33	40.7	182	7	US-11-098-662-118	Sequence 118, Appl
35	33	40.7	182	7	US-11-098-662-132	Sequence 132, Appl
36	33	40.7	183	7	US-11-098-662-136	Sequence 136, Appl
37	33	40.7	183	7	US-11-098-662-130	Sequence 130, Appl
38	33	40.7	200	7	US-11-098-662-4	Sequence 4, Appl
39	33	40.7	200	7	US-11-098-662-20	Sequence 20, Appl
40	33	40.7	310	6	US-10-793-626-478	Sequence 478, Appl
41	33	40.7	310	6	US-10-793-626-1270	Sequence 1270, Appl
42	33	40.7	322	7	US-11-055-822-66	Sequence 66, Appl
43	33	40.7	505	6	US-10-467-657-6228	Sequence 6228, Appl
44	33	40.7	735	7	US-11-184-380-24	Sequence 24, Appl
45	33	40.7	737	7	US-11-128-420-9	Sequence 9, Appl

## ALIGNMENTS

```
RESULT 1
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 1151-4153US2
; CURRENT FILING DATE: 2003-11-24
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IGE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2
Query Match 100.0%; Score 81; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RNDSPICQDYTTTG 15
Db 255 RNDSPICQDYTTTG 269
RESULT 2
US-10-793-626-1780
; Sequence 1780, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
```

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; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1780
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1780

Query Match          46.9%; Score 38; DB 6; Length 1155;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2  RNDSPIQDQYTTT 14
Db      242  NDEPTQDVEHTTT 254

RESULT 3
US-10-689-742-78
; Sequence 78, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766,000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-78

Query Match          44.4%; Score 36; DB 6; Length 543;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1  RNDSPIQDQYTTT 15
Db      69  RNPTLVQDDQYENHG 83

RESULT 4
US-10-467-657-5476
; Sequence 5476, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
```

```
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5476
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5476

Query Match          43.2%; Score 35; DB 6; Length 128;
Best Local Similarity 35.7%; Pred. No. 4.9;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1  RNDSPIQDQYTTT 14
Db      24  RNSATVMADKYTSS 37

RESULT 5
US-11-098-662-136
; Sequence 136, Application US/11098662
; Publication No. US2005024423A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; FILE REFERENCE: 04-05
; CURRENT APPLICATION NUMBER: US/11/098,662
; CURRENT FILING DATE: 2005-04-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 Glu, Ala, and Glu inserted after N-terminal
; OTHER INFORMATION: Met, C175X
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (175)...(175)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
US-11-098-662-136

Query Match          43.2%; Score 35; DB 7; Length 185;
Best Local Similarity 46.2%; Pred. No. 7.4;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3  DSPIQDQYTTTG 15
Db      4  BGPVPTSKPTTTG 16

RESULT 6
US-10-131-826A-538
; Sequence 538, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
```

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 538
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-538

Query Match          42.0%; Score 34; DB 6; Length 310;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RNDSP1QTD 9
Db      175 RNDVPLPTD 183

RESULT 7
US-11-025-834A-13
; Sequence 13, Application US/11025834A
; Publication No. US20050266426A1
; GENERAL INFORMATION:
; APPLICANT: IMHOFF, BEAT ALBERT
; APPLICANT: AURRAND-LIONS, MICHEL
; TITLE OF INVENTION: PERFORMANCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASO
; FILE REFERENCE: 011422-0314432
; CURRENT APPLICATION NUMBER: US/11/025,834A
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/524,531
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EP 99,200746.8
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 310
; TYPE: PRT
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; ORGANISM: Mus musculus
US-11-025-834A-13

Query Match          42.0%; Score 34; DB 7; Length 310;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RNDSP1QTD 9
Db      175 RNDVPLPTD 183

RESULT 8
US-11-025-834A-15
; Sequence 15, Application US/11025834A
; Publication No. US20050266426A1
; GENERAL INFORMATION:
; APPLICANT: IMHOFF, BEAT ALBERT
; APPLICANT: AURRAND-LIONS, MICHEL
; TITLE OF INVENTION: CONFLUENCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASO
; FILE REFERENCE: 011422-0314432
; CURRENT APPLICATION NUMBER: US/11/025,834A
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/524,531
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EP 99,200746.8
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-025-834A-15

Query Match          42.0%; Score 34; DB 7; Length 310;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RNDSP1QTD 9
Db      175 RNDVPLPTD 183

RESULT 9
US-10-467-657-5634
; Sequence 5634, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA, Maria Rita
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: MASIGNANI, Vega
; APPLICANT: MONACI, Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5634
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5634

Query Match          42.0%; Score 34; DB 6; Length 354;
Best Local Similarity 45.5%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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QY      2  NDSPIQTDQYT 12
Db      178 SDQPIGEYVT 188

RESULT 10
US-10-821-234-1148
; Sequence 1148, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1148
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1148

Query Match      42.0%; Score 34; DB 6; Length 362;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  RNDSPIQTD 9
Db      227 RNDVPLPTD 235

RESULT 11
US-10-821-234-997
; Sequence 997, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 997
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-997

Query Match      42.0%; Score 34; DB 6; Length 428;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3  DSPIQTDQYTTG 15
Db      268 ESPVQYAAVTVG 280

RESULT 12
US-10-763-712A-75
; Sequence 75, Application US/10763712A
; Publication No. US20050266541A1
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; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Geobacter metallireducens
US-10-763-712A-75

Query Match      42.0%; Score 34; DB 6; Length 790;
Best Local Similarity 53.8%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1  RNDSPIQTDQYTT 13
Db      517 RNDKPLVTWCTT 529

RESULT 13
US-11-108-172-1102
; Sequence 1102, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
```

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; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1102
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-662-1102

Query Match      42.0%; Score 34; DB 7; Length 840;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 NDSPIQTDQ 10
        |::|||
Db      506 NEEPMETDQ 514

RESULT 14
US-11-098-662-114
; Sequence 114, Application US/11098662
; Publication No. US20050244423A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Sivakumar, Pallavar V.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; FILE REFERENCE: 04-05
; CURRENT APPLICATION NUMBER: US/11/098,662
; CURRENT FILING DATE: 2005-04-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 114
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 C170X, truncated after N-terminal Methionine
; OTHER INFORMATION: and Glycine
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (170)...(170)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
US-11-098-662-114

Query Match      40.7%; Score 33; DB 7; Length 180;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 PIQTDQYTTTG 15
        |::|||
Db      1 PVPISKPPTTG 11

RESULT 15
US-11-098-662-32
; Sequence 32, Application US/11098662
; Publication No. US20050244423A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Sivakumar, Pallavar V.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; FILE REFERENCE: 04-05
; CURRENT APPLICATION NUMBER: US/11/098,662
```

```
; CURRENT FILING DATE: 2005-04-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 32
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 mutant C171S
US-11-098-662-32

Query Match      40.7%; Score 33; DB 7; Length 181;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 PIQTDQYTTTG 15
        |::|||
Db      2 PVPISKPPTTG 12
```

Search completed: December 12, 2005, 20:19:48  
Job time : 3.4569 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 12.6724 Seconds  
(without alignments)  
113.889 Million cell updates/sec

Title: US-10-758-165A-1

Perfect score: 81

Sequence: 1 RNDSPQTDQYTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	53.1	664	T20420	hypothetical prote
2	42	51.9	1008	T23986	hypothetical prote
3	42	51.9	1067	D96545	probable DNA polym
4	41	50.6	1117	S63399	probable membrane
5	40	49.4	234	T49737	hypothetical prote
6	40	49.4	1157	F97255	fusion of alpha-gl
7	40	49.4	2094	S33124	cupr protein - huma
8	39	48.1	187	UC4806	core protein G - p
9	39	48.1	187	S22331	gene G protein - p
10	39	48.1	294	T08408	transcription fact
11	39	48.1	514	S72443	DNA-binding protei
12	39	48.1	564	HMVYDA	hemagglutinin prec
13	39	48.1	587	F85084	probable achilla-li
14	39	48.1	940	T01834	hypothetical prote
15	39	48.1	2161	A45389	genome polypeptide
16	39	48.1	138344	138344	ctitin, cardiac mus
17	38.5	47.5	1157	S49247	paraspinal crystal
18	38	46.9	173	S55150	hypothetical prote
19	38	46.9	201	T23492	hypothetical prote
20	38	46.9	205	T31489	hypothetical prote
21	38	46.9	254	F81265	cyto9 protein homol
22	38	46.9	281	AD2052	hypothetical prote
23	38	46.9	321	B32801	fibrial adhesion p
24	38	46.9	321	JR0115	zinc-finger protei
25	38	46.9	429	EB4410	GTP-binding protei
26	38	46.9	450	A10345	probable heat shoc
27	38	46.9	468	T08139	shaggy-like protei
28	38	46.9	612	C90374	hypothetical prote
29	38	46.9	996	S76194	hypothetical prote

30	38	46.9	1158	2	AF1852	hypothetical prote
31	38	46.9	1450	2	A44027	165K myofibrillar
32	38	46.9	1465	2	S43529	165K protein, skel
33	38	46.9	1562	2	T07323	DNA-directed RNA p
34	38	46.9	1969	2	T38495	hypothetical prote
35	37.5	46.3	272	2	B69688	glutamate racemase
36	37.5	46.3	590	2	S63193	hypothetical prote
37	37	45.7	136	2	F84234	hypothetical prote
38	37	45.7	219	2	B71841	hypothetical prote
39	37	45.7	245	2	T23844	hypothetical prote
40	37	45.7	268	2	A71966	hypothetical prote
41	37	45.7	298	2	A70238	hypothetical prote
42	37	45.7	429	2	T06296	extensin-like prote
43	37	45.7	502	2	E71963	probable cardioli
44	37	45.7	521	2	A48650	agrociclopine utili
45	37	45.7	521	2	A13244	hypothetical prote

#### ALIGNMENTS

RESULT 1  
T20420  
hypothetical protein E02H4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20420  
R:Barlow, K.  
submitted to the EMBL Data Library, November 1995  
A:Reference number: Z19273  
A:Accession: T20420  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-664 <WILL>  
A:Cross-References: UNIPROT:Q19038; UNIPARC:UPI0000129186; EMBL:Z68003; PIDN:CAA91975.1;  
A:Experimental source: clone E02H4  
C:Genetics:  
A:Gene: CESP:E02H4.1  
A:Map position: X  
A:Intons: 57/3; 102/3; 135/3; 166/1; 191/1; 221/2; 254/3; 314/2; 355/2; 386/1; 472/3; 5  
C:Superfamily: human amloride-sensitive sodium channel protein; fibronectin type I repe

Query Match 53.1% Score 43; DB 2; Length 664;  
Best Local Similarity 80.0% Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PQQDQYTTT 14  
DB 536 PQQDQYTTT 545

RESULT 2  
T23986  
hypothetical protein C05D2.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T23986  
R:Du, Z.  
submitted to the EMBL Data Library, February 1998  
A:Description: The sequence of C. elegans cosmid C05D2.  
A:Reference number: Z21260  
A:Accession: T23986  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1008 <DUZ>  
A:Cross-References: UNIPARC:UPI0000178734; EMBL:AF047651; PIDN:AA02723.1; GSPDB:GN00021  
A:Experimental source: strain Bristol N2; clone C05D2  
C:Genetics:  
A:Gene: CESP:C05D2.6  
A:Map position: 3  
A:Intons: 23/1; 53/3; 141/1; 231/3; 307/3; 325/2; 420/1; 466/3; 499/3; 522/2; 594/1; 75

Query Match 51.9% Score 42; DB 2; Length 1008;

Best Local Similarity 58.3%; Pred. No. 39;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPQTQDTT 12  
| | | | |  
| | | | |  
Db 41 REDPVTQTYT 52

## RESULT 3

D96545

probable DNA polymerase A family protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: D96545

R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,

Chun, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hultzar, L.

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzalli,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D96545

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1067 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9C6J5; UNIPARC:UPI0000048370; GB:AE005173; NID:g11094700; F

C:Genetics:

A:Gene: PBA12.8

A:Map position: 1

Query Match

Best Local Similarity 42.9%; Pred. No. 41;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTQDTT 15  
: | | | | : | | :  
: | | | | : | | :  
Db 625 SDSPLSTENFTTASG 638

## RESULT 4

S63399

probable membrane protein YNR067C - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein N3547

C:Species: Saccharomyces cerevisiae

C&gt;Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004

C:Accession: S63399

R:Ducrestioeft, A.; Floeth, M.; Filtz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S62944

A:Accession: S63399

A:Molecule type: DNA

A:Residues: 1-1117 &lt;DUE&gt;

A:Cross-references: UNIPROT:P53753; UNIPARC:UPI000013BACB; EMBL:Z71682; NID:g1302597; P1

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YNR067C

A:Cross-references: SGD:S0005350

A:Map position: 14R

C:Keywords: transmembrane protein

F:6-22/Domain: transmembrane #status predicted &lt;TMM&gt;

Query Match

Best Local Similarity 50.6%; Score 41; DB 2; Length 1117;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTQDTT 13  
| | | | |  
| | | | |  
Db 430 NDSPIQTINKFTT 441

RESULT 5  
T49737  
hypothetical protein B24B19.90 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C&gt;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 18-Aug-2000

C:Accession: T49737

R:Schulte, U.; Aign, V.; Heiseisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49737

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 &lt;SCH&gt;

A:Cross-references: UNIPARC:UPI0000179DBA; EMBL:ALJ56192; GSPDB:GN00116; NCSP:B24B19.90

A:Experimental source: BAC clone B24B19; strain OR74A

C:Genetics:

A:Gene: NCSP:B24B19.90

A:Map position: 6

A:Insertions: 133/2

C:Superfamily: Neurospora crassa hypothetical protein B24B19.90

Query Match

Best Local Similarity 49.4%; Score 40; DB 2; Length 234;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIQTQDTT 14  
: | | | |  
: | | | |  
Db 65 PVPTQTYTT 74

## RESULT 6

P97255

fusion of alpha-glucosidase (family 31 glycosyl hydrolase) and glycosidase (TREA/MaIs fan

C:Species: Clostridium acetobutylicum

C&gt;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C:Accession: P97255

R:Noiling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clof

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: P97255

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1157 &lt;KUR&gt;

A:Cross-references: UNIPROT:Q97F62; UNIPARC:UPI00000D755C; GB:AE001437; PIDN:AAK80833.1;

C:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC2891

Query Match

Best Local Similarity 49.4%; Score 40; DB 2; Length 1157;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTQDTT 13  
: | | | | : | | :  
: | | | | : | | :  
Db 889 NESDVFTQTYTT 900

## RESULT 7

S33124

tpr protein - human

N:Alternate names: kinase-related transforming protein (tpr-met); protein with promoter 1

C:Species: Homo sapiens (man)

C&gt;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004

C:Accession: S33124; S23740; S00928; G01185

R:Michell, P.J.; Cooper, C.S.

Oncogene 7, 2329-2333, 1992

A:Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive coil

A:Reference number: S33124; MUID:93064711; PMID:1437155

A:Accession: S33124

A:Status: preliminary; nucleic acid sequence not shown; translation not shown



A:Molecule type: mRNA  
A:Residues: 1-2094 <MIT>  
A:Cross-references: UNIPROT:O15624; UNIPROT:O9UE33; UNIPARC:UPI000017CBF3; EMBL:X66397;  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
R:Mitcheil, P.J.; Cooper, C.S.  
Oncogene 7, 383-388, 1992  
A:Title: Nucleotide sequence analysis of human tpr cDNA clones.  
A:Reference number: S23740; MUID:92195670; PMID:1549355  
A:Accession: S23740  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-725, 'L' <MT2>  
A:Cross-references: UNIPARC:UPI000062253; EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID  
R:King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.  
Oncogene 2, 617-619, 1988  
A:Title: Tpr homologues activate met and raf.  
A:Reference number: S00928; MUID:88262257; PMID:3387099  
A:Accession: S00928  
A:Molecule type: mRNA  
A:Residues: 1-31, 'R', '33-142 <KIN>  
A:Cross-references: UNIPARC:UPI000016B112; EMBL:X06672; NID:g37255; PIDN:CAA68681.1; PID  
R:Greco, A.  
submitted to the EMBL Data Library, December 1995  
A:Reference number: H00592  
A:Accession: G01185  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 144-228 <GRE>  
A:Cross-references: UNIPARC:UPI00000711D7; EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; F  
C:Genetics:  
A:Gene: GDB:TPR  
A:Cross-references: GDB:128821; OMIM:189940  
A:Map position: 1q25-1q25  
A:Introns: 177/3

Query Match 49.4%; Score 40; DB 2; Length 2094;  
Best Local Similarity 70.0%; Pred. No. 2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PIOTDQYTTT 14  
Db 1922 PLOSDQOYTTT 1931

RESULT 8  
core protein G - phage phi-K  
C:Species: phage phi-K  
C:Date: 15-Aug-1996 #sequence revision 15-Oct-1996 #text\_change 09-Jul-2004  
C:Accession: JC4806; B04253; A04253  
R:Kodaira, K.; Oki, M.; Kakikawa, M.; Kimoto, H.; Takeko, A.  
J. Biochem. 119, 1062-1069, 1996  
A:Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant ph  
A:Reference number: JC4804; MUID:96424987; PMID:8827438  
A:Accession: JC4806  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-187 <KOD>  
A:Cross-references: UNIPROT:Q38042; UNIPARC:UPI0000138658; EMBL:X60333; NID:g1478118; PI  
R:Sims, J.; Capon, D.; Dressler, D.  
J. Biol. Chem. 254, 12615-12628, 1979  
A:Title: dnag (primase)-dependent origins of DNA replication. Nucleotide sequences of th  
A:Reference number: A92247; MUID:80049950; PMID:387790  
A:Accession: B04253  
A:Molecule type: DNA  
A:Residues: 165-187 <SIM>  
A:Cross-references: UNIPARC:UPI000009COFB  
C:Comment: This protein is one of the structural components of the bacteriophage capsid.  
C:Genetics:  
A:Gene: G  
A:Superfamily: phage phi-X174 gene G protein  
C:Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;  
Best Local Similarity 40.0%; Pred. No. 19;  
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPLOTQYTTTG 15  
Db 8 KHDTRIQTSRFSVTG 22

RESULT 9  
gene G protein - phage alpha-3  
C:Species: phage alpha-3  
C:Date: 10-Mar-1994 #sequence revision 10-Mar-1994 #text\_change 09-Jul-2004  
C:Accession: S22331; C04253; A04253  
R:Kodaira, K.I.; Nakano, K.; Okada, S.; Takeko, A.  
Biochim. Biophys. Acta 1130, 277-288, 1992  
A:Title: Nucleotide sequence of the genome of the bacteriophage alpha3: interrelationshi  
A:Reference number: S22324; MUID:92223109; PMID:1532908  
A:Accession: S22331  
A:Molecule type: DNA  
A:Residues: 1-187 <KOD>  
A:Cross-references: UNIPROT:P31281; UNIPARC:UPI0000113352; EMBL:X60322; NID:g14775; PIDN  
R:Sims, J.; Capon, D.; Dressler, D.  
J. Biol. Chem. 254, 12615-12628, 1979  
A:Title: dnag (primase)-dependent origins of DNA replication. Nucleotide sequences of th  
A:Reference number: A92247; MUID:80049950; PMID:387790  
A:Accession: C04253  
A:Molecule type: DNA  
A:Residues: 165-187 <SIM>  
A:Cross-references: UNIPARC:UPI0000000389; GB:J02444; GB:M10725; NID:g16103; PIDN:AAA32  
C:Comment: This protein is one of the structural components of the bacteriophage capsid.  
C:Genetics:  
A:Gene: G  
A:Superfamily: phage phi-X174 gene G protein  
C:Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;  
Best Local Similarity 40.0%; Pred. No. 19;  
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPLOTQYTTTG 15  
Db 8 KHDTRIQTSRFSVTG 22

RESULT 10  
transcription factor homolog F18B3.150 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text\_change 09-Jul-2004  
C:Accession: T08408  
R:Queller, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salancub  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: T08409  
A:Accession: T08408  
A:Molecule type: DNA  
A:Residues: 1-294 <QUR>  
A:Cross-references: UNIPROT:Q9SVL2; UNIPARC:UPI00000A322F; EMBL:AL049862; GSPDB:GND0061;  
A:Experimental source: cultivar Columbia; BAC clone F18B3  
C:Genetics:  
A:Gene: ATSP:F18B3.150  
A:Map position: 3  
A:Introns: 172/3

Query Match 48.1%; Score 39; DB 2; Length 294;  
Best Local Similarity 75.0%; Pred. No. 33;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPIOTDQY 11  
Db 201 APVOTDQY 208

## RESULT 11

S72443

DNA-binding protein WRKY1 - parsley

C/Species: Petroselinum crispum (parsley)

C/Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 31-Dec-2004

C/Accession: S72443

R/Rushon, P.J.; Tovar Torres, J.; Parniske, M.; Wernert, P.; Hahlbrock, K.; Somesich, I

EMBO J. 15, 5690-5700, 1996

A/Title: Interaction of elicitor-induced DNA-binding proteins with elicitor response ele

A/Reference number: S72443; MUID:97051827; PMID:8896462

A/Accession: S72443

A/Molecule type: mRNA

A/Residues: 1-514 &lt;RUS&gt;

A/Cross-references: UNIPROT:Q40827; UNIPARC:UPI00000A1FF5; EMBL:U48831; NID:G1431871; P

C/Keywords: DNA binding

Query Match

Best Local Similarity 48.1%; Score 39; DB 2; Length 514;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DSPIQDQYTT 12

DB 53 DSPIQNNNT 62

## RESULT 12

HMIYDA

hemagglutinin precursor - influenza A virus

N/Contains: hemagglutinin HA1; hemagglutinin HA2

C/Species: influenza A virus

C/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 16-Jun-2000

C/Accession: B39987; A04057; F3157

R/Nobusawa, E.; Aoyama, T.; Kato, H.; Suzuki, Y.; Tateo, Y.; Nakajima, K.

A/Title: Comparison of complete amino acid sequences and receptor-binding properties and

A/Reference number: A39987; MUID:9120697; PMID:2024485

A/Accession: B39987

A/Molecule type: genomic RNA

A/Residues: 1-564 &lt;NOB&gt;

A/Cross-references: UNIPARC:UPI000012C4DB; GB:D90307; NID:G221309; PIDN:BAH1437.1; PID:

A/Experimental source: strain A/duck/Alberta/60/76 [H1N5]

R/Air, G.M.

Proc. Natl. Acad. Sci. U.S.A. 78, 7639-7643, 1981

A/Title: Sequence relationships among the hemagglutinin genes of 12 subtypes of influenza

A/Reference number: A93902; MUID:82150925; PMID:6174976

A/Accession: A04057

A/Molecule type: genomic RNA

A/Residues: 1-38, 'L', '40-51', 'G', '53-101 &lt;AIR&gt;

A/Cross-references: UNIPARC:UPI0000170F31; GB:J02104; NID:G324135; PIDN:AAA43180.1; PID:

A/Experimental source: strain A/duck/Alberta/60/76 [H12]

A/Note: the signal sequence and the amino end of the HA1 chain comprise residues 1-17 and

C/Genetics:

A/Map position: segment 4

C/Superfamily: influenza virus hemagglutinin

C/Keywords: glycoprotein; hemagglutinin; homotrimer; transmembrane protein

F/1-17/Domain: signal sequence #status predicted &lt;SIG&gt;

F/18-342/Product: hemagglutinin HA1 #status predicted &lt;HA1&gt;

F/343-564/Product: hemagglutinin HA2 #status predicted &lt;HA2&gt;

F/555-551/Domain: transmembrane #status predicted &lt;TM&gt;

F/27,28,140,151,152,222,302,309,496,523/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match

Best Local Similarity 48.1%; Score 39; DB 1; Length 564;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14

DB 174 PVQTDYKNT 183

## RESULT 13

## F85084

probable athlia-like protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C/Accession: F85084

R/Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A/Reference number: A85001; MUID:20083488; PMID:10617198

A/Accession: F85084

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-587 &lt;STO&gt;

A/Cross-references: UNIPROT:Q9W072; UNIPARC:UPI0000095893; GB:NC\_001268; NID:G7267490; P

A/Genes: AT4g08490

A/Map position: 4

Query Match

Best Local Similarity 48.1%; Score 39; DB 2; Length 587;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 DSPIQDQYTTT 14

DB 401 DTPQDQNPPT 412

## RESULT 14

T01834

hypothetical protein T15F16.4 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004

C/Accession: T01834

R/Antoniou, B.; Le, T.

submitted to the EMBL Data Library, August 1998

A/Description: The sequence of A. thaliana T15F16.

A/Reference number: Z14443

A/Accession: T01834

A/Status: translated from GB/EMBL/DBD

A/Molecule type: DNA

A/Residues: 1-940 &lt;ANT&gt;

A/Cross-references: UNIPROT:O81471; UNIPARC:UPI000009DA3B; EMBL:AF076275; NID:G3293582; I

A/Experimental source: cultivar Columbia

A/Map position: 4

A/Introns: 108/1; 340/1

A/Note: T15F16.4

Query Match

Best Local Similarity 48.1%; Score 39; DB 2; Length 940;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 DSPIQDQYTTT 14

DB 754 DTPQDQNPPT 765

## RESULT 15

A45389

genome polyprotein - canine distemper virus (strain Onderstepoort)

N/Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase

C/Species: canine distemper virus

C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C/Accession: A45389

R/Stidnu, W.S.; Wenomna, J.P.; Cook, S.D.; Dowling, P.C.; Udem, S.A.

Virology 193, 50-65, 1993

A/Title: Canine distemper virus L gene: sequence and comparison with related viruses.

A/Reference number: A45389; MUID:93174968; PMID:8438585

A/Accession: A45389

A/Molecule type: genomic RNA

A/Residues: 1-2161 &lt;STD&gt;

A/Cross-references: UNIPROT:P24658; UNIPARC:UPI0000172721; GB:L13195; NID:G289531; PID:G

C;Genetics:

A;Gene: L

C;Superfamily: parainfluenza virus RNA-directed RNA polymerase  
C;Keywords: ATP; nucleotidyltransferase; RNA biosynthesis; RNA replication

Query March 48.1%; Score 39; DB 1; Length 2161;

Best Local Similarity 63.6%; Pred. No. 3.1e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYT 12

Db 1656 NDKPILIDQYS 1666

Search completed: December 12, 2005, 20:43:45  
Job time : 14.6724 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 81.4655 Seconds  
(without alignments)  
129.907 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSP1QTDYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	54.3	558	2	Q6FW7_CANGA
2	43	53.1	340	2	Q4SKB2_TERNG
3	43	53.1	511	2	Q5HK05_STRAB
4	43	53.1	511	2	Q8CMU2_STRAP
5	43	53.1	516	2	Q7RHP3_PLAYO
6	43	53.1	664	1	DELI_CABEL
7	43	53.1	699	2	Q819P8_9BIVA
8	43	53.1	809	2	Q4N289_TREPA
9	43	53.1	5261	2	Q4UFT9_THEAN
10	42	51.9	273	2	Q6WVK1_NEUCR
11	42	51.9	455	2	Q8BD16_PSEPK
12	42	51.9	516	2	Q45133_CAEEL
13	42	51.9	700	2	Q24781_BACSP
14	42	51.9	1049	2	Q8W105_ARATH
15	42	51.9	1056	2	Q5ZG34_MAGGR
16	42	51.9	1067	2	Q9CG05_ARATH
17	42	51.9	1857	2	Q8TW75_METAC
18	41	50.6	235	2	Q87R22_VIBPA
19	41	50.6	189	2	Q4L7X7_STAHJ
20	41	50.6	264	2	Q4WVW6_BACCE
21	41	50.6	299	2	Q6CTV1_KLULA
22	41	50.6	339	2	Q8RBP9_THERTN
23	41	50.6	360	2	Q8AS18_BACTN
24	41	50.6	414	2	Q5TRD3_ANGCA
25	41	50.6	429	2	Q757X1_ASHGO
26	41	50.6	662	2	Q6FN92_CASHG
27	41	50.6	713	2	Q5QV82_IDILO
28	41	50.6	860	2	Q6TWS3_9BACT
29	41	50.6	1117	1	YN56_YEAST
30	40	49.4	99	2	Q60S58_CABER
31	40	49.4	213	2	Q5WCK0_BACSK

32	40	49.4	234	2	Q7RUA3_NEUCR	Q7RUA3 neuropeptide
33	40	49.4	236	2	Q56PA2_9METZ	Q56PA2 uncultured
34	40	49.4	255	2	Q54236_DICDI	Q54236 dictyosteli
35	40	49.4	258	2	Q4FM13_9RICK	Q4FM13 candidatu
36	40	49.4	305	2	Q4IPN7_GIBZE	Q4IPN7 gibberella
37	40	49.4	341	2	Q4W9K8_ASPFU	Q4W9K8 aspergillus
38	40	49.4	356	2	Q9VM59_DROME	Q9VM59 drosophila
39	40	49.4	374	2	Q61257_9BILA	Q61257 escarpia sp
40	40	49.4	374	2	Q25407_LAMSP	Q25407 lamellibrac
41	40	49.4	397	1	ATG5_NEUCR	ATG5 neuropeptide
42	40	49.4	441	2	Q6BMG4_DBBHA	Q6BMG4 debaryomyce
43	40	49.4	442	2	Q81BX8_BACCR	Q81BX8 bacillus ce
44	40	49.4	492	2	Q5MQD6_9INFA	Q5MQD6 influenza a
45	40	49.4	492	2	Q8B2W2_9INFA	Q8B2W2 influenza a

## ALIGNMENTS

RESULT 1	Q6FW7_CANGA	PRELIMINARY;	PRT;	558 AA.
ID	Q6FW7_CANGA			
AC	Q6FW7_			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Candida glabrata strain CBS138 chromosome M complete sequence.			
GN	OrderedContigsNames=CAGL0M03003g;			
OS	Candida glabrata (Yeast) (Torulopsis glabrata).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.			
OX	NCBI_TaxID=5478;			
RN	[1]			
RC	STRAIN=ATCC 2001 / CBS 138;			
RX	PubMed=15229592; DOI=10.1038/nature02579;			
RA	Dubon B., Sherman D., Fischer G., Durrens P., Casaregola S.,			
RA	Lafontaine I., de Montigny J., Marck C., Nevegilise C., Talla E.,			
RA	Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,			
RA	Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,			
RA	Boisrame A., Boyer D., Fathnad C., Ferry-Dumazet H., Groppi A.,			
RA	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,			
RA	Hantreux F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,			
RA	Kerret A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,			
RA	Nicoud J.-M., Nikoleki M., Oztas S., Ozler-Kalogeropoulos O.,			
RA	Pellenz S., Potier S., Richard G.-F., Straub M.-L., Sileau A.,			
RA	Swennen D., Tekata F., Wesolowski-Louvel M., Westhof E., Wirth B.,			
RA	Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,			
RA	Bouchier C., Caudron B., Scarpetti C., Galliard C., Weissbach J.,			
RA	Wincker P., Souciet J.-L.,			
RT	"Genome evolution in yeasts."			
RL	Nature 430:35-44(2004).			
EMBL	CR380959; CAG62453.1; -; Genomic DNA.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0005215; P:transporter activity; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR007114; MFS_1.			
DR	InterPro; IPR011701; MFS_1.			
DR	Pfam; PF07690; MFS_1; 1.			
DR	PROSITE; PS50850; MFS; 1.			
KW	Complete proteome.			
SO	SEQUENCE 558 AA; 61176 MW; 05760736C3F432D CRC64;			

Query Match 54.3%; Score 44; DB 2; Length 558;  
Best Local Similarity 57.1%; Pred. No. 58;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 RNDSP1QTDYTTTG 15  
||||| :|||  
Db 69 RNDSP1QTDYTTTG 82

RESULT 2

```
Q4SKB2.TETNG
ID Q4SKB2.TETNG PRELIMINARY; PRT; 340 AA.
AC Q4SKB2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome 13 SCAP14566, whole genome shotgun sequence.
GN ORFNames=GSTENG0016807001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxId=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ubin C., Castelli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Cattoi L., Poulin J., De Bernardis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouy J.,
RA Pella G., Lardier G., Chapple C., McKernan K.O., McEwan P., Bosak S.,
RA Kellis M., Volt J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope: Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014566; CAF98920.1; -; Genomic DNA.
SQ SEQUENCE 340 AA; 36745 MW; 1E282568C07674E5 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 340;
Best Local Similarity 53.3%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 RNDSPIDQDTTGG 15
Db 322 RLDPLSADONATTG 336

RESULT 3
OSHKOS.STAEQ PRELIMINARY; PRT; 511 AA.
AC OSHKOS;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE 5'-nucleotidase family protein.
GN OrderedLocustNames=SERP2288;
OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=176279;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1126/DB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uitterlbeck T.R., Lee C.,
RA Dmitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
```

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RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
DR EMBL; CP000029; AAW53170.1; -; Genomic DNA.
DR TIGR; SERP2288; -;
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0009166; P:nucleotide catabolism; IEA.
DR InterPro; IPR008334; 5'-Nucleotidase_C.
DR InterPro; IPR006146; 5'-Nucleotidase_N.
DR InterPro; IPR006179; 5'-Nucleotidase.
DR Pfam; PF02872; 5_nucleotid_C; 1.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR01607; APYRASEFAMLY.
DR PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
KM Complete proteome.
SQ SEQUENCE 511 AA; 57847 MW; F160793204D4149C CRC64;

Query Match 53.1%; Score 43; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSPIQTDQYTT 13
Db 444 NDAPIGSDQIYT 455

RESULT 4
OSCMU2.STAEP PRELIMINARY; PRT; 511 AA.
ID OSCMU2;
AC OSCMU2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 26, Last annotation update)
DE Lactococcal phosphatase-like protein.
GN OrderedLocustNames=SE2258;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1282;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 12228;
RX PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
DR EMBL; AEO16751; AAC05900.1; -; Genomic DNA.
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0009166; P:nucleotide catabolism; IEA.
DR InterPro; IPR008334; 5'-Nucleotidase_C.
DR InterPro; IPR006146; 5'-Nucleotidase_N.
DR InterPro; IPR006179; 5'-Nucleotidase.
DR Pfam; PF02872; 5_nucleotid_C; 1.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR01607; APYRASEFAMLY.
DR PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
KM Complete proteome.
SQ SEQUENCE 511 AA; 57798 MW; 47487BE2096ADEC6 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSPIQTDQYTT 13
Db 444 NDAPIGSDQIYT 455

RESULT 5
```

```

07RHP3 PLAYO
ID 07RHP3_PLAYO PRELIMINARY; PRT; 516 AA.
AC 07RHP3;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE GAF domain protein.
GN Name=PY03941;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiolini S.V., Suh B.B., Koel J.T.W., Pertia M.,
RA Silva J.C., Emolaeva M.D., Allen J.E., Senguttu J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.B., Riedmiller S.B., Feldlyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoatli A., Cummings L.M.,
RA Florens L., Yates J.R. II, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC EMBL; AABL01001174; EAA15729.1; -; Genomic_DNA.
DR GO; GO:0016829; F1yase activity; IEA.
KW Lyase.
SQ
SEQUENCE 516 AA; 62120 MW; 8CBA858FA3C373FC CRC64;

Query Match 53.1%; Score 43; DB 2; Length 516;
Best Local Similarity 54.5%; Pred. No. 80;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPQDTQY 11
Db 53 XNDSPVSTDRY 63

RESULT 6
DEB1 CAEEL
ID DEB1_CAEEL STANDARD; PRT; 664 AA.
AC Q19038;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Degenerin del-1.
GN Name=del-1; ORFNames=E02H4.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Bristol N2;
RX PubMed=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
CC -1- FUNCTION: Probable sodium channel subunit.

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CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the amiloride-sensitive sodium channel
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U76403; AAB39735.1; -; mRNA.
DR EMBL; Z68003; CA91975.1; -; Genomic_DNA.
DR PIR; T20420; T20420.
DR Ensemble; E02H4.1; Caenorhabditis elegans.
DR Wormbase; WBGen0000952; del-1.
DR WormPep; E02H4.1; CE05547.
DR InterPro; IPR004726; Deg-1.
DR InterPro; IPR01873; Na+channel_ASC.
DR PANTHER; PTHR11690; Na+channel_ASC; 1.
DR Pfam; PF00858; ASC; 1.
DR PRINTS; PR01078; AMINACHANNEL.
DR TIGRFAMs; TIGR00867; deg-1; 1.
DR PROSITE; PS01206; ASC; 1.
KW Complete proteome; Glycoprotein; Ion transport; Ionic channel; Sodium;
KW Sodium channel; Sodium transport; Transmembrane; Transport.
FT TOPO_DOM 1 67
FT TRANSMEM 68 88
FT TOPO_DOM 89 607
FT TRANSMEM 608 628
FT TOPO_DOM 629 664
FT CARBOHYD 241 241
FT CARBOHYD 300 300
FT CARBOHYD 394 394
FT CARBOHYD 508 508
FT CARBOHYD 562 562
SQ
SEQUENCE 664 AA; 75474 MW; 0D19C8EF79688F8D CRC64;

Query Match 53.1%; Score 43; DB 1; Length 664;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIGTDQYTTT 14
Db 536 PQQDQYTTT 545

RESULT 7
Q819P8_9BIVA
ID Q819P8_9BIVA PRELIMINARY; PRT; 699 AA.
AC Q819P8;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN Name=Amy;
OS Corbicula fluminea.
OC Corbiculata; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Corbiculidae; Corbiculidae; Corbicula.
OX NCBI_TaxID=45949;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Da Lage J.-L., Van Wormhoudt A., Cariou M.-L.;
RT "Diversity and evolution of the alpha-amylase genes in Animals.";
RL Biologia 57:181-189(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14704857; DOI=10.1007/s00018-003-3334-Y;
RA Da Lage J.-L., Feller G., Janecsek S.;
RT "Horizontal gene transfer from Eukarya to bacteria and domain
RT shuffling: the alpha-amylase model.";
RL Cell. Mol. Life Sci. 61:97-109(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.

```

RA Da Lage J.-L.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF468016; AA017927.2; -; Genomic\_DNA.  
DR HSSP; P04745; 1SMD.  
DR GO; GO:0004556; F:alpha-amylase activity; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0005975; F:carbohydrate metabolism; IEA.  
DR InterPro; IPR006048; Alpha-amyl\_C.  
DR InterPro; IPR006047; Alpha-amyl\_cat.  
DR InterPro; IPR006046; Alp\_amyl\_cat\_sub.  
DR Pfam; PF00128; Alpha-amylase; 1.  
DR Pfam; PF02806; Alpha-amylase\_C; 1.  
DR PRINTS; PR00110; ALPHAMYLASE.  
DR SMART; SM00642; Amy; 1.  
DR SMART; SM00632; Amy; 1.  
SQ SEQUENCE 699 AA; 76544 MW; 25D57008165B04CB CRC64;

Query Match 53.1%; Score 43; DB 2; Length 699;  
Best Local Similarity 46.7%; Pred. No. 1.1e+02;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NDSPIQTDQYTTTG 15  
Db 241 QSNPPIKTSQYTSIG 255

## RESULT 8

QAN289\_THEPA PRELIMINARY; PRT; 809 AA.  
AC QAN289;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=rp04\_0468;

OS Theileria parva.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.

OX NCBI\_Taxid=5675;

RN [1]

NUCLEOTIDE SEQUENCE.

RC STRAIN=Muguga;

RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,

RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weisman J.,

RA Jiang L., Lynn J., Weaver B., Shoab A., Wasawo D., Crabtree J.,

RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,

RA Silva J.C., Uterback T.R., Feldblyum T.V., Perlea M., Allen J.,

RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,

RA Venter J.C., Fraser C.M., Nene V.;

RT "genome sequence of Theileria parva, a bovine pathogen that transforms

RT lymphocytes.";

RL Science 309:134-137(2005).

RN [2]

NUCLEOTIDE SEQUENCE.

RC STRAIN=Muguga;

RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,

RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,

RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiao L.,

RA Lynn J., Weaver B., Shoab A., Wasawo D., Crabtree J., Wortman J.R.,

RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,

RA Uterback T., Feldblyum T., Perlea M., Allen J., Taracha E.L.,

RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,

RA Fraser C.M., Nene V.;

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

CC -; CUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AAGK0100004; EAN31820.1; -; Genomic\_DNA.

KM Hypothetical protein.

SQ SEQUENCE 809 AA; 92620 MW; 58FA8368C3613471 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 809;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTTG 15  
Db 526 NNSPTNSNSETTTG 539

## RESULT 9

Q4UFT9\_THEAN PRELIMINARY; PRT; 5261 AA.  
AC Q4UFT9;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Sfil-subtelomeric related protein family member, putative.

GN ORFNames=TA16050;

OS Theileria annulata.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.

OX NCBI\_Taxid=5874;

RN [1]

NUCLEOTIDE SEQUENCE.

RC STRAIN=Ankara isolate clone C9;

RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,

RA Hall N., Barrell B.G.;

RT "The chromosome 2 sequence of Theileria annulata.";

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR940348; CA174027.1; -; Genomic\_DNA.

DR InterPro; IPR007480; DUF529.

DR Pfam; PF04385; PAINT; 54.

KM Nucleotide-binding.

SQ SEQUENCE 5261 AA; 603934 MW; 79941BB6659B78E CRC64;

Query Match 53.1%; Score 43; DB 2; Length 5261;  
Best Local Similarity 53.8%; Pred. No. 1.2e+03;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPIQTDQYTTT 14  
Db 4887 NDNPLTNDYTTT 4899

## RESULT 10

Q6MK1\_NEUCR PRELIMINARY; PRT; 273 AA.  
AC Q6MK1;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Hypothetical protein B8J22.210.

GN Name=B8J22.210;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI\_Taxid=5141;

RN [1]

NUCLEOTIDE SEQUENCE.

RP Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,

RA Mykatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

NUCLEOTIDE SEQUENCE.

RA German Neurospora genome project;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX842627; CA576297.1; -; Genomic\_DNA.

KM Hypothetical protein.

SQ SEQUENCE 273 AA; 29666 MW; 86F5D77647F13873 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 273;  
Best Local Similarity 57.1%; Pred. No. 59;



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Matches      8; Conservative      1; Mismatches      5; Indels      0; Gaps      0;
Qy           2 NDSP1QTDQYTTG 15
           |||:|:|:|
Db          151 NTDH1HDSYTSYG 164

RESULT 11
Q88D16_PSEPK PRELIMINARY; PRT; 455 AA.
AC Q88D16_1998 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Membrane protein, putative.
GN OrderedLocustName=PP4839;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Bauman M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Meazzer A., Utechtack T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Weidner H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tummeler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016792; AAN70408.1; -; Genomic_DNA.
DR TIGR; PP4839; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008237; F:metalloproteinase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:protein catabolism and peptidolysis; IEA.
DR InterPro; IPR005075; Peptid_1.
DR Pfam; PF03413; Pept_2.
DR Pfam; PF03923; Pept_1.
DR Complete proteome.
KW SEQUENCE 455 AA; 50581 MW; 9DDC64470ED713A5 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 455;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy           1 RNDSP1QTDQYTTG 12
           |||:|:|:|
Db          325 RNDATLHVDTY 336

RESULT 12
Q45133_CABEL PRELIMINARY; PRT; 516 AA.
AC Q45133_1998 (TREMBlrel. 06, Created)
DT 01-JUN-2003 (TREMBlrel. 23, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein COSD2.6.
GN ORFNames=COSD2.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

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RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; AF047651; AAK67208.2; -; Genomic_DNA.
DR Ensembl; COSD2.6; Caenorhabditis elegans.
DR WormBase; WBGene00015468; COSD2.6.
DR WormPep; COSD2.6; CB32115.
DR InterPro; IPR006578; MADP.
DR PROSITE; PS51029; MADP.1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 516 AA; 58256 MW; 95968B5A0855743 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 516;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy           1 RNDSP1QTDQYTTG 12
           |||:|:|:|
Db          41 REDPVKTQY 52

RESULT 13
Q24781_BACSP PRELIMINARY; PRT; 700 AA.
AC Q24781_1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Alpha-amylase precursor.
GN Name=baa;
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NO.195;
RX MEDLINE=20407125; PubMed=10947962; DOI=10.1042/0264-6021.3500477;
RA Sumitani J., Tottori T., Kawaguchi T., Arai M.;
RT "New type of starch-binding domain: the direct repeat motif in the C-
RT terminal region of Bacillus sp. no. 195 alpha-amylase contributes to
RT starch binding and raw starch degrading.";
RL Biochem. J. 350:477-484 (2000).
DR EMBL; AB006823; BAA22082.1; -; Genomic_DNA.
DR HSSP; P29957; 1B01.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; Alp_1.
DR InterPro; IPR006048; Alp_1_cat.
DR InterPro; IPR006047; Alp_1_cat.
DR InterPro; IPR005085; CBM_25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase_1.
DR Pfam; PF02806; Alpha-amylase_C_1.
DR Pfam; PF03423; CBM_25; 2.
DR PRINTS; PR00110; ALPHAMYLAASE.
DR SMART; SM00642; Amyy; 1.
DR SMART; SM00632; Amyy; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 700 AA; 73569 MW; 1A6F3B9218F88AC0 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 700;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy           1 RNDSP1QTDQYTTG 15
           |||:|:|:|
Db          256 RANEP1QPEBYTSNG 270

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RESULT 14  
ID 08W105 ARATH PRELIMINARY; PRT; 1049 AA.  
AC 08W105\_1  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE A1G50840/FBA12.8 (Poli-like A DNA polymerase) (Putative DNA  
DE polymerase A family protein).  
GN Name=A1G50840;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,  
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ichida T., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15993837; DOI=10.1016/j.brc.2005.06.052;  
RA Mori Y., Kimura S., Saitome A., Kasei N., Sakaguchi N., Uchiyama Y.,  
RA Ishibashi T., Yamamoto T., Chiku H., Sakaguchi K.;  
RT "Plastic DNA polymerases from higher plants, Arabidopsis thaliana.";  
RL Biochem. Biophys. Res. Commun. 334:43-50(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,  
RA Tang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,  
RA Deng C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ichida T., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,  
RA Davis R.W., Ecker J.R., Theologis A.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: A1G50840; AL58915.1; -; mRNA.  
DR EMBL: AY091072; BA010873.1; -; mRNA.  
DR HSSP: P19821; IKTQ.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0008408; F:3'-5' exonuclease activity; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR GO: GO:0003887; F:DNA-directed DNA polymerase activity; IEA.  
DR GO: GO:0006260; P:DNA replication; IEA.  
DR InterPro: IPR002562; 3\_5\_exonuclease.  
DR InterPro: IPR001098; DNA\_pol.  
DR InterPro: IPR002298; DNA\_pol.  
DR InterPro: IPR012337; RNaseH fold.  
DR Pfam: PF004612; 3\_5\_exonuc; I.  
DR Pfam: PF00476; DNA\_pol\_A; 1.  
DR PRINTS: PR00868; DNAPOL.  
DR SMART: SM00474; 35XOC; 1.  
DR SMART: SM00482; POLAC; 1.  
SQ SEQUENCE 1049 AA; 117147 MW; 5D48466D69798DA1 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 1049;  
Best Local Similarity 42.9%; Pred. No. 2.8e+02;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPIOTDQYTTTG 15  
Db 625 SDSPLSTENTTAGS 638

RESULT 15  
ID 052G34 MAGGR PRELIMINARY; PRT; 1056 AA.  
AC 052G34\_1  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
DE ORFNames=MG01452.4;  
GN Magnaporthe oryzae 70-15.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.  
OX NCBI\_TaxID=242507;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
RA Alt-Zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
RA Arachchi H., Armbruster J., Bachantlang P., Baldwin J., Barry A.,  
RA Bayul T., Blitsheseyn B., Bloom T., Bye J., Boguslavsky L.,  
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,  
RA Calvo S., Camarata J., Campo K., Chang J., Cheshtang Y., Citroen M.,  
RA Collymore A., Considine T., Cook A., Cooke P., Cornu B., Cuomo C.,  
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Filzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierre S.,  
RA Ghitke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,  
RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,  
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
RA Landrad-toh K., Liu X., Lokytsang T., Lokytsang Y., Lucien O.,  
RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,  
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
RA McCarthy M., McDonough S., Mcghee T., Melrim J., Menes L.,  
RA Mesirov J., Mihalovich A., Mihova T., Mikkelson T., Mlenga V., Moru K.,  
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'Donnell P., Okawa O., O'Leary S., Omotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Ramau R., Ray V., Raymond C.,  
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schuppach R., Seaman C., Settillali S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,  
RA Spencer B., Stalker J., Strange-Thomann N., Stavropoulos S.,  
RA Stetson K., Stone C., Stone S., Stubbs M., Talans J., Tchinga P.,  
RA Tenzing P., Teafaye S., Theodore J., Thoultsang Y., Topham K.,  
RA Towey S., Teamia T., Tsomo N., Vallee D., Vassiliev H.,  
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,  
RA Zimmer A., Zody M., Lander E.;  
RL "The genome sequence of Magnaporthe oryzae.";  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Zhu H., Blackmon B.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: AUC0100053; EA55801.1; -; Genomic\_DNA.  
KM Hypothetical protein.  
SQ SEQUENCE 1056 AA; 116594 MW; 57BF6982798C69 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 1056;  
Best Local Similarity 52.9%; Pred. No. 2.8e+02;  
Matches 9; Conservative 3; Mismatches 3; Indels 2; Gaps 1;  
QY 1 RNDSPICQTDQ--YTTTG 15  
:|:|:|:|:|:  
Db 124 KNDVPVQTFDADIQSTTG 140

Search completed: December 12, 2005, 20:41:02  
Job time : 84.4655 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:43:06 ; Search time 112.667 Seconds  
(without alignments)  
58.497 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNSDPVREOQATTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	8	ADR10602 Cat IGE e
2	48	56.5	15	8	ADR10601 Dog IGE e
3	39	45.9	15	8	ADR10607 Pig IGE e
4	37	43.5	15	8	ADR10603 Horse IGE
5	35	41.2	15	7	ADCG4568 Horse Imm
6	32	37.6	11	5	AAU79709 Synthetic
7	30	35.3	10	3	AAAB38098 Human ABC
8	29	34.1	6	4	AAAB5476 Human elia
9	29	34.1	15	2	AAAB55733 dsDNA-dep
10	29	34.1	15	8	ADR97089 Cysteine
11	28.5	33.5	12	2	AAW56548 Toxin fra
12	28	32.9	9	2	AAW76034 LM609 gra
13	28	32.9	9	4	AAAB61392 Mutant VL
14	28	32.9	9	6	ABAB19830 Enhanced
15	28	32.9	9	6	ABAB62303 Surface s
16	28	32.9	9	7	ADG71862 Enhanced
17	28	32.9	9	8	ADJ58043 Murine IM
18	28	32.9	9	8	ADJ73181 CDR3 of t
19	28	32.9	10	5	ABG98755 F protein
20	28	32.9	13	2	AAAR79898 Fusion pr
21	28	32.9	15	7	ADAB62941 Human 98P
22	28	32.9	15	7	ADAB63829 Human 98P
23	27	31.8	8	2	AAW59312 Non-Polio
24	27	31.8	9	3	AAAB10015 H. pylori

25	27	31.8	9	4	AAAB6095 H. pylori
26	27	31.8	9	4	AAAB6063 H. pylori
27	27	31.8	9	5	ABAB9231 CD45RO/RB
28	27	31.8	9	5	AAU72845 Anti-NG2
29	27	31.8	9	5	AAU72853 Anti-NG2
30	27	31.8	9	9	ADY80269 CDR3 from
31	27	31.8	10	5	ABG98754 F protein
32	27	31.8	13	2	AAAB63411 Peptide f
33	27	31.8	13	4	AAAB9483 Hepatitis
34	27	31.8	14	4	AAAB97114 Human pep
35	27	31.8	14	8	ADT40356 hSARS vlr
36	27	31.8	14	8	ADT379773 SARS vlr
37	27	31.8	14	8	ADT37886 hSARS vlr
38	26	30.6	8	2	AAV04462 Active mi
39	26	30.6	9	6	ABP74676 Human SCP
40	26	30.6	9	6	AAAB38100 Human COU
41	26	30.6	9	7	ADCG09535 Epitope w
42	26	30.6	9	8	ADN28303 Human CD3
43	26	30.6	10	2	AAV04464 Active mi
44	26	30.6	10	2	AAV04463 Active mi
45	26	30.6	10	3	AAV51451 AAV VP3 d

ALIGNMENTS

RESULT 1  
ADR10602 standard; peptide, 15 AA.  
ID ADR10602  
AC ADR10602;  
XX  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.  
XX  
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW cat.  
XX  
OS Felis catus.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
XX (UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hammerberg B;  
XX  
XX WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian IGE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC cat IGE 5.91 recognition site.

XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQOATW 15  
 |||||  
 Db 1 HNDSPVTEQOATW 15

RESULT 2

ID ADR10601 standard; peptide; 15 AA.

XX ADR10601;

DT 21-OCT-2004 (first entry)

DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

PN WO2004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.

XX Sequence 15 AA;

Query Match 56.5%; Score 48; DB 8; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 0.23;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPPVTEQOATT 14  
 |||||  
 Db 2 NDSPPVTEQOATT 14

RESULT 3

ID ADR10607 standard; peptide; 15 AA.

XX ADR10607;

DT 21-OCT-2004 (first entry)

DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

XX pig.

PN WO2004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC pig IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 45.3%; Score 39; DB 8; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 9.5;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPPVTEQOATT 14  
 |||||  
 Db 2 NDAVQADRHSTT 14

RESULT 4

ID ADR10603 standard; peptide; 15 AA.

```

XX AC ADR10603;
XX XX
XX DT 21-OCT-2004 (first entry)
XX XX
XX DE Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.
XX XX
XX KM Antiaesthetic; Antiallergic; Immunosuppressive; IGF; dog; asthma;
XX XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX KM horse.
XX OS Equus caballus.
XX PN MO2004065936-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX PS (UYN(-) UNIV NORTH CAROLINA STATE.
XX PA Hammerberg B;
XX PI WPI; 2004-593545/57.
XX DR WPI; 2004-593545/57.
XX XX
XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful
XX PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX PT or treating asthma or anaphylactic shock.
XX PS
XX PS Example 6; Page 9; 14pp; English.
XX CC The present invention relates to a novel monoclonal antibody (I) that
XX CC specifically binds to a mammalian IGE epitope, where the epitope is
XX CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX CC (I) is useful for testing an allergen reactivity of an IGE sample. The
XX CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX CC and corn allergens. The sample is a biological sample collected from a
XX CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX CC antibodies recognise epitopes on canine IGE corresponding to amino acid
XX CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
XX CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX CC of IGE from cat and horse, but did not exhibit cross-reactivity with
XX CC either pig or human epsilon-chains of IGE. The present sequence is the
XX CC horse IGE 5.91 recognition site.
XX CC
XX SQ Sequence 15 AA;
XX
XX Query Match 43.5%; Score 37; DB 8; Length 15;
XX Best Local Similarity 53.8%; Pred. No. 22;
XX Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 NDSPTRTQOQATT 14
XX : : : : :
XX Db 2 NNVLITQDOQATT 14
XX
XX
XX RESULT 5
XX ADR64568
XX ID ADR64568 standard; peptide; 15 AA.
XX AC ADR64568;
XX XX
XX DT 18-DEC-2003 (first entry)
XX XX
XX DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.
XX XX
XX KM Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX KW

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```

OS OS Equus caballus.
XX XX
XX PN US2003087314-A1.
XX XX
XX PD 08-MAY-2003.
XX PF 08-NOV-2001; 2001US-00052788.
XX PR 08-NOV-2001; 2001US-00052788.
XX PS (REGC ) UNIV CALIFORNIA.
XX PA Gershwin LJ, Pettigrew HD, Kalina WV;
XX PI WPI; 2003-765437/72.
XX DR WPI; 2003-765437/72.
XX XX
XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
XX PT polypeptide that induces production of antibodies which specifically bind
XX PT to equine immunoglobulin E.
XX PS
XX PS Example 1; Page 8; 14pp; English.
XX CC The invention relates to an immunogenic composition comprising an
XX CC isolated polypeptide having an amino acid sequence that is at least 80%
XX CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
XX CC equine immunoglobulin E (the composition induces production of an
XX CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
XX CC polypeptides are not explicitly identified in the specification. Also
XX CC included are a composition comprising an antibody that specifically binds
XX CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
XX CC specifically binds to equine IGE made by the process of immunising an
XX CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
XX CC antibody that specifically binds to equine IGE (involving immunising an
XX CC animal with a composition further comprising an isolated polypeptide (the
XX CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-
XX CC (S6)), and collecting antiserum from the animal) and a kit for detection
XX CC of equine IGE in a biological sample comprising the antibody and means
XX CC for detecting specific binding of the antibody to equine IGE. The
XX CC antibody is useful for detecting equine IGE protein in a biological
XX CC sample (serum) which involves contacting the sample with the antibody,
XX CC thus forming an antigen/antibody complex, and detecting the presence or
XX CC absence of the antigen/antibody complex. The antibody and antigen are
XX CC immobilised on a solid surface. The antibody is labelled such that the
XX CC complex can be detected. The complex is detected using a second labelled
XX CC antibody. The peptides are useful for generating antibodies specific for
XX CC IGE which can serve as a diagnostic test for allergy. The present
XX CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
XX CC peptide from the early portion of the C4 region.
XX CC
XX SQ Sequence 15 AA;
XX
XX Query Match 41.2%; Score 35; DB 7; Length 15;
XX Best Local Similarity 66.7%; Pred. No. 49;
XX Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 VRTQOQATT 14
XX : : : : :
XX Db 1 IOTDQOQATT 9
XX
XX
XX RESULT 6
XX AAU79709
XX ID AAU79709 standard; peptide; 11 AA.
XX AC AAU79709;
XX XX
XX DT 15-JUL-2002 (first entry)
XX XX
XX DE Synthetic peptide CPP-2 used in invention of DRL90.
XX XX
XX KM Human; tissue-specific secretory polypeptide; DRL90; infection; cancer;
XX KW immune disease; digestive disease; circulatory disease;
XX endocrine disease; infertility; cytostatic; immunomodulator;

```

KW antimicrobial; vasotropic; antifertility; hormonal; CPP-2.  
 XX Synthetic.  
 XX WO200224908-A1.  
 XX  
 PD 28-MAR-2002.  
 XX  
 XX 21-SEP-2001; 2001WO-JP008223.  
 PF  
 XX 22-SEP-2000; 2000JP-00293985.  
 PR 29-SEP-2000; 2000JP-00302839.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Ito Y, Tanaka H, Nishimura A, Ogi K;  
 XX  
 DR WPI; 2002-330018/36.  
 XX  
 PT New tissue-specific secretory polypeptides applicable in diagnosis of and  
 PT remedies for cancer, immune diseases, infection, digestive diseases,  
 PT circulatory diseases, endocrine diseases and infertility.  
 XX  
 PS Example 8; Page 80; 11pp; Japanese.  
 XX  
 CC The present invention relates to the isolation of a novel tissue-specific  
 CC secretory polypeptide, DRJ90, and the polynucleotide sequence encoding  
 CC it. The DRJ90 polypeptide and encoding DNA are useful for diagnosing and  
 CC treating cancer, immune diseases, infection, digestive diseases,  
 CC circulatory diseases, endocrine diseases and infertility. The present  
 CC sequence for synthetic peptide CPP-2 is used in the examples of the  
 CC present invention  
 CC  
 XX Sequence 11 AA;  
 SQ  
 Query Match 37.6%; Score 32; DB 5; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 SPVRECOA 12  
 ||: ||: ||  
 2 SPITKQA 10  
 DB  
 RESULT 7  
 AAB38098  
 ID AAB38098 standard; peptide; 10 AA.  
 XX  
 AC AAB38098;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 FHA-3 mutant exon 41-encoded peptide fragment, SEQ ID NO:65.  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; T; familial HDL deficiency; FHA; polymorphism;  
 KW cerebrovascular disease; coronary artery disease; coronary restenosis;  
 KW Alzheimer's disease; peripheral vascular disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055318-A2.  
 OS  
 PD 21-SEP-2000.  
 PF  
 XX 15-MAR-2000; 2000WO-IB000532.  
 XX  
 PR 15-MAR-1999; 99US-0124702P.  
 PR 08-JUN-1999; 99US-0138048P.

PR 17-JUN-1999; 99US-0139600P.  
 PR 01-SEP-1999; 99US-0151977P.  
 XX  
 XX (VYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENON-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Wilson AR, Pimstone SN;  
 XX  
 XX WPI; 2000-587528/55.  
 DR N-PSDB; AAC69168.  
 XX  
 PT New ABC1 polypeptide is useful for treating diseases associated with ABC1  
 PT biological activity, e.g. Alzheimer's disease, Huntington's disease and  
 PT cancer.  
 XX  
 XX Example; Fig 6E; 229p; English.  
 XX  
 CC The invention relates to the human ABC1 cholesterol transporter protein  
 CC (B38082) and to nucleic acid sequences (CG9120) which encode it. ABC1 is  
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
 CC proteins, and plays a crucial role in cholesterol transport, particularly  
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 CC located on chromosome 9q31, and mutations in this gene are associated  
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 CC are distinguishable in that TD is an autosomal recessive disorder, while  
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 CC cholesterol") in the blood correlate with a high risk of cardiovascular  
 CC disease, particularly coronary artery disease, but also cerebrovascular  
 CC disease, coronary restenosis, and peripheral vascular disease.  
 CC Conversely, a high level of HDL has protective effects against  
 CC cardiovascular disease. The invention provides genetic constructs and  
 CC transgenic cells and non-human animals comprising human ABC1 nucleic  
 CC acids, and methods of gene therapy for the treatment or prevention of  
 CC cardiovascular disease comprising the administration of an expression  
 CC vector encoding ABC1 or an active fragment thereof. The invention also  
 CC encompasses compounds which mimic ABC1 activity, compounds which  
 CC stimulate ABC1 expression and methods of screening for such compounds. It  
 CC further relates to methods for determining whether a patient has an  
 CC increased risk for cardiovascular disease due to polymorphisms in the  
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or  
 CC prevent cardiovascular disease, especially coronary artery disease,  
 CC cerebrovascular disease, coronary restenosis or peripheral vascular  
 CC disease. They may also be used in the treatment of diseases associated  
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as GenBank Accession No: A012376.1. The  
 CC present sequence represents a human ABC1 cholesterol transporter peptide  
 CC fragment used in the exemplifications of the invention  
 CC  
 XX Sequence 10 AA;  
 SQ  
 Query Match 35.3%; Score 30; DB 3; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 NDSVRECO 11  
 ||: ||: ||  
 1 NDSVRRERQ 10  
 DB  
 RESULT 8  
 AAB55476  
 ID AAB55476 standard; peptide; 6 AA.  
 XX  
 AC AAB55476;  
 XX  
 DT 07-MAR-2001 (first entry)  
 XX  
 DE Human elastase variant segment peptide SEQ ID NO:46.



XX Human; elastase; variant; substrate; mutant; mutagenesis; histidine;  
 KM human neutrophil elastase; H43A; cytosolic; proteolysis; ADEPT;  
 KW antibody-directed enzyme activated prodrgng therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20068363-A2.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PF 04-MAY-2000; 2000WO-US006692.  
 XX  
 PR 05-MAY-1999; 99US-0132640P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Carter PJ, Dall'acqua W, Rodrigues M;  
 XX  
 DR WPI; 2001-007389/01.  
 XX  
 PT Elastase variant (H43A) having altered substrate specificity useful for  
 PT antibody-directed enzyme activated prodrgng therapy.  
 XX  
 PS Example 4; Fig 3; 79pp; English.  
 XX  
 CC The present invention describes a purified elastase variant (I) with an  
 CC amino acid sequence different from that of a precursor elastase, the  
 CC difference comprising a substitution of an active site histidine residue  
 CC corresponding to residue 43 in human neutrophil elastase with a different  
 CC amino acid residue so that (I) has substrate specificity substantially  
 CC different from the precursor elastase. (I) has cytosolic activity, and  
 CC can be used in antibody-directed enzyme activated prodrgng therapy. The  
 CC elastase variant can be used to cleave a particular substrate, especially  
 CC those containing histidine residues at the substrate site. Site-specific  
 CC proteolysis is useful in therapeutic applications, e.g. for antibody-  
 CC directed enzyme activated prodrgng therapy (ADEPT). AAC8022, AAC8023 and  
 CC AAB55432 to AAB55526 represent sequences used in the exemplification of  
 CC the present invention  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 34.1%; Score 29; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. NO. 2e+06; 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 QOATTW 15  
 Db 1 QOHTTW 6  
 RESULT 9  
 AAR55733  
 ID AAR55733 standard; peptide; 15 AA.  
 XX  
 AC AAR55733;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 16-NOV-1994 (first entry)  
 DE dedNA-dependent kinase inhibitor.  
 XX  
 KW dedNA-dependent kinase inhibitor; fatty acyl-peptide; conjugate;  
 KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DNA;  
 KW eicosapentaenoic acid; EPA; antitumor.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9412530-A1.  
 XX  
 PD 09-JUN-1994.  
 XX  
 PF 29-NOV-1993; 93WO-HU000065.

XX  
 PR 30-NOV-1992; 92US-00984293.  
 XX  
 PA (BIOS-) BIOSIGNAL KUTATO PEPTIDESZNO KFT.  
 PA (SYNT-) SYNTHETIC PEPTIDES INC.  
 XX  
 PI Keri G, Hodges RS, Cachia PJ, Szederkenyi F, Horvath A, Balogh A;  
 PI Vadasz Z;  
 XX  
 DR WPI; 1994-200194/24.  
 XX  
 PT New fatty acyl-peptide conjugates for inhibiting cell proliferation -  
 PT more active than free peptide, partic. for treating tumours, virus-  
 PT infected cells, psoriasis, etc.  
 XX  
 PS Disclosure; Fig 1; 45pp; English.  
 XX  
 CC The peptides given in AAR55718-48 can each be conjugated through an amide  
 CC linkage with a polyunsaturated fatty acid moiety, such as docosahexaenoic  
 CC acid or eicosapentaenoic acid, to improve antiproliferative activity. The  
 CC dedNA-dependent kinase inhibitor given in AAR55733 competes with native  
 CC kinases associated with neoplastic cell proliferation or transformation,  
 CC psoriasis, etc. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 15 AA;  
 Query Match 34.1%; Score 29; DB 2; Length 15;  
 Best Local Similarity 40.0%; Pred. NO. 5.8e+02; 2; Indels 0; Gaps 0;  
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HNDSPVRETO 10  
 Db 6 YNDNPMEEEE 15  
 RESULT 10  
 ADR97089  
 ID ADR97089 standard; peptide; 15 AA.  
 XX  
 AC ADR97089;  
 XX  
 DT 02-DEC-2004 (first entry)  
 DE Cysteine protease inhibitory protein fragment #2.  
 XX  
 KW antinflammatory; vasotropic; immunostimulator;  
 KW cysteine protease inhibitory protein; diagnosis; Behcet's disease;  
 KW Harada's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004078975-A1.  
 XX  
 PD 16-SEP-2004.  
 XX  
 PF 05-MAR-2004; 2004WO-JP002902.  
 XX  
 PR 05-MAR-2003; 2003JP-00059082.  
 XX  
 PA (SENP ) SENJU PHARM CO LTD.  
 XX  
 PI Katunuma N, Shiota H;  
 PI WPI; 2004-668624/65.  
 DR Novel cysteine protease inhibitory protein, useful as diagnostic marker  
 PT for diagnosing Behcet's disease and Harada's disease.  
 XX  
 PS Disclosure; SEQ ID NO 4; 64pp; Japanese.  
 XX  
 CC A cysteine protease inhibitory protein (I) having the amino acid sequence  
 CC ADR97086 at its N-terminal and exhibiting the molecular weight of 31 kDa,  
 CC is new. (I) is useful for screening a compound or its salt having

CC activity of promoting or inhibiting the function of (I). (I) enables  
CC diagnosis, prevention or treatment of Behcet's disease or Harada's  
CC disease. This sequence is a fragment of the cysteine protease inhibitory  
CC protein.

XX Sequence 15 AA;

Query Match 34.1%; Score 29; DB 8; Length 15;  
Best Local Similarity 38.5%; Pred. No. 5.8e+02;  
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
Dy 3 DSPVTEQOATW 15  
Db 3 DPAHPPEQPLW 15

# RESULT 11

AAW56548  
ID AAW56548 standard; peptide; 12 AA.

XX AAW56548;

XX 07-AUG-1998 (first entry)

DE Toxin fragment of Tcac of the bacterium Photorhabdus luminescens.

XX Photorhabdus luminescens W-14; nematode; symbiotic; Heterorhabditis; tca;  
XX tcb; tcc; tcd; insecticidal activity; toxin; Lepidoptera; Coleoptera;  
XX Hymenoptera; Diptera; Dictyoptera; Acarina; Homoptera; Southern;  
XX Western corn rootworm; Colorado potato beetle; mealworm; boll weevil;  
XX turf grub; beetle armyworm; black cutworm; cabbage looper; codling moth;  
XX corn earworm; European corn borer; Tobacco hornworm; budworm.

XX Photorhabdus luminescens.

XX WO9808932-A1.

XX 05-MAR-1998.

XX 05-MAY-1997; 97WO-US007657.

XX 28-AUG-1996; 96US-00705484.

XX 06-NOV-1996; 96US-00743699.

XX 06-NOV-1996; 96WO-US018003.

XX (DOWC ) DOWELANCO.

XX (WISC ) WISCONSIN ALUMNI RES FOUND.

XX Ensign UC, Bowen DJ, Petrell J, Fatig R, Schoonover S;  
XX Firench-Constant RH, Rochelleau TA, Blackburn MB, Hey TD, Merlo DJ;  
XX Orr GL, Roberts JR, Strickland JA, Guo L, Cliche TA, Sukhapinda K;  
XX WPI; 1998-179427/16.

PT Isolated toxins from Photorhabdus luminescens strains - useful for  
PT control of insect pests.

XX Claim 30; Page 151; 321pp; English.

XX The present sequence represents a fragment of the toxic protein Tcac  
XX (encoded by gene tcaC) of the bacterium Photorhabdus luminescens (W-14).  
XX This is a symbiotic bacterium of the nematodes of the Heterorhabditis  
XX genus. The bacterium has at least 4 distinct genomic regions, tca, tcb,  
XX tcb, and tcd. Peptide products are produced from these regions that are  
XX associated with insecticidal activity. The native toxins are secreted  
XX proteins. The proteins are toxic to insects upon exposure and especially  
XX when ingested. The nucleic acid sequence can be used to produce  
XX transgenic plants, baculoviruses or microbial hosts for toxin production.  
XX They can be used to control insects pests from the Lepidoptera.  
XX Coleoptera, Hymenoptera, Diptera, Dictyoptera, Acarina or Homoptera  
XX orders, especially the Southern or Western corn rootworm, Colorado potato  
XX beetle, mealworm, boll weevil, turf grub, beetle armyworm, black cutworm,  
XX cabbage looper, codling moth, corn earworm, European corn borer or

CC tobacco hornworm or budworm  
XX Sequence 12 AA;

Query Match 33.5%; Score 28.5; DB 2; Length 12;  
Best Local Similarity 53.8%; Pred. No. 5.5e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;  
Dy 3 DSPVTEQOATW 15  
Db 3 DSP---EVSITW 12

# RESULT 12

AAW76034  
ID AAW76034 standard; protein; 9 AA.

XX AAW76034;

XX 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDR3 protein fragment #3.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;  
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;  
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;  
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;  
XX macular degeneration; osteoporosis; primer; V-L region; CDR;  
XX complementarity determining region.

XX Mus sp.

XX WO9833919-A2.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US001826.

XX 30-JAN-1997; 97US-00791391.

XX (IXSY-) IXSYS INC.

XX Huse WD, Glaser SM;

XX WPI; 1998-437472/37.

XX N-PSDB; AAV49871.

PT Humanised antibody, vitaxin, that binds selectively to alphabeta3  
PT integrin - and related grafted antibodies based on murine monoclonal  
PT LM609, also related nucleic acid, used to treat, prevent or diagnose  
PT angiogenesis or restenosis.

XX Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody  
XX LM609 heavy and light chain variable region. LM609 and the antibody  
XX vitaxin bind selectively to integrin alphabeta3 and can be used to  
XX inhibit binding of alphabeta3 to a ligand and thus block integrin-  
XX mediated signal transduction. This is useful in the treatment, prevention  
XX and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis  
XX and restenosis (but also e.g. (non-)immune inflammation, diabetic  
XX retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid  
XX arthritis, macular degeneration, osteoporosis etc.). The antibodies  
XX contain non-murine framework regions so are suitable for use in humans.  
XX Enhanced types of LM609 have affinity more than 90 times greater than  
XX that of parent the parent antibody

XX Sequence 9 AA;

Query Match 32.9%; Score 28; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 QOATW 15  
 DB 1 QOSTW 6  
 RESULT 13  
 AAB61392  
 ID AAB61392 standard; peptide; 9 AA.  
 XX  
 AC AAB61392;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Mutant VL CDR3 peptide #2.  
 XX  
 KW LM609; grafted antibody; alphavbeta.3 integrin; angiogenesis;  
 KW inflammatory; cancer; retina; restenosis; osteoporosis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200078815-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 23-JUN-2000; 2000WO-US017454.  
 XX  
 PR 24-JUN-1999; 99US-00339922.  
 XX  
 PA (MOLE-) APPLIED MOLECULAR EVOLUTION.  
 XX  
 PI Huse WD, Wu H;  
 XX  
 DR WPI; 2001-050110/06.  
 XX  
 PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 PT to alpha(v)beta(3) integrin, useful in the diagnosis and treatment of  
 PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 PT osteoporosis.  
 XX  
 PS Disclosure; Page 41; 132pp; English.  
 XX  
 CC The present invention relates to enhanced LM609 grafted antibodies  
 CC exhibiting selective binding affinity to alphavbeta.3 integrin or their  
 CC functional fragments. The antibodies or their functional fragments can be  
 CC used in the diagnosis and treatment of alphavbeta.3-mediated diseases  
 CC such as angiogenesis, inflammatory diseases (such as psoriasis and  
 CC chronic articular rheumatism), disorders associated with inappropriate or  
 CC inopportunity invasion of vessels (such as diabetic retinopathy,  
 CC neovascular glaucoma and cancer disorders such as tumours and Kaposi's  
 CC sarcoma), retinal diseases (such as macular degeneration), restenosis and  
 CC osteoporosis  
 CC  
 SQ Sequence 9 AA;  
 QY 10 QOATW 15  
 DB 1 QOSTW 6  
 Query Match 32.9%; Score 28; DB 4; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

KW LM609; antibody; grafted antibody; alpha\_vbeta.3; angiogenesis; CDR;  
 KW alpha\_vbeta.3-mediated disease; complementarity determining region;  
 KW restenosis.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003028009-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 06-JUL-2001; 2001US-00900590.  
 XX  
 PR 30-JAN-1998; 98US-00016061.  
 XX  
 PA (IXSY-) IXSYS INC.  
 XX  
 PI Huse WD;  
 XX  
 DR WPI; 2003-492042/46.  
 DR N-PSDB; ACD30189.  
 XX  
 PT New Vitaxin or LM609 grafted antibody exhibiting selective binding  
 PT affinity to alphavbeta.3. The Vitaxin or LM609 grafted  
 PT disease e.g., angiogenesis or restenosis.  
 XX  
 PS Claim 65; Page 12; 71pp; English.  
 XX  
 CC The invention relates to a Vitaxin or LM609 grafted antibody, exhibiting  
 CC selective binding affinity to alpha\_vbeta.3. The Vitaxin or LM609 grafted  
 CC antibody is useful for treating an alpha\_vbeta.3-mediated disease e.g.  
 CC angiogenesis or restenosis. The present sequence represents the amino  
 CC acid sequence of a LM609 complementarity determining region  
 CC  
 SQ Sequence 9 AA;  
 QY 10 QOATW 15  
 DB 1 QOSTW 6  
 Query Match 32.9%; Score 28; DB 6; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
 ABR62303  
 ID ABR62303 standard; peptide; 9 AA.  
 XX  
 AC ABR62303;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE Surface simulation synthetic peptide useful in HIV-1 vaccine.  
 XX  
 KW Surface simulation synthetic peptide; SSSP; HIV-1; vaccine; anti-HIV;  
 KW vitruide; epitope.  
 XX  
 OS Human immunodeficiency virus 1.  
 OS Synthetic.  
 OS  
 PN WO2003048186-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 23-NOV-2002; 2002WO-US037664.  
 XX  
 PR 01-DEC-2001; 2001US-00012806.  
 XX  
 PA (CREV/) CREVECOEUR H.  
 XX  
 PI Crevecoeur H;  
 XX  
 DR WPI; 2003-558941/52.

XX Configuration of synthetic peptides useful for treating hyper-variable  
PT viral pathogen e.g. HIV, involves identifying non-sequential conserved  
PT residues in selected viral proteins and designing a sequence from image  
PT scan of the residues.

XX  
PS Disclosure; Page 27; 55pp; English.

XX  
CC The present sequence is that of a surface simulation synthetic peptide  
CC (SSSP) corresponding to a non-sequential conserved residue epitope of HIV  
CC -1 glycoprotein gp120 required for viral pathogenicity. It is an example  
CC of SSSPs of the invention, which incorporate amino acid sequences that  
CC simulate the 3-dimensional spatial positions of non-sequential conserved  
CC residues necessary for viral pathogenicity. The SSSPs are useful for  
CC incorporation into vaccines effective in eliciting an effective broad  
CC spectrum immune response against hyper-variable viral pathogens such as  
CC HIV-1, and in diagnostic kits. SSSPs provide a reliable strategy for  
CC allowing the immune system to process and recognise discontinuous  
CC epitopes and to mount immune responses to the 3-dimensional  
CC configurations of targeted proteins

XX  
SQ Sequence 9 AA;

Query Match 32.9%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. NO. 2e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPV RTEQ 11  
:| |||:  
Db 1 NPCTREKQ 8

Search completed: December 12, 2005, 21:11:36  
job time : 114.667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:20:00 ; Search time 27 Seconds  
(without alignments)  
45.931 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:\*

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2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/1aa/PCITUS\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	35.3	10	US-09-526-193A-65	Sequence 65, Appl
2	28.5	33.5	12	US-08-851-567B-2	Sequence 2, Appl
3	28	32.9	9	US-09-339-922A-88	Sequence 88, Appl
4	28	32.9	9	US-09-016-061-88	Sequence 88, Appl
5	28	32.9	13	5223254-6	Patent No. 5223254
6	27	31.8	13	US-08-836-075A-166	Sequence 166, App
7	27	31.8	13	US-09-878-281A-244	Sequence 244, App
8	27	31.8	15	US-08-221-583-56	Sequence 56, Appl
9	27	31.8	15	PCR-US95-04018-56	Sequence 56, Appl
10	26	30.6	10	US-08-981-392-53	Sequence 53, Appl
11	26	30.6	10	US-09-620-091-436	Sequence 436, App
12	26	30.6	10	US-09-908-322-53	Sequence 53, Appl
13	26	30.6	12	US-09-620-091-172	Sequence 172, Appl
14	26	30.6	14	US-08-321-668-28	Sequence 28, Appl
15	26	30.6	14	US-08-837-941-28	Sequence 28, Appl
16	26	30.6	15	US-09-148-712-23	Sequence 23, Appl
17	25	29.4	10	US-08-203-716-13	Sequence 13, Appl
18	25	29.4	10	US-08-383-434-7	Sequence 7, Appl
19	25	29.4	10	US-08-649-197-7	Sequence 7, Appl
20	25	29.4	10	US-08-440-179-13	Sequence 13, Appl
21	25	29.4	10	US-08-748-117A-1	Sequence 1, Appl
22	25	29.4	10	US-08-597-346-1	Sequence 1, Appl
23	25	29.4	10	US-08-679-350-1	Sequence 1, Appl
24	25	29.4	10	US-09-039-657-13	Sequence 13, Appl
25	25	29.4	10	US-09-421-954-1	Sequence 1, Appl
26	25	29.4	10	US-09-623-548A-1263	Sequence 1263, Ap
27	25	29.4	10	US-09-657-276-1263	Sequence 1263, Ap

28	25	29.4	10	6	5422425-8	Patent No. 5422425
29	25	29.4	11	1	US-08-456-670B-38	Sequence 38, Appl
30	25	29.4	11	2	US-09-372-036-38	Sequence 38, Appl
31	25	29.4	12	1	US-08-203-716-21	Sequence 21, Appl
32	25	29.4	12	1	US-08-440-179-21	Sequence 21, Appl
33	25	29.4	12	2	US-09-039-657-21	Sequence 21, Appl
34	25	29.4	13	2	US-09-117-608-2	Sequence 2, Appl
35	25	29.4	14	1	US-08-354-685-3	Sequence 3, Appl
36	25	29.4	14	2	US-08-665-643A-2	Sequence 2, Appl
37	25	29.4	14	2	US-09-693-746-93	Sequence 93, Appl
38	25	29.4	15	1	US-07-616-910-55	Sequence 55, Appl
39	25	29.4	15	1	PCR-US91-08497-55	Sequence 55, Appl
40	24	28.2	8	4	US-08-203-716-22	Sequence 22, Appl
41	24	28.2	8	1	US-08-440-179-22	Sequence 22, Appl
42	24	28.2	8	2	US-09-039-657-22	Sequence 2, Appl
43	24	28.2	9	1	US-08-233-081B-6	Sequence 6, Appl
44	24	28.2	10	1	US-08-203-716-17	Sequence 17, Appl
45	24	28.2	10	1	US-08-203-716-19	Sequence 19, Appl

## ALIGNMENTS

RESULT 1  
US-09-526-193A-65  
Sequence 65, Application US/09526193A  
Patent No. 6617122  
GENERAL INFORMATION:  
APPLICANT: Hayden, Michael R.  
APPLICANT: Brooks-Wilson, Angela R.  
APPLICANT: Pimstone, Simon N.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING  
FILE REFERENCE: 50110/002805  
CURRENT APPLICATION NUMBER: US/09/526,193A  
CURRENT FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 60/124,702  
PRIOR FILING DATE: 1999-03-15  
PRIOR APPLICATION NUMBER: 60/138,048  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: 60/139,600  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: 60/151,977  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 287  
SOFTWARE: FastrSeq for Windows Version 4.0  
SEQ ID NO 65  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-526-193A-65

Query Match 35.3%; Score 30; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 58;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSVPVTEQQ 11  
DB 1 NDSVPVTEQQ 10

RESULT 2  
US-08-851-567B-2  
Sequence 2, Application US/08851567B  
Patent No. 6528484  
GENERAL INFORMATION:  
APPLICANT: Ensign, Jerald C  
APPLICANT: Bowen, David J  
APPLICANT: Petell, James  
APPLICANT: Faticig, Raymond  
APPLICANT: Schoonover, Sue  
APPLICANT: Firench-Constant, Richard  
APPLICANT: Rocheleau, Thomas A.

```

; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Cliche, Todd A.
; APPLICANT: Sukhapiinda, Kitiari
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,567B
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.93804
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-851-567B-2

Query Match      33.5%; Score 28.5; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy      3 DSPVTEQQTW 15
      ||| |
      ||| |
Db      3 DSP---EVSITW 12

RESULT 3
; US-09-339-922A-88
; Sequence 88, Application US/09339922A
; Patent No. 6531580
; GENERAL INFORMATION:

```

```

; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; US-09-339-922A-88

Query Match      32.9%; Score 28; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      10 QOATW 15
      ||| |
      ||| |
Db      1 QOSTW 6

RESULT 4
; US-09-016-061-88
; Sequence 88, Application US/09016061
; Patent No. 6596850
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaeser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-88

Query Match      32.9%; Score 28; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;

```

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 QOATW 15  
|||:|  
Db 1 QOSTW 6

RESULT 5  
5223254-6  
Patent No. 5223254  
APPLICANT: PARADISO, PETER R.; HILDEETH, STEPHEN W.; HU,  
BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARIMUGHAM, RASAPPA  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES  
NUMBER OF SEQUENCES: 17  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/247,017  
FILING DATE: 20-SEP-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 102,180  
FILING DATE: 29-SEP-1987  
SEQ ID NO: 6:  
LENGTH: 13  
5223254-6

Query Match 32.9%; Score 28; DB 6; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPTREQ 11  
|||:|  
Db 2 NDMPTINDOK 11

RESULT 6  
US-08-836-075A-166  
Sequence 166, Application US/08836075A  
Patent No. 6180768  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT  
APPLICANT: STUYVER, LIEVEN  
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 6.0 / ASCII text output  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,075A  
FILING DATE: 21 Apr 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/04155  
FILING DATE: 23 Oct 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94870166.9  
FILING DATE: 21 Oct 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95870076.7  
FILING DATE: 28 Jun 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: KAMMERER, PATRICIA A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: INNS:004  
INFORMATION FOR SEQ ID NO: 166:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-836-075A-166

Query Match 31.8%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTGQATW 15  
|||:|  
Db 1 VRTGQSRWC 10

RESULT 7  
US-09-878-281A-244  
Sequence 244, Application US/09878281A  
Patent No. 6762024  
GENERAL INFORMATION:  
APPLICANT: Innogenetics N.V.  
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
FILE REFERENCE: 35  
CURRENT APPLICATION NUMBER: US/09/878,281A  
CURRENT FILING DATE: 2001-06-12  
NUMBER OF SEQ ID NOS: 284  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 244  
LENGTH: 13  
TYPE: PRT  
ORGANISM: hepatitis C virus  
US-09-878-281A-244

Query Match 31.8%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTGQATW 15  
|||:|  
Db 1 VRTGQSRWC 10

RESULT 8  
US-08-221-583-56  
Sequence 56, Application US/08221583  
Patent No. 5486595  
GENERAL INFORMATION:  
APPLICANT: Heavner, George A.  
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595stris  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25.mdetctMod.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,583  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: CCO-0185  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-221-583-56

Query Match 31.8%; Score 27; DB 1; Length 15;  
Best Local Similarity 46.2%; Pred. No. 3.1e+02;  
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQT 13  
Db 1 HLPQPVSTRSQHT 13

RESULT 9  
PCT-US95-04018-56  
Sequence 56, Application PC/RUS9504018  
GENERAL INFORMATION:  
APPLICANT: Heavner, George A.  
APPLICANT: Kruszynski, Marian  
APPLICANT: Mervic, Miljenko  
APPLICANT: Weber, Robert W.  
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSEE: Norris  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04018  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,580  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,583  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,581  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: CCOR-0232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-04018-56

Query Match 31.8%; Score 27; DB 4; Length 15;  
Best Local Similarity 46.2%; Pred. No. 3.1e+02;  
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQT 13  
Db 1 HLPQPVSTRSQHT 13

RESULT 10  
US-08-981-392-53  
Sequence 53, Application US/08981392  
Patent No. 6262025  
GENERAL INFORMATION:  
APPLICANT: Ish-Horowitz, David  
APPLICANT: Henrique, Domingos Manuel Pinto  
APPLICANT: Lewis, Julian Hart  
APPLICANT: Altavanti-Tsakonas, Spyridon  
APPLICANT: Gray, Grace  
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES  
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/981,392  
FILING DATE: 22-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Antler, Adriane M.  
REGISTRATION NUMBER: 32,605  
REFERENCE/DOCKET NUMBER: 7326-038  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-981-392-53

Query Match 30.6%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VRTEQQ 11  
Db 5 VRTEQE 10

RESULT 11  
US-09-620-091-436  
Sequence 436, Application US/09620091  
Patent No. 6716811  
GENERAL INFORMATION:  
APPLICANT: CWIRLA, STEVEN E.  
APPLICANT: BALU, PALANI  
APPLICANT: DUFFIN, DAVID J.  
APPLICANT: PIPLANI, SONILA  
APPLICANT: MERRILL, BARBARA MCEOWEN  
APPLICANT: SCHATZ, PETER JOSEPH  
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY



TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
FILE REFERENCE: 0300-0014  
CURRENT APPLICATION NUMBER: US/09/620,091  
CURRENT FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 491  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 436  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-620-091-436

Query Match 30.6%; Score 26; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNSDPV 6  
|||:  
1 HNSSPM 6

Db 1 HNSSPM 6

RESULT 12  
US-09-908-322-53  
Sequence 53, Application US/09908322  
Patent No. 6783956  
GENERAL INFORMATION:  
APPLICANT: Ish-Horowitz, David  
Henrique, Domingos Manuel Pinto  
Lewis, Julian Hart  
Artavanis-Teakonas, Spyridon  
Gray, Grace  
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
VERTERATE DELTA GENE AND METHODS BASED THEREON  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/908,322  
FILING DATE: 17-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/981,392  
FILING DATE: 22-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7336-123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-09-908-322-53

Query Match 30.6%; Score 26; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VRTEQ 11  
|||:  
5 VRTEQ 10

Db 5 VRTEQ 10

RESULT 13  
US-09-620-091-172  
Sequence 172, Application US/09620091  
Patent No. 6716811  
GENERAL INFORMATION:  
APPLICANT: CIRILA, STEVEN E.  
APPLICANT: BALU, PALANI  
APPLICANT: DUFFIN, DAVID J.  
APPLICANT: PIPLANI, SUNILA  
APPLICANT: MERRILL, BARBARA MCEOWEN  
APPLICANT: SCHATZ, PETER JOSEPH  
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
FILE REFERENCE: 0300-0014  
CURRENT APPLICATION NUMBER: US/09/620,091  
CURRENT FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 491  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 172  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-620-091-172

Query Match 30.6%; Score 26; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNSDPV 6  
|||:  
2 HNSSPM 7

Db 2 HNSSPM 7

RESULT 14  
US-08-321-668-28  
Sequence 28, Application US/08321668  
Patent No. 3663859  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VAREPOLOMEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/321,668  
FILING DATE: 12-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: /note= hu p55 TNF-R mutant  
OTHER INFORMATION: construct V 173 P  
US-08-321-668-28

Query Match 30.6%; Score 26; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 4.2e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 DSPVTEQOATT 14  
::| |||  
Db 2 ENPKGTDSGTT 13

RESULT 15  
US-08-837-941-28  
Sequence 28, Application US/08837941  
Patent No. 5766917  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARFOLOMEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,941  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/321,668  
FILING DATE: 12-OCT-1994  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: /note= hu p55 TNF-R mutant  
OTHER INFORMATION: construct V 173 P  
US-08-837-941-28

Query Match 30.6%; Score 26; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 4.2e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 DSPVTEQOATT 14  
::| |||  
Db 2 ENPKGTDSGTT 13

Search completed: December 12, 2005, 21:00:45  
Job time : 27 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 12, 2005, 20:30:45 ; Search time 92.6667 Seconds  
(without alignments)  
67.634 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	5	US-10-758-165-2
2	48	56.5	15	5	US-10-758-165-1
3	39	45.9	15	5	US-10-758-165-7
4	37	43.5	15	5	US-10-758-165-3
5	35	41.2	15	4	US-10-052-788-4
6	32	37.6	11	4	US-10-381-089-18
7	32	37.6	15	4	US-10-381-089-8
8	30	35.3	10	4	US-10-452-510-65
9	30	35.3	10	4	US-10-617-334-65
10	30	35.3	10	4	US-10-744-465-65
11	30	35.3	10	4	US-10-833-679-65
12	30	35.3	10	4	US-10-818-279-65
13	28.5	33.5	12	4	US-10-262-794A-2
14	28	32.9	9	3	US-09-900-590-88
15	28	32.9	9	4	US-10-012-806A-39
16	28	32.9	9	4	US-10-305-231-88
17	28	32.9	9	4	US-10-463-847-88
18	28	32.9	10	4	US-10-432-234A-250
19	27	31.8	9	3	US-09-842-776A-39
20	27	31.8	9	4	US-10-239-656-31
21	27	31.8	9	4	US-10-239-656-41
22	27	31.8	9	4	US-10-467-546-21
23	27	31.8	9	5	US-10-666-332-21
24	27	31.8	10	4	US-10-432-234A-249
25	27	31.8	13	3	US-09-851-138-166
26	27	31.8	13	3	US-09-899-046-244
27	27	31.8	13	3	US-09-878-281-244

28	27	31.8	13	3	US-09-873-224-244	Sequence 244, App
29	27	31.8	14	5	US-10-808-187-1344	Sequence 1344, Ap
30	27	31.8	14	5	US-10-807-807-1344	Sequence 1344, Ap
31	26	30.6	9	4	US-10-117-937-560	Sequence 560, App
32	26	30.6	9	4	US-10-428-335-103	Sequence 103, App
33	26	30.6	9	5	US-10-883-020-19	Sequence 19, App
34	26	30.6	9	6	US-11-067-064-560	Sequence 560, App
35	26	30.6	9	6	US-11-067-159-560	Sequence 560, App
36	26	30.6	10	3	US-09-908-332-53	Sequence 53, App1
37	26	30.6	10	3	US-09-783-931-53	Sequence 53, App1
38	26	30.6	10	4	US-10-117-937-561	Sequence 561, App
39	26	30.6	10	5	US-10-659-207-436	Sequence 436, App
40	26	30.6	10	6	US-11-067-064-561	Sequence 561, App
41	26	30.6	10	6	US-11-067-159-561	Sequence 561, App
42	26	30.6	11	4	US-10-203-754A-7	Sequence 7, App1
43	26	30.6	11	4	US-10-607-834-11	Sequence 11, App1
44	26	30.6	12	5	US-10-468-543-9	Sequence 9, App1
45	26	30.6	12	5	US-10-659-207-172	Sequence 172, App

## ALIGNMENTS

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RESULT 1
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2
```

Query Match 100.0%; Score 85; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.3e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 HNDSPVTEQQTW 15
|||
Db 1 HNDSPVTEQQTW 15
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RESULT 2
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1
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Query Match 56.5%; Score 48; DB 5; Length 15;

Best Local Similarity 61.5%; Pred. No. 0.23;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NDSFPRTEQQAATT 14  
| | | | | | | |  
| | | | | | | |  
Db 2 NDSPIQTDQYTT 14

RESULT 3  
US-10-758-165-7  
; Sequence 7, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758.165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-7

Query Match 45.9%; Score 39; DB 5; Length 15;  
Best Local Similarity 46.2%; Pred. No. 9;  
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFPRTEQQAATT 14  
| | | | | | | |  
| | | | | | | |  
Db 2 NDAFVQADRHSTT 14

RESULT 4  
US-10-758-165-3  
; Sequence 3, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758.165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Equus caballus  
US-10-758-165-3

Query Match 43.5%; Score 37; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 20;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFPRTEQQAATT 14  
| | | | | | | |  
| | | | | | | |  
Db 2 NNVLQTDQQAATT 14

RESULT 5  
US-10-052-788-4  
; Sequence 4, Application US/10052788  
; Publication No. US20030087314A1  
; GENERAL INFORMATION:  
; APPLICANT: Gershwin, Laurel J.  
; APPLICANT: Pettigrew, Howard David

; APPLICANT: Kalina, Warren V.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for  
; TITLE OF INVENTION: Induction of Anti-IgE Antibodies  
; FILE REFERENCE: 023070-121000US  
; CURRENT APPLICATION NUMBER: US/10/052,788  
; CURRENT FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:epitope peptide  
; OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon  
US-10-052-788-4

Query Match 41.2%; Score 35; DB 4; Length 15;  
Best Local Similarity 66.7%; Pred. No. 46;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 VRTGQAATT 14  
| | | | | | | |  
| | | | | | | |  
Db 1 IQTDQAATT 9

RESULT 6  
US-10-381-089-18  
; Sequence 18, Application US/10381089  
; Publication No. US20040053276A1  
; GENERAL INFORMATION:  
; APPLICANT: ITO, Yasuaki  
; APPLICANT: TANAKA, Hideyuki  
; APPLICANT: NISHIMURA, Atsushi  
; APPLICANT: OGI, Kazuhito  
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA  
; FILE REFERENCE: 2789 usOP  
; CURRENT APPLICATION NUMBER: US/10/381,089  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: JP 2000-293985  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: JP 2000-302839  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO 18  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide Cpp1-2  
US-10-381-089-18

Query Match 37.6%; Score 32; DB 4; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.le+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12  
| | | | | | | |  
| | | | | | | |  
Db 2 SPVTEKQA 10

RESULT 7  
US-10-381-089-8  
; Sequence 8, Application US/10381089  
; Publication No. US20040053276A1  
; GENERAL INFORMATION:  
; APPLICANT: ITO, Yasuaki  
; APPLICANT: TANAKA, Hideyuki  
; APPLICANT: NISHIMURA, Atsushi  
; APPLICANT: OGI, Kazuhito  
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA

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FILE REFERENCE: 2789 USOP
; CURRENT APPLICATION NUMBER: US/10/361,089
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2000-293985
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP 2000-302839
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human
US-10-381-089-8

Query Match      37.6%; Score 32; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 SPVTEQQA 12
      ||| |||
Db      1 SPILTEKQA 9

RESULT 8
US-10-452-510-65
; Sequence 65, Application US/10452510
; Publication No. US20040005666A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-93
; CURRENT APPLICATION NUMBER: US/10/452,510
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-452-510-65

Query Match      35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPVTEQQ 11
      ||| |||
Db      1 NDEVRRERQ 10

RESULT 9
US-10-617-334-65
; Sequence 65, Application US/10617334
; Publication No. US20040058869A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-91
; CURRENT APPLICATION NUMBER: US/10/617,334
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/526,193
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; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: PatentIn 3.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-334-65

Query Match      35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPVTEQQ 11
      ||| |||
Db      1 NDEVRRERQ 10

RESULT 10
US-10-744-465-65
; Sequence 65, Application US/10744465
; Publication No. US20040157250A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pimstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-92
; CURRENT APPLICATION NUMBER: US/10/744,465
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 10/617,334
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-744-465-65

Query Match      35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPVTEQQ 11
      ||| |||
Db      1 NDEVRRERQ 10

RESULT 11
US-10-833-679-65
; Sequence 65, Application US/10833679
; Publication No. US20040185508A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
```

APPLICANT: Brooks-Wilson, Angela R.  
PIMSTONE, Simon N.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
FILE REFERENCE: 760050-135  
CURRENT APPLICATION NUMBER: US/10/833,679  
CURRENT FILING DATE: 2004-04-28  
PRIOR APPLICATION NUMBER: 10/452,510  
PRIOR FILING DATE: 2003-06-02  
PRIOR APPLICATION NUMBER: 10/617,334  
PRIOR FILING DATE: 2003-07-10  
PRIOR APPLICATION NUMBER: 09/526,193  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 60/124,702  
PRIOR FILING DATE: 1999-03-15  
PRIOR APPLICATION NUMBER: 60/138,048  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: 60/139,600  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: 60/151,977  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 287  
SOFTWARE: PatentIn 3.0  
SEQ ID NO 65  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-833-679-65

Query Match 35.3%; Score 30; DB 4; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSFPRTEQ 11  
Db 1 NDEVRERQ 10

RESULT 12  
US-10-818-279-65  
Sequence 65, Application US/10818279  
Publication No. US20050136421A1  
GENERAL INFORMATION:  
APPLICANT: Hayden, Michael R.  
APPLICANT: Brooks-Wilson, Angela R.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
FILE REFERENCE: 760050-126  
CURRENT APPLICATION NUMBER: US/10/818,279  
CURRENT FILING DATE: 2004-04-05  
PRIOR APPLICATION NUMBER: 10/745,377  
PRIOR FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: 10/617,334  
PRIOR FILING DATE: 2003-07-10  
PRIOR APPLICATION NUMBER: 09/526,193  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 60/124,702  
PRIOR FILING DATE: 1999-03-15  
PRIOR APPLICATION NUMBER: 60/138,048  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: 60/139,600  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: 60/151,977  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 287  
SOFTWARE: PatentIn 3.0  
SEQ ID NO 65  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-818-279-65

Query Match 35.3%; Score 30; DB 5; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.3e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 NDSFPRTEQ 11  
Db 1 NDEVRERQ 10

RESULT 13  
US-10-262-794A-2  
Sequence 2, Application US/10262794A  
Publication No. US20030207806A1  
GENERAL INFORMATION:  
APPLICANT: Ensign, Jerald C  
APPLICANT: Bowen, David J  
APPLICANT: Petrell, James  
APPLICANT: Fatig, Raymond  
APPLICANT: Schoonover, Sue  
APPLICANT: French-Constant, Richard  
APPLICANT: Rocheleau, Thomas A.  
APPLICANT: Blackburn, Michael B.  
APPLICANT: Hey, Timothy D.  
APPLICANT: Merlo, Donald J.  
APPLICANT: Orr, Gregory L.  
APPLICANT: Roberts, Jean L.  
APPLICANT: Strickland, James A.  
APPLICANT: Guo, Lining  
APPLICANT: Ciche, Todd A.  
APPLICANT: Sukhapiinda, Kitiari  
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dow Agrosciences Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/262,794A  
FILING DATE: 02-OCT-2002  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,567  
FILING DATE: 05-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/063,615  
FILING DATE: 18-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/395,497  
FILING DATE: 28-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/007,255  
FILING DATE: 06-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/608,423  
FILING DATE: 28-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/705,484  
FILING DATE: 28-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296..93804  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-10-262-794A-2

Query Match 33.5% Score 28.5; DB 4; Length 12;  
Best Local Similarity 53.8%; Pred. No. 5.1e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 3 DSPVTEQOATW 15  
|||  
3 DSP---EVSITW 12

## RESULT 14

US-09-900-590-88  
Sequence 88, Application US/09900590  
Publication No. US20030028009A1  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
Glaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
Antibodies, Nucleic Acids Encoding Same and Methods of Use  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/900,590  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/016,061  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 2965  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 88:  
US-09-900-590-88

Query Match 32.9% Score 28; DB 3; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QOATW 15  
||:|:  
1 QOSTW 6

## RESULT 15

US-10-012-806A-39  
Sequence 39, Application US/10012806A  
Publication No. US20030125518A1  
GENERAL INFORMATION:  
APPLICANT: CREVICOER, HARRY  
TITLE OF INVENTION: SURFACE SIMULATION SYNTHETIC PEPTIDES USEFUL IN THE  
TREATMENT OF HYPER-VARIABLE VIRAL PATHOGENS  
FILE REFERENCE: 2001-Crev1  
CURRENT APPLICATION NUMBER: US/10/012,806A  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 39  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-012-806A-39

Query Match 32.9% Score 28; DB 4; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SPVTEQ 11  
:|:|:  
Db 1 NPCRTEQ 8

Search completed: December 12, 2005, 21:05:29  
Job time : 93.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:00:56 ; Search time 4.66667 Seconds  
(without alignments)  
17,950 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 8641

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	31.8	9	7	US-11-108-135-12
2	24	28.2	13	6	US-10-511-559-627
3	24	28.2	13	6	US-10-511-559-628
4	23	27.1	13	6	US-10-511-559-626
5	22	25.9	12	7	US-11-010-748A-270
6	22	25.9	12	7	US-11-058-735-37
7	22	25.9	13	6	US-10-511-559-625
8	21	24.7	9	6	US-10-997-201A-39
9	21	24.7	7	6	US-11-093-274-18
10	21	24.7	13	6	US-10-511-559-752
11	21	24.7	13	6	US-10-511-559-753
12	21	24.7	13	6	US-10-511-559-754
13	21	24.7	13	6	US-10-511-559-755
14	21	24.7	15	7	US-11-006-119-37
15	20	23.5	6	7	US-11-129-143-161
16	20	23.5	6	7	US-11-129-143-162
17	20	23.5	6	7	US-11-129-143-163
18	20	23.5	6	7	US-11-129-143-164
19	20	23.5	6	7	US-11-129-143-165
20	20	23.5	8	6	US-10-989-226-49
21	20	23.5	8	6	US-10-989-226-50
22	20	23.5	9	7	US-11-010-748A-265
23	20	23.5	9	7	US-11-010-748A-266
24	20	23.5	9	7	US-11-010-748A-267

26	20	23.5	9	7	US-11-010-748A-268	Sequence 268, App
27	20	23.5	9	7	US-11-010-748A-271	Sequence 271, App
28	20	23.5	10	7	US-11-053-076-242	Sequence 242, App
29	20	23.5	10	7	US-11-053-076-247	Sequence 247, App
30	20	23.5	10	7	US-11-093-274-16	Sequence 16, Appl
31	20	23.5	10	7	US-11-093-274-17	Sequence 17, Appl
32	20	23.5	12	6	US-10-632-150-84	Sequence 3189, Ap
33	20	23.5	12	6	US-11-054-515-3189	Sequence 84, Appl
34	20	23.5	13	6	US-11-073-457-84	Sequence 199, App
35	20	23.5	13	6	US-10-511-559-199	Sequence 200, App
36	20	23.5	13	6	US-10-511-559-200	Sequence 201, App
37	20	23.5	13	6	US-10-511-559-201	Sequence 202, App
38	20	23.5	13	6	US-10-511-559-202	Sequence 882, App
39	20	23.5	13	6	US-10-511-559-203	Sequence 883, App
40	20	23.5	13	6	US-10-511-559-882	Sequence 105, App
41	20	23.5	15	7	US-11-022-562-105	Sequence 106, App
42	20	23.5	15	7	US-11-022-562-106	Sequence 107, App
43	20	23.5	15	7	US-11-022-562-107	Sequence 7, Appl
44	20	23.5	15	7	US-11-022-562-107	
45	19	22.4	8	6	US-10-416-047-7	

## ALIGNMENTS

```
RESULT 1
US-11-108-135-12
; Sequence 12, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Taillon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; TITLE OF INVENTION: Fc-gamma-RIIb-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 286 Light chain variable region - CDR3
US-11-108-135-12

Query Match      31.8% ; Score 27 ; DB 7 ; Length 9 ;
Best Local Similarity 66.7% ; Pred. No. 2.8e+04 ;
Matches 4 ; Conservative 1 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

QY      10 QOATW 15
Db      1 QOANTW 6

RESULT 2
US-10-511-559-627
; Sequence 627, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
```

```

; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 627
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-627
```

```

Query Match          28.2%; Score 24; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 NDSVPRTQ 10
Db      5 NDSTNRITK 13
```

```

RESULT 3
US-10-511-559-628
; Sequence 628, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-628
```

```

Query Match          28.2%; Score 24; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 NDSVPRTQ 10
Db      4 NDSTNRITK 12
```

```

RESULT 4
US-10-511-559-626
; Sequence 626, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
```

```

; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 626
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-626
```

```

Query Match          27.1%; Score 23; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 NDSVPRT 9
Db      6 NDSTNRITK 13
```

```

RESULT 5
US-11-010-748A-270
; Sequence 270, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHAW, Burhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 270
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of seq. No. 263
US-11-010-748A-270
```

```

Query Match          25.9%; Score 22; DB 7; Length 9;
Best Local Similarity 33.3%; Pred. No. 2; Seq+04;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 HNSDPVTE 9
Db      1 HNESLISQ 9
```

```

RESULT 6
US-11-058-735-37
; Sequence 37, Application US/11058735
; Publication No. US20050261475A1
; GENERAL INFORMATION:
```

APPLICANT: TSENG, HUANG-CHUN  
APPLICANT: TSAI, LI-HUEI  
TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR  
FILE REFERENCE: PHOSPHOPROTEOMIC ANALYSES  
CURRENT APPLICATION NUMBER: US/11/058,735  
CURRENT FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,748  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 37  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-058-735-37

Query Match 25.9%; Score 22; DB 7; Length 12;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSPVTEQO 11  
Db 2 DAAVTEER 10

RESULT 7  
US-10-511-559-625  
Sequence 625, Application US/10511559  
Publication No. US20050256304A1  
GENERAL INFORMATION:  
APPLICANT: JONES, Tim  
APPLICANT: BAKER, Matthew  
APPLICANT: CARR, Francis, J.  
TITLE OF INVENTION: MODIFIED FACTOR VIII  
FILE REFERENCE: MER-133  
CURRENT APPLICATION NUMBER: US/10/511,559  
CURRENT FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: PCT/EP03/04063  
PRIOR FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: EP 02008712.8  
PRIOR FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: EP 03006554.4  
PRIOR FILING DATE: 2003-03-24  
NUMBER OF SEQ ID NOS: 1147  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 625  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-625

Query Match 25.9%; Score 22; DB 6; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSVPT 8  
Db 7 NDSTNRT 13

RESULT 8  
US-10-997-201A-39  
Sequence 39, Application US/10997201A  
Publication No. US20050249739A1  
GENERAL INFORMATION:  
APPLICANT: Marasco, Wayne  
APPLICANT: Sui, Jianhua

TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof  
FILE REFERENCE: 20363-026  
CURRENT APPLICATION NUMBER: US/10/997,201A  
CURRENT FILING DATE: 2004-11-24  
PRIOR APPLICATION NUMBER: 60/524,840  
PRIOR FILING DATE: 2003-11-25  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 39  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-997-201A-39

Query Match 24.7%; Score 21; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 QOATW 15  
Db 1 QORSNW 6

RESULT 9  
US-11-093-274-18  
Sequence 18, Application US/11093274  
Publication No. US20050266008A1  
GENERAL INFORMATION:  
APPLICANT: Graziano, Robert  
APPLICANT: Cardarelli, Josephine M.  
APPLICANT: Kempe, Thomas  
APPLICANT: Cutler, Beth  
APPLICANT: Srinivasan, Mohan  
TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES  
FILE REFERENCE: 04280/1201101-US1  
CURRENT APPLICATION NUMBER: US/11/093,274  
CURRENT FILING DATE: 2005-03-28  
PRIOR APPLICATION NUMBER: 60/557,741  
PRIOR FILING DATE: 2004-03-29  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Version 3.2  
SEQ ID NO 18  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-093-274-18

Query Match 24.7%; Score 21; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 QOATW 15  
Db 1 QORSNW 6

RESULT 10  
US-10-511-559-752  
Sequence 752, Application US/10511559  
Publication No. US20050256304A1  
GENERAL INFORMATION:  
APPLICANT: JONES, Tim  
APPLICANT: BAKER, Matthew  
APPLICANT: CARR, Francis, J.  
TITLE OF INVENTION: MODIFIED FACTOR VIII  
FILE REFERENCE: MER-133  
CURRENT APPLICATION NUMBER: US/10/511,559  
CURRENT FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: PCT/EP03/04063  
PRIOR FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: EP 02008712.8  
PRIOR FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: EP 03006554.4

```
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 752
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-752
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 VRTSEQOANTT 14
Db      5 VATESSAKT 13
```

## RESULT 11

```
US-10-511-559-753
; Sequence 753, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 753
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-753
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 VRTSEQOANTT 14
Db      4 VATESSAKT 12
```

## RESULT 12

```
US-10-511-559-754
; Sequence 754, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
```

```
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 754
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-754
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 VRTSEQOANTT 14
Db      3 VATESSAKT 11
```

## RESULT 13

```
US-10-511-559-755
; Sequence 755, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 755
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-755
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 VRTSEQOANTT 14
Db      1 VATESSAKT 9
```

## RESULT 14

```
US-11-006-119-37
; Sequence 37, Application US/11006119
; Publication No. US20050260691A1
; GENERAL INFORMATION:
; APPLICANT: Ndao, Momar
; APPLICANT: Caifrey, Rebecca
; APPLICANT: Spithill, Terry
; APPLICANT: Li, Hongshan
; APPLICANT: Poduet, Vladimir
; APPLICANT: Perichon, Regis
; APPLICANT: Ciplergen Biosystems, Inc.
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
; FILE REFERENCE: 016866-012130US
```

```

; CURRENT APPLICATION NUMBER: US/11/006,119
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/527,153
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 60/565,093
; PRIOR FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/625,519
; PRIOR FILING DATE: 2004-11-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal
; OTHER INFORMATION: truncation 24.7 kDa fragment of Apolipoprotein A-I
; OTHER INFORMATION: (APOA-I) Chagas disease biomarker tryptic digest
; OTHER INFORMATION: fragment peptide
US-11-006-119-37

```

```

Query Match          24.7%  Score 21;  DB 7;  Length 15;
Best Local Similarity 57.1%  Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      5  PVTEQQ 11
       |||||
Db      5  PLRAELQ 11

```

```

RESULT 15
US-11-129-143-161
; Sequence 161, Application US/11/29143
; Publication No. US20050266518a1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum
US-11-129-143-161

```

```

Query Match          23.5%  Score 20;  DB 7;  Length 6;
Best Local Similarity 60.0%  Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1  HNDSP 5
       |||||
Db      2  HDDLP 6

```

```

Search completed: December 12, 2005, 21:17:40
Job time : 4.66667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:05:42 ; Search time 18 Seconds

(without alignments)  
80.181 Million cell updates/sec

Title: US-10-758-165A-2

Perfect score: 85

Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	27.1	11	2	S71304
2	22	25.9	15	2	PA0062
3	21	24.7	12	2	141235
4	21	24.7	13	2	PH0138
5	20	23.5	11	2	152980
6	20	23.5	15	2	S39012
7	20	23.5	15	2	B60763
8	19	22.4	9	2	A61357
9	19	22.4	10	2	A61337
10	19	22.4	11	2	A29806
11	19	22.4	11	2	A49037
12	19	22.4	12	2	ES8502
13	19	22.4	13	2	A60458
14	19	22.4	13	2	S36887
15	19	22.4	14	2	S74128
16	19	22.4	14	2	PN0147
17	19	22.4	15	2	JN0263
18	19	22.4	15	2	A36527
19	18	21.2	6	2	S76764
20	18	21.2	11	2	UQ2317
21	18	21.2	12	2	PD0021
22	18	21.2	12	2	C30503
23	18	21.2	13	2	S33273
24	18	21.2	13	2	S47376
25	18	21.2	14	2	PH1625
26	18	21.2	14	2	PH1627
27	18	21.2	15	2	P00195
28	18	21.2	15	2	S32677
29	18	21.2	15	2	PA0020

30	18	21.2	15	2	PA0058	protein QF200022 -
31	18	21.2	15	2	A49177	22K protein p1, mi
32	18	21.2	15	2	A53594	cainexin - mouse (
33	17	20.0	5	2	PT0580	T-cell receptor be
34	17	20.0	6	2	A31263	dihydrofolate redu
35	17	20.0	7	2	S33246	neuroendocrine pe
36	17	20.0	8	2	PT0030	inulinase (EC 3.2.
37	17	20.0	8	2	I57018	gene Cfr protein
38	17	20.0	9	2	PT0247	Ig heavy chain CRD
39	17	20.0	10	2	S66248	processing enzyme,
40	17	20.0	10	2	A60722	cryptic fibrillar p
41	17	20.0	10	2	S39030	lysoyl-bradykinin -
42	17	20.0	11	2	H54346	pyruvate synthase
43	17	20.0	11	2	B49037	TCR gamma V-J regi
44	17	20.0	11	2	C49037	TCR gamma V-J regi
45	17	20.0	11	2	A61512	variant surface gl

## ALIGNMENTS

## RESULT 1

S71304 amine oxidase (copper-containing) (EC 1.4.3.6) II - *Aspergillus niger* (fragment)  
C.Species: *Aspergillus niger*  
C.Date: 12-Feb-1998 #sequence\_revision 01-May-1998 #text\_change 09-Jul-2004

C.Accession: S71304

R.Frederick, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tanno, H.; Halata, M.; Asano

Bur, J. Biochem. 237, 255-265, 1996

A.Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc

A.Reference number: S71303; PMID:96203933; PMID:8620882

A.Accession: S71304

A.Molecule type: protein

A.Residues: 1-11 <FR>

A.Cross-References: UNIPROT:Q7M504; UNIPARC:UPI000017B3B7

C.Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquione

## Query Match

Best Local Similarity 100.0%; Pred. No. 6.7e+02; Length 11;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 NDSF 4

## RESULT 2

PA0062 fumarate hydratase (EC 4.2.1.2) - fungus (*Fusarium sporotrichioides*) (fragment)

C.Species: *Fusarium sporotrichioides*

C.Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C.Accession: PA0062

R.Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JPIB, October 1994

A.Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrich*

A.Reference number: PA0051

A.Accession: PA0062

A.Molecule type: protein

A.Residues: 1-15 <CHO>

A.Cross-References: UNIPROT:Q7M4Z3; UNIPARC:UPI000017B3FD

C.Keywords: carbon-oxygen lyase; hydro-lyase

## Query Match

Best Local Similarity 55.6%; Pred. No. 1.4e+03; Length 15;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 4 SPVTEQQA 12

1 SGTRESDA 9

## RESULT 3

I41235

glutamine-tRNA ligase (EC 6.1.1.18) - Escherichia coli (fragment)  
C/Species: Escherichia coli  
C/Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 03-Jun-2002  
C/Accession: 141235  
R/Hoben, P.; Uemura, H.; Yamao, F.; Cheung, A.; Swanson, R.; Summer-Smith, M.; Soli, D.  
Fed. Proc. 43, 2972-2976, 1984  
A/Title: Misaminoacylation by glutamyl-tRNA synthetase: relaxed specificity in wild-type  
A/Reference number: 141235; PMID:85051900; PMID:6389180  
A/Accession: 141235  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-12 <RES>  
A/Cross-references: UNIPARC:UPI000016F1B4; GB:M16470; NID:G146170; PIDN:AAA69006.1; PID:  
C/Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 24.7%; Score 21; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 QATTW 15  
Db 3 EAETW 7

RESULT 4  
PH0138  
T-cell receptor beta chain V-D-J region C8 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
C/Accession: PH0138  
R/Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlage, M.; Richert, J.; Brostoff, S.; Le  
J. Exp. Med. 173, 19-24, 1991  
A/Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context  
A/Reference number: PH0135; PMID:91086843; PMID:1702137  
A/Accession: PH0138  
A/Molecule type: mRNA  
A/Residues: 1-13 <MAR>  
A/Cross-references: UNIPARC:UPI000017C3AC  
C/Keywords: T-cell receptor

Query Match 24.7%; Score 21; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 ATTW 15  
Db 4 ASTW 7

RESULT 5  
I52980  
glucocerebrosidase - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C/Accession: I52980; I55971  
R/Reiner, O.; Wigderson, M.; Horowitz, M.  
DNA 7, 107-116, 1988  
A/Title: Structural analysis of the human glucocerebrosidase genes.  
A/Reference number: I52980; MUID:88195776; PMID:3359914  
A/Accession: I52980  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-11 <RES>  
A/Cross-references: UNIPARC:UPI000016A981; GB:M18916; NID:G183023; PIDN:AAA35878.1; PID:  
A/Accession: I55971  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-11 <RES>  
A/Cross-references: UNIPARC:UPI000016A981; GB:M18917; NID:G183025; PIDN:AAA35879.1; PID:

Query Match 23.5%; Score 20; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPVR 7  
Db 5 SPVR 8

RESULT 6  
S39012  
proteinnase - Thermus sp.  
C/Species: Thermus sp.  
C/Date: 18-Feb-1994 #sequence\_revision 19-Apr-1996 #text\_change 07-May-1999  
C/Accession: S39012  
R/Freeman, S.A.; Peek, K.; Prescott, M.; Daniel, R.  
Biochem. J. 295, 463-469, 1993  
A/Title: Characterization of a chelator-resistant proteinase from Thermus strain Rt4A2.  
A/Reference number: S39012; MUID:94058984; PMID:8240244  
A/Accession: S39012  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <FRE>  
A/Cross-references: UNIPARC:UPI000008BFF9  
A/Note: 13-Ala was also found

Query Match 23.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 QOATW 15  
Db 3 QSPVTW 8

RESULT 7  
B60763  
endo-1,3-beta-glucanase (EC 3.2.1.-), 40K - Bacillus circulans (strain WL-12) (fragment)  
C/Species: Bacillus circulans  
C/Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C/Accession: B60763  
R/Fiske, M.J.; Tobey-Fletcher, K.L.; Fuchs, R.L.  
J. Gen. Microbiol. 136, 2377-2383, 1990  
A/Title: Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-beta-glucanase  
A/Reference number: A60763; MUID:91178514; PMID:2127800  
A/Accession: B60763  
A/Molecule type: protein  
A/Residues: 1-15 <FIS>  
A/Cross-references: UNIPROT:Q7M110; UNIPARC:UPI000017AC94  
C/Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth on c  
C/Keywords: glycosidase; hydrolase

Query Match 23.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 ATTW 15  
Db 1 ATTW 4

RESULT 8  
A61357  
phyllocaerulein - Sauvage's leaf frog  
C/Species: Phyllomedusa sauvagei (Sauvage's leaf frog)  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C/Accession: A61357  
R/Anastasi, A.; Bertecchini, G.; Cai, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.  
Br. J. Pharmacol. 37, 198-206, 1969  
A/Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like nona  
A/Reference number: A61357; MUID:70005484; PMID:5824931  
A/Accession: A61357  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <ANA>  
A/Cross-references: UNIPROT:Q7LZC4; UNIPARC:UPI000017668D



C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:3/Binding site: sulfate (Tyr) (covalent) #status experimental  
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4% Score 19; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 QOATW 15  
DB 1 QDYTGW 6

## RESULT 9

A61337 caerulein - frog (Hyla caerulea)

C:Species: Hyla caerulea

C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999

C:Accession: A61337

R:Anastasi, A.; Erpamer, V.; Edean, R.

Arch. Biochem. Biophys. 125, 57-68, 1968

A:Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the

A:Reference number: A61337; MUID:68238534; PMID:5649531

A:Accession: A61337

A:Molecule type: protein

A:Residues: 1-10 <AN>

A:Cross-references: UNIPARC:UPI0000126DCC

C:Comment: The last five amino acids and the carboxyl terminal amide group of this neuro

C:Comment: This amphibian skin peptide can cause a sustained lowering of blood pressure

C:Superfamily: gastrin

C:Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid; se

F:4/Binding site: sulfate (Tyr) (covalent) #status experimental

F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4% Score 19; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 EQOATW 15  
DB 1 QOQDTGW 7

## RESULT 10

A29806 acidic proline-rich protein HP43b - golden hamster (fragment)

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993

C:Accession: A29806

R:Mechanico, H.; Ann, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.

J. Biol. Chem. 262, 12344-12350, 1987

A:Title: Induction of proline-rich proteins in hamster salivary glands by isoproterenol

A:Reference number: A29811; MUID:87308247; PMID:3040740

A:Accession: A29806

A:Molecule type: protein

A:Residues: 1-11 <MEH>

A:Cross-references: UNIPARC:UPI000017C60F

Query Match 22.4% Score 19; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSP 5  
DB 4 YEDSP 8

## RESULT 11

A49037 TCR gamma V-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: A49037

R:Esquerre, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.

Bar. J. Immunol. 22, 491-498, 1992

A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T

A:Reference number: A49037; MUID:92164730; PMID:1311262

A:Accession: A49037

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-11 <EZO>

A:Cross-references: UNIPARC:UPI00001154FA; GB:S90637; MID:9246288; PIDN:AAB21547.1; PID:

A:Experimental source: dendritic epidermal T-cell lines

A>Note: sequence extracted from NCBI backbone (NCBI:90637, NCBI:90641)

Query Match 22.4% Score 19; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 QATW 15  
DB 6 RSTW 10

RESULT 12  
B58502 43.2K bile stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004

C:Accession: B58502

R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: B58502

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <BIN>

A:Cross-references: UNIPROT:Q7MID0; UNIPARC:UPI000017A8D4

A:Experimental source: human bile with stones

A>Note: a secondary sequence DVXIGVAGS was also found

Query Match 22.4% Score 19; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSPV 6  
DB 6 NEQPV 10

RESULT 13  
A60458 protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain G02)  
N:Alternate names: protocatechuate oxygenase  
C:Species: Moraxella sp.

C:Date: 20-Feb-1993 #sequence\_revision 20-Feb-1993 #text\_change 07-May-1999

C:Accession: A60458

R:Sterliades, R.; Belmont, J.

Appl. Environ. Microbiol. 55, 340-347, 1989

A:Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Morax

A:Reference number: A60458; MUID:89245845; PMID:2541659

A:Accession: A60458

A:Molecule type: protein

A:Residues: 1-13 <STB>

A:Cross-references: UNIPARC:UPI000017A9FE

A>Note: two forms P and G of the alpha subunit yielded identical amino terminal sequence

Query Match 22.4% Score 19; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 4.1e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 RTEQOATW 15  
 | | : | :  
 Db 3 RTAKFAPTY 11

## RESULT 14

S36887  
 ribosomal protein S14 - Mycobacterium bovis (fragments)  
 C:Species: Mycobacterium bovis  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
 C:Accession: S36887  
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
 FEBS Lett. 331, 9-14, 1993  
 A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac  
 A:Reference number: S36887; MUID:94009653; PMID:8405418  
 A:Accession: S36887  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-2;3-12;13 <OH>  
 A:Cross-references: UNIPARC:UPI0000061DAD; UNIPARC:UPI000011BC65; UNIPARC:UPI000017AD47  
 C:Keywords: protein biosynthesis; ribosome

Query Match 22.4%; Score 19; DB 2; Length 13;  
 Best Local Similarity 37.5%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 VRTEQOAT 13  
 | | : | :  
 Db 6 VKNQRAT 13

## RESULT 15

S74128  
 superoxide dismutase (EC 1.15.1.1) 1 (N1) - Streptomyces coelicolor (fragment)  
 C:Species: Streptomyces coelicolor  
 C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
 C:Accession: S74128  
 R:Kim, E.U.; Kim, H.P.; Hah, Y.C.; Roe, J.H.  
 Eur. J. Biochem. 241, 178-185, 1996  
 A:Title: Differential expression of superoxide dismutases containing N1 and Fe/Zn in Str  
 A:Reference number: S74128; MUID:97054607; PMID:8898904  
 A:Accession: S74128  
 A:Molecule type: protein  
 A:Residues: 1-14 <KIM>  
 A:Cross-references: UNIPARC:UPI000017AE10  
 A:Experimental source: ATCC 10147  
 C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Keywords: metalloprotein; nickel; oxidoreductase; tetramer

Query Match 22.4%; Score 19; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HNDSP 5  
 | | : | :  
 Db 1 HGDLF 5

Search completed: December 12, 2005, 21:18:42  
 Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:59:31 ; Search time 114 Seconds  
(without alignments)  
92.833 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BIOSUM62  
Gapo 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	28.2	10	Q9F9H5_HELIPY	Q9F9H5 helicobacte
2	24	28.2	11	Q6LBJ0_MOUSE	Q6LBJ0 mus musculi
3	23	27.1	11	Q7M504_ASPNG	Q7M504 aspergillus
4	22	25.9	11	Q47602_ECOLI	Q47602 escherichia
5	22	25.9	13	Q50117_MYCLE	Q50117 mycobacteri
6	22	25.9	15	Q7M423_FUSSP	Q7M423 fusarium sp
7	21.5	25.3	15	Q9TS39_PPRIM	Q9TS39 gorilla gor
8	21	24.7	9	Q798K5_STRLI	Q798K5 streptomyce
9	21	24.7	9	Q9R635_CHLTR	Q9R635 chlamydia t
10	21	24.7	11	Q5EDJ3_LBGRN	Q5EDJ3 legionella
11	21	24.7	13	EBE5_HUMAN	EBE5 homo sapien
12	21	24.7	13	Q9SB03_ORISA	Q9SB03 oryza sativ
13	21	24.7	14	Q7IGS6_9HYME	Q7IGS6 andrena n.
14	21	24.7	14	Q9LCS1_AZCVI	Q9LCS1 azotobacter
15	21	24.7	14	Q6SCH4_9GEMI	Q6SCH4 tomato leaf
16	20.5	24.1	14	R1PL_LURCY	R1PL luffa cylin
17	20	23.5	8	Q9T2W0_YEAST	Q9T2W0 saccharomyc
18	20	23.5	9	Q71066_9PARA	Q71066 canine dist
19	20	23.5	10	Q86D30_TRYCR	Q86D30 trypanosoma
20	20	23.5	11	Q8TDA8_HUMAN	Q8TDA8 homo sapien
21	20	23.5	12	Q6JDGO_CANFA	Q6JDGO canis famil
22	20	23.5	12	Q9BOV3_MOUSE	Q9BOV3 mus musculi
23	20	23.5	13	Q718T2_9PARA	Q718T2 newcastle d
24	20	23.5	14	SODN_STRGR	SODN streptomyce
25	20	23.5	14	Q71GM6_9HYME	Q71GM6 andrena eri
26	20	23.5	14	Q6LDN2_BACST	Q6LDN2 bacillus st
27	20	23.5	15	Q71GV6_9HYME	Q71GV6 andrena sim
28	20	23.5	15	Q71H38_9HYME	Q71H38 andrena aur
29	20	23.5	15	Q9RS31_9DEIN	Q9RS31 thermus ch
30	20	23.5	15	Q7M110_BACCI	Q7M110 bacillus ci
31	19	22.4	7	Q8JEB1_9HIV1	Q8JEB1 human immun

32	19	22.4	9	1	CAER_PHYSA	Q71ZC4 phylomedus
33	19	22.4	9	2	Q71H00_9HYME	Q71H00 andrena iso
34	19	22.4	10	1	CAE12_LITCI	P62540 litorea cit
35	19	22.4	10	1	CAE12_LITSP	P62541 litorea sp1
36	19	22.4	10	1	CAER_LITXA	P56264 litorea xan
37	19	22.4	10	2	Q9QVE5_9MURI	Q9QVE5 mus sp. pro
38	19	22.4	10	2	Q33EAI_9NEOB	Q33EAI eleutheroda
39	19	22.4	10	2	P84487_LITCE	P84487 litorea cae
40	19	22.4	12	2	Q7M1D0_9BACT	Q7M1D0 unidentified
41	19	22.4	12	2	Q98Z40_9HIV1	Q98Z40 human immun
42	19	22.4	13	2	Q7YRDI_BISBO	Q7YRDI bison bonas
43	19	22.4	13	2	Q7YRI4_BOVIN	Q7YRI4 bos taurus
44	19	22.4	13	2	P97140_BORBU	P97140 botreilia bu
45	19	22.4	13	2	Q535S7_9PERC	Q535S7 channa argu

## ALIGNMENTS

RESULT 1					
ID	Q9F9H5_HELIPY	PRELIMINARY;	PRT;	10 AA.	
AC	Q9F9H5_				
DT	01-MAR-2001 (TREMBlrel. 16, Created)				
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)				
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)				
DE	Glutamate racemase (Fragment).				
GN	Name=glr;				
OS	Helicobacter pylori (Campylobacter pylori).				
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;				
OC	Helicobacteriaceae; Helicobacter.				
OX	NCBI_TaxID=210;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=Indiat75A;				
RX	MEDLINE=20270152; PubMed=10809702;				
RA	DOI=10.1128/JB.182.11.3210-3218.2000;				
RA	Keruliyte D., Mukhopadhyay A.K., Velapattino B., Su W.W., Pan Z.J.,				
RA	Garcia C., Hernandez V., Valdez Y., Mistry R.S., Gilman R.H., Yuan Y.,				
RA	Gao H., Alarcon T., Lopez-Brea M., Balakrish Nair G., Chowdhury A.,				
RA	Datta S., Shirai M., Nakazawa T., Ally R., Segal I., Wong B.C.,				
RA	Lam S.K., Olat F.O., Boren T., Engstrand L., Torres O., Schneider R.,				
RA	Thomas J.E., Czinn S., Berg D.E.;				
RT	"Differences in genotypes of Helicobacter pylori from different human				
RL	populations.";				
DR	J. Bacteriol. 182:3210-3218(2000).				
FT	EMBL; AF190663; AAG18486.1; -; Genomic_DNA.				
FT	NON TER				
SQ	SEQUENCE 10 AA; 1273 MW; CAD126337B133DC6 CRC64;				
Query Match					
Best Local Similarity 57.1%; Pred. No. 3.1e+03;					
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY	9 EQQATTW 15				
	: :				
DB	1 EKQAKW 7				
RESULT 2					
ID	Q6LBJO_MOUSE				
AC	Q6LBJO_				
DT	05-JUL-2004 (TREMBlrel. 27, Created)				
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)				
DE	Topoisomerase I (Fragment).				
GN	Name=TopI; Synonyms=TOP;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				

```

RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=Balb/c; TISSUE=Liver;
RA MEDLINE=94250690; PubMed=8193161;
RX Baumgartner B., Heiland S., Kunze N., Richter A., Knippers R.;
RT "Conserved regulatory elements in the type I DNA topoisomerase gene
RT promoter of mouse and man.";
RL Biochim. Biophys. Acta 1218:123-127(1994).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=Balb/c; TISSUE=Liver;
RA Baumgartner B.;
RX Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X70958; CA50294.1; -; Genomic_DNA.
DR MGI; MGI:98788; TopI.
DR GO; GO:0006260; P:DNA replication; IMP.
KM Isomerase.
FT NON_TER
SQ SEQUENCE 11 AA; 1240 MW; 95183AD41E721EA CRC64;

Query Match 28.2%; Score 24; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDS 4
DB 7 HNDS 10

RESULT 3
Q7M504_ASPNG PRELIMINARY; PRT; 11 AA.
AC Q7M504;
DT 01-MAR-2004 (TREMBlrel. 26; Created)
DT 01-MAR-2004 (TREMBlrel. 26; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Amino oxidase (Copper-containing) (EC 1.4.3.6) II (Fragment).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP PROTEIN SEQUENCE.
RA Fiebot I., Tamaki H., Ishida H., Pec P., Luhova L., Tsuno H.,
RA Halata M., Asano Y., Kato Y., Matsushita K., Toyana H., Kumagai H.,
RA Adachi O.;
RT "Two distinct quinoprotein amino oxidases are induced by n-butylamine
RT in the mycelia of Aspergillus niger AKU 3302: purification,
RT characterization, cDNA cloning and sequencing.";
RL Eur. J. Biochem. 237:255-265(1996).
DR PIR; S71304; S71304.
DR GO; GO:0008131; F:amine oxidase activity; IEA.
FT NON_TER
SQ SEQUENCE 11 AA; 1158 MW; 21BBPDC4472DC7 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NDSP 5
DB 1 NDSP 4

RESULT 4
Q47602_ECOLI PRELIMINARY; PRT; 11 AA.
AC Q47602;
DT 01-NOV-1996 (TREMBlrel. 01; Created)
DT 01-NOV-1996 (TREMBlrel. 01; Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19; Last annotation update)
DE Release protein (Fragment).

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GN Name=Rease;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63620; AAA24558.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 25.9%; Score 22; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 7.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 RTEQATTW 15
DB 3 RDDQLFTLW 11

RESULT 5
Q50117_MYCLE PRELIMINARY; PRT; 13 AA.
ID Q50117_MYCLE PRELIMINARY;
AC Q50117;
DT 01-NOV-1996 (TREMBlrel. 01; Created)
DT 01-NOV-1996 (TREMBlrel. 01; Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23; Last annotation update)
DE U650W.
OS Mycobacterium lepreae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Robinson K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15184; AAA63055.1; -; Genomic_DNA.
SQ SEQUENCE 13 AA; 1503 MW; CAABP1429DEDS12 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 9.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DSPVR 7
DB 3 DEPRV 7

RESULT 6
Q7M423_FUSSP PRELIMINARY; PRT; 15 AA.
ID Q7M423_FUSSP PRELIMINARY;
AC Q7M423;
DT 01-MAR-2004 (TREMBlrel. 26; Created)
DT 01-MAR-2004 (TREMBlrel. 26; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Fumarate hydratase (EC 4.2.1.2) (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP PROTEIN SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyura Y., Ueno Y., Tabuchi K., Tsugita A.;
RL Submitted (OCT-1994) to the PIR data bank.

```

DR PIR; PA0062; PA0062.  
 DR GO; GO:0004333; F: fumarate hydratase activity; IEA.  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1668 MW; 805C8118C239DE05 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 15;  
 Best Local Similarity 55.6%; Pred. No. 1.1e+04;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12  
 DB 1 SQRTESDA 9

RESULT 7  
 ID Q9TS39\_9PRIM PRELIMINARY; PRT; 15 AA.  
 AC Q9TS39;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Dopamine D5 (Fragment).  
 OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Gorilla.  
 OX NCBI\_TaxID=9593;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92068184; PubMed=1958184;  
 RA Nguyen T., Sunahara R., Marchese A., Van Tol H.H., Seeman P.,  
 RA O'Dowd B.F.;  
 RT "Transcription of a human dopamine D5 pseudogene";  
 RL Biochem. Biophys. Res. Commun. 181:16-21(1991).  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1637 MW; 39D8326BA63B908 CRC64;

Query Match 25.3%; Score 21.5; DB 2; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 1 HNDSPVTEQOATW 15  
 DB 1 HRD-----QNASW 8

RESULT 8  
 ID Q798K5\_STRLI PRELIMINARY; PRT; 9 AA.  
 AC Q798K5;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE AmB protein (Fragment).  
 GN Name=amB.  
 OS Streptomyces lividans.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=1916;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=96332731; PubMed=9666116; DOI=10.1016/S0378-1119(98)00265-0;  
 RA Yin X.H., Getraud C., Franco F.X., Guerin M., Virolle M.J.;  
 RT "amC, another amyloid gene maps close to the amB locus in  
 RT Streptomyces lividans TK24.";  
 RL Gene 215:171-180(1998).  
 DR EMBL; Z86113; CAB06815.1; -, Genomic\_DNA.  
 FT NON\_TER 9  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 970 MW; F334C75A1A44871 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.2e+06;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVR 7  
 DB 4 NTSPAR 9

RESULT 9  
 ID Q9R635\_CHLTR PRELIMINARY; PRT; 9 AA.  
 AC Q9R635;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Major outer membrane protein variable domain IV, MOMP VD IV  
 DE (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92040090; PubMed=1718870;  
 RA Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.;  
 RT "Functional and structural mapping of Chlamydia trachomatis species-  
 RT specific major outer membrane protein epitopes by use of neutralizing  
 RT monoclonal antibodies";  
 RL Infect. Immun. 59:4147-4153(1991).  
 DR PIR; S16034; S16034.  
 FT NON\_TER 1  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTW 15  
 DB 1 TTW 3

RESULT 10  
 ID Q5EDJ3\_LEGN PRELIMINARY; PRT; 11 AA.  
 AC Q5EDJ3;  
 DT 10-MAY-2005 (TREMBLrel. 30, Created)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DE Putative acyl carrier protein (Fragment).  
 OS Legionella pneumophila.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.  
 OX NCBI\_TaxID=446;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=02/41.  
 RA Newton H.J., Hartland E.L.;  
 RT "Subtractive hybridization reveals DNA fragments present in Legionella  
 RT pneumophila, strain 02/41, and absent in Legionella mldadei, strain  
 RT 02/42.";  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY902880; AAM83806.1; -, Genomic\_DNA.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1159 MW; DCC78B8601ADC66 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 EQOAT 13  
 DB 3 QOQAT 7

```
RESULT 11
EP65 HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=90004678; PubMed=2507249;
RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins.";
RL Ciba Found. Symp. 145:102-118(1989).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR GO: GO:0005737; C:cytoplasm; NAS.
KW Direct protein sequencing; Glycoprotein.
FT CARBOHYD 2
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;

Query Match 24.7%; Score 21; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSPV 6
DB 1 DSPV 4

RESULT 12
Q9SB03 ORYSA PRELIMINARY; PRT; 13 AA.
ID Q9SB03_ORYSA
AC Q9SB03;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Waxy (Fragment).
OS Name=Waxy;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98384837; PubMed=9718725;
RA Hirano H., Eizuguchi M., Sano Y.;
RT "A single base change altered the regulation of the Waxy gene at the
RT post-transcriptional level during domestication of rice.";
RL Mol. Biol. Evol. 15:978-987(1998).
DR EMBL; AB008794; BAA32471.1; -; Genomic_DNA.
DR Gramene; Q9SB03; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1281 MW; 999F8DE570FC5A1 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 1.4e+04;
```

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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 SPVRTGQART 14
DB 2 SALTTSQATS 12

RESULT 13
Q71GS6 9HYME PRELIMINARY; PRT; 14 AA.
ID Q71GS6_9HYME
AC Q71GS6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena n. sp. 'goth'.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205171;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Larkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF04376; AAG07723.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1692 MW; 79E3B922A4E7BE5B CRC64;

Query Match 24.7%; Score 21; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 1.5e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPV RTE 9
DB 6 NEIPMTK 13

RESULT 14
Q9LCS1 AZOVI PRELIMINARY; PRT; 14 AA.
ID Q9LCS1_AZOVI
AC Q9LCS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Levan sucrase (Fragment).
OS Name=sacB;
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DW136;
RA Maldonado R., Casadesus J.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249381; CAB76429.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1623 MW; 8DC9108BA1B18745 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPV RTEQ 11
DB 5 NDSILMDQTF 14

RESULT 15
```

Q65CH4\_9GEMI  
ID Q65CH4\_9GEMI PRELIMINARY; PRT; 14 AA.  
AC Q65CH4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Coat protein (Fragment).  
GN Name=AV1;  
OS Tomato leaf curl Sinaloa virus.  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=71186;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Nil;  
RX PubMed=15789265; DOI=10.1007/s00705-005-0509-x;  
RA Rojas A., Kvarnheden A., Marcenaro D., Valkonen J.P.T.;  
RT "Sequence characterization of Tomato leaf curl Sinaloa virus and  
RT Tomato severe leaf curl virus: Phylogeny of New World begomoviruses  
RT and detection of recombination.";  
RL Arch. Viro. 150:1281-1291(2005).  
DR EMBL; AJ508778; CAD48516.1; -; Genomic\_DNA.  
KW Capsid protein.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1573 MW; 571284313A0594D3 CRC64;  
Query Match 24.7%; Score 21; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 11 QATTW 15  
:| |  
Db 7 KATAW 11

Search completed: December 12, 2005, 21:17:23  
Job time : 116 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 81.3362 Seconds  
(without alignments)  
81.030 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNSPVRTTEQATTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	ADRI0602	Adri0602 Cat IGE e
2	85	100.0	431	ADG73237	ADG73237 Cat immun
3	85	100.0	496	ABP96580	ABP96580 Cat IGE h
4	85	100.0	496	ABU09338	ABU09338 Feline Ig
5	85	100.0	496	ABU09336	ABU09336 Feline Ig
6	85	100.0	496	ADG73251	ADG73251 Cat parti
7	85	100.0	496	ADG73225	ADG73225 Cat parti
8	48	56.5	15	ADRI0601	Adri0601 Dog IGE e
9	48	56.5	312	AAI79995	AAI79995 Dog immun
10	48	56.5	417	AAW23067	AAW23067 Canine Ig
11	48	56.5	426	AAK97753	AAK97753 Canine Ig
12	48	56.5	426	ABP96583	ABP96583 Dog IGE h
13	47	55.3	84	ABU55745	ABU55745 Tree coct
14	46	54.1	449	ABR60974	ABR60974 Drosophyl
15	45	52.9	321	AAE12007	AAE12007 Streptomy
16	45	52.9	321	ABG73760	ABG73760 S. catlie
17	44	51.8	673	ABR71738	ABR71738 Drosophyl
18	43	50.6	470	ADG27897	ADG27897 Bacterial
19	43	50.6	696	ADK67175	ADK67175 Plant ful
20	42	49.4	87	AAU55965	AAU55965 Propionib
21	42	49.4	87	ABM52485	ABM52485 Propionib
22	42	49.4	178	ABR83494	ABR83494 Human zin
23	42	49.4	178	ADB65732	ADB65732 Human pro
24	42	49.4	197	ABO60445	ABO60445 Human gen

25	42	49.4	296	ADA54799	ADA54799 Human pro
26	42	49.4	296	AAO27216	AAO27216 Human zin
27	42	49.4	349	AAW79729	AAW79729 Human pro
28	42	49.4	430	AAW78745	AAW78745 Human pro
29	42	49.4	536	ADY18750	ADY18750 PRO polyp
30	42	49.4	537	AAE33775	AAE33775 Human nuc
31	41	48.2	70	AAU59982	AAU59982 Propionib
32	41	48.2	70	ABM56501	ABM56501 Propionib
33	41	48.2	152	AAI18098	AAI18098 Peptide #
34	41	48.2	152	ABR37133	ABR37133 Peptide #
35	41	48.2	152	AAU30608	AAU30608 Peptide #
36	41	48.2	152	ABR22444	ABR22444 Protein #
37	41	48.2	152	AAW70271	AAW70271 Human bon
38	41	48.2	152	AAW57851	AAW57851 Human bra
39	41	48.2	152	AAU05733	AAU05733 Peptide #
40	41	48.2	349	AAU30476	AAU30476 Novel hum
41	41	48.2	647	AAU92695	AAU92695 C glutami
42	41	48.2	812	ABG19065	ABG19065 Novel hum
43	41	48.2	1194	ADP29882	ADP29882 Human sec
44	41	48.2	1527	ABG08603	ABG08603 Novel hum
45	41	48.2	1664	ABG14228	ABG14228 Novel hum

## ALIGNMENTS

RESULT 1	
ID	ADRI0602 standard; peptide, 15 AA.
ADRI0602	
AC	ADRI0602;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.
KW	Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody; cat.
XX	
OS	Felis catus.
XX	
PN	WO2004065936-A2.
XX	
PD	05-AUG-2004.
XX	
PF	15-JAN-2004; 2004WO-US003566.
XX	
PR	16-JAN-2003; 2003US-0440472P.
XX	
PA	(UNNC-) UNIV NORTH CAROLINA STATE.
XX	
PI	Hammerberg B;
XX	
DR	WPI; 2004-593545/57.
XX	
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful for testing an allergen reactivity of IGE sample, detecting mammalian IGE or treating asthma or anaphylactic shock.
PT	
PS	Example 6; Page 9; 14pp; English.
XX	
CC	The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IGE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IGE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IGE corresponding to amino acid residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
CC either pig or human epsilon-chains of IgE. The present sequence is the  
CC cat IgE 5.91 recognition site.

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.7e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATW 15  
|||||  
DB 1 HNDSPVTEQOATW 15

RESULT 2

ADG73237 standard; protein; 431 AA.

XX  
AC ADG73237;

DT 11-MAR-2004 (first entry)

DE Cat immunoglobulin E (IgE) constant region.

XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;  
KM immune response; IgE-mediated response; allergy; cat; constant region.

XX  
OS Felis catus.

XX  
PN US2003216565-A1.

XX  
PD 20-NOV-2003.

XX  
PF 07-APR-2003; 2003US-00409772.

XX  
PR 07-JAN-1999; 99US-0115033P.

XX  
PR 07-JAN-2000; 2000US-00479614.

XX  
PA (MCCA/) MCCALL C.

XX  
PA (WEBE/) WEBER E.

XX  
PI Mccall C, Weber E;

XX  
XX WPI; 2004-010802/01.

XX  
DR N-PSDB; ADG73236.

XX  
PT New isolated nucleic acid molecule encoding a portion of a feline IgE

XX  
PT heavy chain protein, useful for treating and/or eliciting feline immune

XX  
PT responses for IgE-mediated responses, such as allergies.

XX  
PS Claim 12; SEQ ID NO 14; 44pp; English.

XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a

XX  
CC portion of a feline IgE heavy chain protein. The methods and compositions

XX  
CC of the present invention are useful for eliciting feline immune responses

XX  
CC for and/or treating IgE-mediated responses, such as allergies. This is

XX  
CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.

XX  
SQ Sequence 431 AA;

Query Match 100.0%; Score 85; DB 8; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATW 15  
|||||  
DB 362 HNDSPVTEQOATW 376

RESULT 3

ABP96580  
ID ABP96580 standard; protein; 496 AA.

XX  
AC ABP96580;

XX  
DT 28-MAY-2003 (first entry)

DE Cat IgE heavy chain amino acid sequence SEQ ID NO:25.

XX  
XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;

XX immune response; major histocompatibility complex; MHC; immunogenic;

XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;

XX dermatological; antiinflammatory; IgE-mediated condition; food allergy;

XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;

XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;

XX  
XX urticaria hives.

XX  
OS Felis catus.

XX  
PN W02003015716-A2.

XX  
XX 27-FEB-2003.

XX  
PF 08-AUG-2002; 2002WO-US026986.

XX  
PR 13-AUG-2001; 2001US-0312120P.

XX  
PA (IGET-) IGE THERAPEUTICS INC.

XX  
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX  
XX WPI; 2003-268242/26.

XX  
DR Example 7; Page 145-147; 187pp; English.

XX  
XX The present invention describes a method (M1) for identifying peptides

XX  
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin

XX  
CC E (IgE), comprising providing a test peptide (T) suspected of being able

XX  
CC to bind to major histocompatibility complex (MHC) class I molecule, and

XX  
CC evaluating (T) for ability to elicit in a mammal a CTL response to

XX  
CC naturally processed and presented IgE peptides, where a peptide that

XX  
CC induces such a response is identified. Also described are compositions:

XX  
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);

XX  
CC (C2) comprising at least one isolated polynucleotide encoding (I); and

XX  
CC (C3) comprising antigen-presenting cells that recognise at least one (I).

XX  
CC Where C1-3 are able to bind to at least one MHC class I molecule and to

XX  
CC elicit in a mammal a CTL response to naturally processed and presented

XX  
CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,

XX  
CC vasotropic, dermatological, antiinflammatory and cyrostatic activities,

XX  
CC and can be used as inducers of a CTL response against IgE, and in

XX  
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a

XX  
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as

XX  
CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic

XX  
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are

XX  
CC useful for treating atopic hypersensitivity conditions (such as allergic

XX  
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-

XX  
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria

XX  
CC hives). The present sequence represents an IgE heavy chain amino acid

XX  
CC sequence, which is given in an example from the present invention

XX  
SQ Sequence 496 AA;

Query Match 100.0%; Score 85; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATW 15  
|||||

Db 427 HNDSVPRTEQOATW 441

RESULT 4  
ABU09338  
ID ABU09338 standard; protein; 496 AA.  
XX  
XX ABU09338;  
XX  
XX 27-JUN-2003 (first entry)  
XX  
XX Feline IGE epsilon heavy chain #2.  
XX  
XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
XX IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
XX antibody technology; antiallergic; antiparasitic; cytostatic.  
XX  
XX Felis catus.  
XX  
XX US2003013183-A1.  
XX  
XX 16-JAN-2003.  
XX  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX  
XX (MCCA/) MCCALL C.  
XX (WEBER/) WEBER E.  
XX  
XX Mccall C, Weber E;  
XX  
XX MPI; 2003-391997/37.  
XX N-PSDB; ABX95715.  
XX  
XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or  
XX light chain protein, useful for treating feline IGE-mediated responses  
XX e.g. allergies, parasitic infections or neoplasia.  
XX  
XX Claim 1; Page 37-39; 45pp; English.  
XX  
XX The present invention relates to the isolation of feline immunoglobulin E  
XX (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the  
XX polynucleotide sequences encoding them. The sequences of the invention  
XX are useful for treating feline IGE-mediated immune responses (e.g.  
XX allergies, parasitic infections or neoplasia), in vaccine technology,  
XX small molecule/antibody technology, molecular biology, and various  
XX immunological techniques related to feline IGE and its functions. The  
XX present sequence represents feline IGE epsilon heavy chain #2  
XX  
XX Sequence 496 AA;  
XX  
XX Query Match 100.0%; Score 85; DB 6; Length 496;  
XX Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 HNDSVPRTEQOATW 15  
Db 427 HNDSVPRTEQOATW 441

RESULT 5  
ABU09336  
ID ABU09336 standard; protein; 496 AA.  
XX  
XX ABU09336;  
XX  
XX 27-JUN-2003 (first entry)  
XX  
XX Feline IGE epsilon heavy chain #1.  
XX  
XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
XX IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
XX

KW antibody technology; antiallergic; antiparasitic; cytostatic.  
XX  
XX Felis catus.  
XX  
XX Key Location/Qualifiers  
XX Region 66..496  
XX /note= "This sequence is given as SEQ ID No:14 and is  
XX specifically claimed in Claim 12"  
XX Region 284..309  
XX /note= "This sequence is given as SEQ ID No:11 and is  
XX specifically claimed in Claim 9"  
XX Region 288..305  
XX /note= "This sequence is given as SEQ ID No:8 and is  
XX specifically claimed in Claim 10"  
XX Region 291..302  
XX /note= "This sequence is given as SEQ ID No:5 and is  
XX specifically claimed in Claim 11"  
XX  
XX US2003013183-A1.  
XX  
XX 16-JAN-2003.  
XX  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX  
XX (MCCA/) MCCALL C.  
XX (WEBER/) WEBER E.  
XX  
XX Mccall C, Weber E;  
XX  
XX MPI; 2003-391997/37.  
XX N-PSDB; ABX95715.  
XX  
XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or  
XX light chain protein, useful for treating feline IGE-mediated responses  
XX e.g. allergies, parasitic infections or neoplasia.  
XX  
XX Claim 1; Page 24-25; 45pp; English.  
XX  
XX The present invention relates to the isolation of feline immunoglobulin E  
XX (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the  
XX polynucleotide sequences encoding them. The sequences of the invention  
XX are useful for treating feline IGE-mediated immune responses (e.g.  
XX allergies, parasitic infections or neoplasia), in vaccine technology,  
XX small molecule/antibody technology, molecular biology, and various  
XX immunological techniques related to feline IGE and its functions. The  
XX present sequence represents feline IGE epsilon heavy chain #1  
XX  
XX Sequence 496 AA;  
XX  
XX Query Match 100.0%; Score 85; DB 6; Length 496;  
XX Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 HNDSVPRTEQOATW 15  
Db 427 HNDSVPRTEQOATW 441

RESULT 6  
ADG73251  
ID ADG73251 standard; protein; 496 AA.  
XX  
XX ADG73251;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
XX Cat partial immunoglobulin E (IGE) heavy chain #2.  
XX  
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;  
XX immune response; IGE-mediated response; allergy; cat; heavy chain.  
XX

OS	Felis catus.
XX	US2003216565-A1.
XX	20-NOV-2003.
XX	07-APR-2003; 2003US-00409772.
PE	
XX	07-JAN-1999; 99US-0115033P.
PR	07-JAN-2000; 2000US-00479614.
XX	(MCCA/) MCCALL C.
PA	(WEBE/) WEBER E.
XX	
EI	Mccall C, Weber E;
XX	
DR	WPI; 2004-010802/01.
DR	N-PSTDB; ADG73250.
XX	
PT	New isolated nucleic acid molecule encoding a portion of a feline IGE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
PS	Claim 8; SEQ ID NO 29; 44pp: English.
XX	
CC	The invention describes an isolated nucleic acid molecule (1) encoding a portion of a feline IGE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy chain.
CC	
XX	
SQ	Sequence 496 AA;
Query Match	100.0%; Score 85; DB 8; Length 496;
Best Local Similarity	100.0%; Pred. No. 2.9e+06;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
Oy	1 HNDSPVRTEQQATTW 15       427 HNDSPVRTEQQATTW 441
Db	
RESULT 7	
ID	ADG73225
XX	ADG73225 standard; protein; 496 AA.
AC	ADG73225;
XX	
DT	11-MAR-2004 (first entry)
DE	Cat partial immunoglobulin E (IGE) heavy chain #1.
KW	antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E; immune response; IGE-mediated response; allergy; cat; heavy chain.
XX	
OS	Felis catus.
XX	
PN	US2003216565-A1.
XX	
PD	20-NOV-2003.
XX	
PF	07-APR-2003; 2003US-00409772.
XX	
PR	07-JAN-1999; 99US-0115033P.
RR	07-JAN-2000; 2000US-00479614.
XX	
PA	(MCCA/) MCCALL C.
XX	(WEBE/) WEBER E.
XX	
EI	Mccall C, Weber E;
XX	
DR	WPI; 2004-010802/01.

DR	N-PSDB; ADG73224.
XX	
PT	New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
PT	
XX	
PS	Claim 8; SEQ ID NO 2; 44pp: English.
XX	
CC	The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy chain.
CC	
XX	
SQ	Sequence 496 AA;
Query Match	100.0%; Score 85; DB 8; Length 496;
Best Local Similarity	100.0%; Pred. NO. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 HNDSPVTEQQATTW 15             
Db	427 HNDSFVTEQQATTW 441
RESULT 8	
ID	ADRI0601
ID	ADRI0601 standard; peptide; 15 AA.
AC	ADRI0601;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
XX	
KM	Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW	anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX	
OS	Canis familiaris.
XX	
PN	WO2004065936-A2.
XX	
PD	05-AUG-2004.
XX	
PX	15-JAN-2004; 2004WO-US003566.
XX	
PR	16-JAN-2003; 2003US-0440472P.
XX	
PA	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	
PI	Hammerberg B;
XX	
DR	WPI; 2004-593545/57.
XX	
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful for testing an allergen reactivity of IGE sample, detecting mammalian IGE or treating asthma or anaphylactic shock.
PT	
XX	
PS	Example 6; Page 9; 14pp: English.
XX	
CC	The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IGE epitope, where the epitope is between amino acids 146-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IGE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IGE corresponding to amino acid residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.

XX Sequence 15 AA;

Query Match 56.5%; Score 48; DB 8; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 0.23;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPTREQOQAT 14  
 |||::|:  
 Db 2 NDSPTQDQYTT 14

RESULT 9  
 ID AAY79995 standard; protein; 312 AA.

XX AAY79995;  
 XX 15-MAY-2000 (first entry)

XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

XX MO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

PS Example 1; Page 66-68; 155pp; English.

CC The present invention describes immunoglobulin E (IGE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IGE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IGE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IGE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX Sequence 312 AA;

Query Match 56.5%; Score 48; DB 3; Length 312;  
 Best Local Similarity 61.5%; Pred. No. 7;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 OY 2 NDSPTREQOQAT 14  
 |||::|:  
 Db 256 NDSPTQDQYTT 268

RESULT 10  
 ID AAW23067 standard; protein; 417 AA.

XX AAW23067;

XX 30-JUN-2005 (revised)

XX 16-JUN-2005 (revised)

XX 19-FEB-1998 (first entry)

XX Canine IGE heavy chain constant region (exon 1-4 product).

XX IGE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX Canis familiaris.

XX Key Location/Qualifiers

XX Misc-difference 55 /note= "encoded by ACC"

XX Misc-difference 56 /note= "encoded by TAC"

XX Misc-difference 67 /note= "encoded by GCC"

XX Misc-difference 83 /note= "encoded by NNT"

XX Misc-difference 174 /note= "encoded by GGN"

XX Misc-difference 175 /note= "encoded by NNG"

XX Misc-difference 176 /note= "encoded by TGN"

XX Misc-difference 203 /note= "encoded by TCC"

XX Misc-difference 204 /note= "encoded by GAC"

XX MO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEX LAB INC.

XX Mermer B, Harris RA, Sieffring AE;

XX WPI; 1997-425031/39.

XX N-PSDB; AAT79278.

XX Isolated canine IGE heavy chain constant region DNA - useful to develop  
 PT products for treatment of canine allergies and for immunomodulation in  
 PT dogs.

XX Disclosure; Page 35-39; 59pp; English.

PS This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IGE  
 XX heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat Type I immediate hypersensitivity, and for immunomodulation

CC Revised record issued on 30-JUN-2005 : Typo in comments  
XX Sequence 417 AA;  
SQ

Query Match 56.5%; Score 48; DB 2; Length 417;  
Best Local Similarity 61.5%; Pred. No. 9.8;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFPRTEQQAATT 14  
|||:::|  
Db 353 NDSPIQTDQYTTT 365

RESULT 11  
AAR97753  
ID AAR97753 standard; protein; 426 AA.  
XX  
AC AAR97753;  
XX  
DT 28-AUG-1996 (first entry)  
XX  
DE Canine IGE.  
XX  
KW IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.  
XX  
OS Canis familiaris.  
XX  
PN MO9614867-A1.  
XX  
PD 23-MAY-1996.  
XX  
PF 03-NOV-1995; 95WO-US013795.  
XX  
PR 09-NOV-1994; 94US-00336583.  
PR 09-NOV-1994; 94US-00336891.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Hollis GF, Patel MD;  
XX  
DR WPI: 1996-277321/28.  
DR N-PSDB; AAT29824.  
XX  
XX New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense  
PT therapy, assays, drug screening, etc.  
XX  
PS Claim 11; Page 29-30; 49pp; English.  
XX  
CC The canine IGE amino acid sequence (AAR97753) was deduced from an  
CC isolated gene (AAR29824) obtd. from a canine liver DNA library. The  
CC cloning of the IGE gene allows produ. of large quantities of recombinant  
CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE  
CC can be used in drug development (e.g. small molecule screening, assay  
CC development and anti-IGE antibody generation). Fragments of IGE can be  
CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new  
CC sequence information permits targeted modulation of IGE-mediated immune  
CC responses  
CC  
XX  
SQ Sequence 426 AA;

Query Match 56.5%; Score 48; DB 2; Length 426;  
Best Local Similarity 61.5%; Pred. No. 10;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFPRTEQQAATT 14  
|||:::|  
Db 358 NDSPIQTDQYTTT 370

RESULT 12  
ABP96583  
ID ABP96583 standard; protein; 426 AA.  
XX

AC ABP96583;  
XX  
DT 28-MAY-2003 (first entry)  
XX  
DE Dog IGE heavy chain amino acid sequence SEQ ID NO:28.  
XX  
KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
KW immune response; major histocompatibility complex; MHC; immunogenic;  
KW antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;  
KW dermatological; antiinflammatory; IGE-mediated condition; food allergy;  
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
KW urticaria hives.  
XX  
XX Canis familiaris.  
XX  
PN WO2003015716-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 08-AUG-2002; 2002WO-US026986.  
XX  
PR 13-AUG-2001; 2001US-0312120P.  
XX  
PA (IGET-) IGE THERAPEUTICS INC.  
XX  
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
XX  
DR WPI: 2003-268242/26.  
XX  
DT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
PT against IGE, by identifying peptide eliciting CTL response to IGE  
PT peptides naturally presented by major histocompatibility complex class I  
PT protein.  
XX  
PS Example 7; Page 152-154; 187pp; English.  
XX  
XX The present invention describes a method (M1) for identifying peptides  
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
CC E (IGE), comprising providing a test peptide (T) suspected of being able  
CC to bind to major histocompatibility complex (MHC) class I molecule, and  
CC evaluating (T) for ability to elicit in a mammal a CTL response to  
CC naturally processed and presented IGE peptides, where a peptide that  
CC induces such a response is identified. Also described are compositions:  
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
CC elicit in a mammal a CTL response to naturally processed and presented  
CC IGE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,  
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
CC and can be used as inducers of a CTL response against IGE, and in  
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
CC useful for treating atopic hypersensitivity conditions (such as allergic  
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
CC hives). The present sequence represents an IGE heavy chain amino acid  
CC sequence, which is given in an example from the present invention  
CC  
XX  
SQ Sequence 426 AA;

Query Match 56.5%; Score 48; DB 6; Length 426;  
Best Local Similarity 61.5%; Pred. No. 10;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFPRTEQQAATT 14  
|||:::|  
Db 358 NDSPIQTDQYTTT 370

RESULT 13  
 ABUS5745  
 ID ABUS5745 standard; protein; 84 AA.  
 XX  
 AC ABUS5745;  
 XX  
 DT 17-MAR-2003 (first entry)  
 XX  
 DE Tree cotton growth regulating protein, GAGREP1.  
 XX  
 KM 86; plant; growth regulating protein; PSK; phytoosulphokine-alpha;  
 KM transgenic; marker-assisted breeding; agriculture; horticulture.  
 XX  
 OS Gossypium arboreum.  
 OS  
 PN WO200283901-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 11-APR-2002; 2002WO-EP004035.  
 XX  
 PR 12-APR-2001; 2001US-0283313P.  
 XX  
 PA (CROP-) CROPPESIGN NV.  
 PA (SAUT/) SAUTER M.  
 PI Sauter M, Lonblecke R, Mironov V, Frankard V, Dillen W;  
 PI Lejeune P, Broekaert W;  
 DR WPI; 2003-093023/08.  
 DR N-PSDB; ABX74222.  
 XX  
 PT New isolated GREP nucleic acids and polypeptides controlling or modifying  
 PT the growth characteristics of a plant, useful for a wide application in  
 PT agricultural and horticultural practices, and in vitro plant cell and  
 PT tissue culture.  
 XX  
 PS Claim 5; Fig 22; 156pp; English.  
 XX  
 CC The invention relates to a new isolated nucleic acid encoding a growth  
 CC regulating protein (GREP), where the protein conforms to the GREP  
 CC signature sequence appearing as ABUS5722, and the GREP proteins. Also  
 CC included are a vector comprising a GREP nucleic acid, or a vector  
 CC encoding the rice growth regulating polypeptide OsPSK (phytoosulphokine-  
 CC alpha) where the growth regulating proteins regulate growth and/or  
 CC development response in intact plants, a GREP transgenic plant, a  
 CC transgenic plant comprising the vector, seed/pollen and a harvestable  
 CC part of propagation material from the transgenic plant, a host cell  
 CC comprising the GREP nucleic acid, an antisense molecule consisting of 14-  
 CC 100 nucleotides targeted to the GREP signature nucleotide sequence  
 CC appearing as ABX74197, an anti-GREP antibody which specifically  
 CC recognises a GREP or its fragment, a method for altering growth and/or  
 CC activity of a plant or plant cell/storage organ comprising modulating the  
 CC level and/or activity of a GREP or the rice growth regulating peptide  
 CC OsPSK, a method for downregulating levels of a GREP or OsPSK gene product  
 CC or its activity (comprising administering or exposing GREP or OsPSK  
 CC antibodies or gene products to cells, tissues or organs of a plant) a  
 CC method for identifying an allele with desired features of a gene encoding  
 CC a GREP which comprises isolating alleles for a GREP and testing the  
 CC features of the allele by expression in a transgenic plant, a method for  
 CC identifying an allele of GREP and selecting an allele with desired  
 CC features which comprises the use of genes encoding GREP, or sequences  
 CC located in the genome in the neighbourhood of GREP genes, as molecular  
 CC markers for different GREP alleles and selecting specific GREP alleles by  
 CC marker-assisted breeding and a method for identifying regulatory  
 CC sequences of GREP growth regulating polypeptide genes. The methods and  
 CC compositions are for controlling or modifying the growth characteristics  
 CC of a plant or its organs and tissues, useful for a wide application in  
 CC agricultural and horticultural practices, and in vitro plant cell and  
 CC tissue culture. The present sequence is a growth regulating protein  
 XX  
 SQ Sequence 84 AA;

Query Match 55.3%; Score 47; DB 6; Length 84;  
 Best Local Similarity 61.5%; Pred. No. 2.4;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 NDSPVTRTEQOATT 14  
 DB 32 NDSPAKTQSGGTT 44  
 RESULT 14  
 ABB60974  
 ID ABB60974 standard; protein; 449 AA.  
 XX  
 AC ABB60974;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 9714.  
 XX  
 KM Drosophila; developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 OS  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US0009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 PA  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 PI  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL05077.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 9714; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 449 AA;  
 QY 1 HNDSPVTRTEQOATTW 15  
 DB 133 HNDGFVRCPERBALTW 147  
 RESULT 15  
 AAE12007  
 ID AAE12007 standard; protein; 321 AA.  
 XX  
 AC AAE12007;

```

XX 18-DEC-2001 (first entry)
DT
XX Streptomycetes cattleya modified isopenicillin N synthetase (IPNS) .
DE
XX Isopenicillin N synthetase; IPNS; antibiotic; penicillin; oxygenase;
XX non-haeme iron (II) dependent family; oxidase; mutant; mutacin.
XX Streptomycetes cattleya.
OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 211 /note= "Wild type Glu substituted with Arg"
XX
XX US6284483-B1.
XX
XX 04-SEP-2001.
XX
XX 06-OCT-1999; 99US-00413231.
XX
XX 06-OCT-1999; 99US-00413231.
XX
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX Dilley DR, Kadyrzhanova DK, Wang Z, Warner TM;
XX
XX WPI; 2001-615433/71.
XX
XX Method for producing antibiotics, particularly penicillin G or V,
XX comprises employing a modified isopenicillin N synthetase, in either an
XX organism or a cell-free system under the control of bicarbonate.
XX
XX Claim 2; Col 37-38; 27pp; English.
XX
XX The invention relates to a modified enzyme of a non-haeme iron (II)
XX dependent family of oxygenases and oxidases which renders the enzyme
XX dependent on bicarbonate for activity. The invention also related to a
XX method for producing penicillin G or V comprises employing a modified
XX enzyme, particularly isopenicillin N synthetase (IPNS), in either an
XX organism or a cell-free system, under the control of bicarbonate. The
XX modified enzymes are IPNS, deacetoxycephalosporin C synthetase (DAOCS)
XX and deacetylcephalosporin C synthetase (IDACS). The method is useful for
XX producing antibiotics, particularly penicillin G or V. The method is
XX useful for making organisms useful for making an antibiotic dependent on
XX bicarbonate to make the antibiotic. The present sequence is Streptomycetes
XX cattleya modified isopenicillin N synthetase showing an Arg211 in place
XX of Glu211
XX
XX Sequence 321 AA;
SQ
XX
XX Query Match 52.9%; Score 45; DB 4; Length 321;
XX Best Local Similarity 50.0%; Pred. No. 25;
XX Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 NDBSPRTQOATW 15
XX | : | : | : | : |
XX 61 NESTTMTDRSTW 74

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Search completed: December 12, 2005, 20:30:27  
 Job time : 83.3362 secs



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## OM protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 20.431 Seconds  
(without alignments)  
60.699 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQOATW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	431	2	US-09-479-614-14
2	85	100.0	496	2	US-09-479-614-2
3	85	100.0	496	2	US-09-479-614-29
4	48	56.5	108	2	US-09-281-760E-37
5	48	56.5	312	2	US-09-701-623C-2
6	48	56.5	426	1	US-08-336-583-2
7	48	56.5	426	4	PCT-US95-13795-2
8	46	54.1	210	2	US-09-270-767-45299
9	45	52.9	321	2	US-09-413-231-8
10	44	51.8	181	2	US-09-270-767-43758
11	42	49.4	178	2	US-10-104-047-3886
12	41	48.2	534	2	US-09-605-703B-1364
13	41	48.2	534	2	US-09-605-703B-1362
14	40	47.1	540	2	US-09-949-016-8465
15	40	47.1	540	2	US-09-949-016-9052
16	39	45.9	225	2	US-09-252-991A-17094
17	39	45.9	655	2	US-08-556-422A-3
18	39	45.9	771	1	US-08-121-713D-54
19	39	45.9	771	1	US-08-835-268-54
20	39	45.9	771	1	US-09-060-692-54
21	39	45.9	771	2	US-08-833-391-54
22	39	45.9	771	2	US-09-060-610-54
23	39	45.9	771	4	PCT-US94-10151A-54
24	38	44.7	127	2	US-09-270-767-3906
25	38	44.7	127	2	US-09-270-767-54223
26	38	44.7	528	2	US-09-356-806-8
27	38	44.7	528	2	US-09-949-016-6999

28	38	44.7	530	2	US-09-180-852-2	Sequence 2, Appli
29	38	44.7	649	2	US-09-489-039A-11880	Sequence 11880, A
30	38	44.7	704	2	US-09-107-532A-5612	Sequence 5612, Ap
31	38	44.7	1092	2	US-09-134-000C-6291	Sequence 6291, Ap
32	37.5	44.1	447	2	US-09-252-991A-25916	Sequence 25916, A
33	37.5	44.1	1124	2	US-09-605-703B-2576	Sequence 2576, Ap
34	37	43.5	113	2	US-09-902-540-11193	Sequence 11193, A
35	37	43.5	116	2	US-09-513-959C-8156	Sequence 8156, Ap
36	37	43.5	236	2	US-09-248-796A-15717	Sequence 15717, A
37	37	43.5	249	2	US-09-134-001C-4442	Sequence 4442, Ap
38	37	43.5	249	2	US-09-710-279-106	Sequence 306, App
39	37	43.5	424	2	US-09-248-796A-16232	Sequence 16232, A
40	37	43.5	865	2	US-08-842-382-2	Sequence 2, Appli
41	37	43.5	865	2	US-09-608-821-2	Sequence 2, Appli
42	37	43.5	3546	2	US-09-679-279-13	Sequence 13, Appli
43	36.5	42.9	188	2	US-09-252-991A-24760	Sequence 24760, A
44	36.5	42.9	439	2	US-09-538-092-852	Sequence 952, App
45	36.5	42.9	493	2	US-09-949-016-8063	Sequence 8063, Ap

## ALIGNMENTS

```
RESULT 1
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match          100.0%; Score 85; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. NO. 9.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQOATW 15
      |||||
Db      362 HNDSPVTEQOATW 376

RESULT 2
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
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Query Match 100.0%; Score 85; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNSDPVTEQOATW 15  
|||||  
Db 427 HNSDPVTEQOATW 441

## RESULT 3

US-09-479-614-29  
Sequence 29, Application US/09479614  
Patent No. 6573372  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/09/479,614  
CURRENT FILING DATE: 2000-01-07  
EARLIER APPLICATION NUMBER: 60/115,033  
EARLIER FILING DATE: 1999-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 29  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-09-479-614-29

Query Match 100.0%; Score 85; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNSDPVTEQOATW 15  
|||||  
Db 427 HNSDPVTEQOATW 441

## RESULT 4

US-09-281-760E-37  
Sequence 37, Application US/09281760E  
Patent No. 6734287  
GENERAL INFORMATION:  
APPLICANT: Lawton, Robert  
APPLICANT: Mermer, Brion  
APPLICANT: Francoeur, Greg  
TITLE OF INVENTION: Specific Binding Protein for Treating  
TITLE OF INVENTION: Canine Allergy  
FILE REFERENCE: 01-1275A  
CURRENT APPLICATION NUMBER: US/09/281,760E  
CURRENT FILING DATE: 1999-03-30  
PRIOR APPLICATION NUMBER: 09/058,331  
PRIOR FILING DATE: 1998-04-09  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 37  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (136)..(136)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (413)..(414)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (451)..(451)  
OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (460)..(462)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (500)..(500)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (530)..(530)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (568)..(568)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (847)..(849)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (853)..(853)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1382)..(1382)  
OTHER INFORMATION: "n" stands for any nucleic acid  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1832)..(1832)  
OTHER INFORMATION: "n" stands for any nucleic acid  
US-09-281-760E-37

Query Match 56.5%; Score 48; DB 2; Length 108;  
Best Local Similarity 61.5%; Pred. No. 0.6;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPPVTEQOAT 14  
|||||  
Db 44 NDSPPVTEQOAT 56

## RESULT 5

US-09-701-623C-2  
Sequence 2, Application US/09701623C  
Patent No. 6811782  
GENERAL INFORMATION:  
APPLICANT: Wang Ph.D., Chang Yi  
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
TITLE OF INVENTION: ALLERGY  
FILE REFERENCE: 11514153US1  
CURRENT APPLICATION NUMBER: US/09/701,623C  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US99/13959  
PRIOR FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: 09/100,287  
PRIOR FILING DATE: 1998-06-20  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 312  
TYPE: PRT  
ORGANISM: Dog  
FEATURE:  
OTHER INFORMATION: CH2CH3n of dog Ige  
PUBLICATION INFORMATION:  
AUTHORS: Patel,  
JOURNAL: Immunogenetics  
VOLUME: 41  
PAGES: 282-286  
DATE: 1995  
US-09-701-623C-2

Query Match 56.5%; Score 48; DB 2; Length 312;  
Best Local Similarity 61.5%; Pred. No. 2;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSFVTEQOAT 14  
|||:::|  
Db 256 NDSFVTEQOAT 268

## RESULT 6

US-08-336-583-2  
; Sequence 2, Application US/08336583  
; Patent No. 5629415  
; GENERAL INFORMATION:  
; APPLICANT: HOLLI, GREGORY F.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/336,583  
; FILING DATE: 09-NOV-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E.  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19211  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-6734  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-336-583-2

Query Match 56.5%; Score 48; DB 1; Length 426;  
Best Local Similarity 61.5%; Pred. No. 2.8;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSFVTEQOAT 14  
|||:::|  
Db 358 NDSFVTEQOAT 370

## RESULT 7

PCT-US95-13795-2  
; Sequence 2, Application PC/TUS9513795  
; GENERAL INFORMATION:  
; APPLICANT: HOLLI, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NEW JERSEY

COUNTRY: USA  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13795  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E.  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19211  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-6734  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-13795-2

Query Match 56.5%; Score 48; DB 4; Length 426;  
Best Local Similarity 61.5%; Pred. No. 2.8;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSFVTEQOAT 14  
|||:::|  
Db 358 NDSFVTEQOAT 370

## RESULT 8

US-09-270-767-45299  
; Sequence 45299, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 45299  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-45299

Query Match 54.1%; Score 46; DB 2; Length 210;  
Best Local Similarity 53.3%; Pred. No. 2.8;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HNSFVTEQOAT 15  
|||:::|  
Db 149 HNSFVTEQOAT 163

## RESULT 9

US-09-413-231-8  
; Sequence 8, Application US/09413231  
; Patent No. 6284483  
; GENERAL INFORMATION:  
; APPLICANT: Dille, David R.  
; APPLICANT: Kadyrzhanova, Dina K  
; APPLICANT: Wang, Zhenyong  
; APPLICANT: Warner, Toni M  
; TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

```
; TITLE OF INVENTION: Cephalosporins under the Control of Bicarbonate
; FILE REFERENCE: MS041-453
; CURRENT APPLICATION NUMBER: US/09/413,231
; CURRENT FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
; NAME/KEY: MUTAGEN
; LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNS modified to Arg
US-09-413-231-8

Query Match      52.9%; Score 45; DB 2; Length 321;
Best Local Similarity 50.0%; Pred. No. 6.8;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSFVTEQOATW 15
Db      61 NESTMTDQSTTW 74

RESULT 10
US-09-270-767-43758
; Sequence 43758, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43758
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43758

Query Match      51.8%; Score 44; DB 2; Length 181;
Best Local Similarity 57.1%; Pred. No. 5.3;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 NDSFVTEQOATW 15
Db      62 NCSPIQTEVQAIQW 75

RESULT 11
US-10-104-047-3886
; Sequence 3886, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3886
; LENGTH: 178
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-104-047-3886

Query Match      49.4%; Score 42; DB 2; Length 178;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 HNSFVTEQOATW 15
Db      8 HODFPVKRKRLSTW 22

RESULT 12
US-09-605-703B-1364
; Sequence 1364, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1364
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1364

Query Match      48.2%; Score 41; DB 2; Length 381;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 HNSFVTEQOATW 15
Db      185 HSDKPIRHEALKGW 199

RESULT 13
US-09-605-703B-1362
; Sequence 1362, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1362
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1362
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Query March	48.2%	Score 41	DB 2	Length 534
Best Local Similarity	40.0%	Pred. No. 60		
Matches	6	Conservative	3	Mismatches 6
				Indels 0
				Gaps 0
QY	1	HNDSPVTEQQAATW	15	
Db	185	HSDKPIRHEALWKW	199	

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Db          461 HHDQPVKLERAVW 475
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Search completed: December 12, 2005, 19:37:04
Job time : 21.431 secs

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RESULT 14
US-09-949-016-8465
; Sequence 8465, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8465
; LENGTH: 540
; TYPE: prt
; ORGANISM: Human
US-09-949-016-8465

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RESULT 15
US-09-949-016-9052
; Sequence 9052; Application US/09949016
; Patent No. 6812359
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9052
; LENGTH: 540
; TYPE: prt
; ORGANISM: Human
US-09-949-016-9052

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Query Match	47.1%;	Score 40;	DB 2;	Length 540;
Best Local Similarity	40.0%;	Pred. No. 91;		
Matches	6;	Conservative	5;	Indels 0; Gaps 0

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## OM protein - protein search, using BW model

Run on: December 12, 2005, 19:33:42 ; Search time 66.9828 Seconds  
(without alignments)  
93.568 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNSDPVTEQQTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.dep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.dep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.dep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.dep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.dep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.dep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	US-10-758-165-2	Sequence 2, Appl1
2	85	100.0	431	US-09-479-614-14	Sequence 14, Appl
3	85	100.0	431	US-10-409-772-14	Sequence 14, Appl
4	85	100.0	496	US-09-479-614-2	Sequence 2, Appl1
5	85	100.0	496	US-09-479-614-29	Sequence 29, Appl
6	85	100.0	496	US-10-214-524-25	Sequence 25, Appl
7	85	100.0	496	US-10-409-772-2	Sequence 2, Appl1
8	85	100.0	496	US-10-409-772-29	Sequence 29, Appl
9	48	56.5	15	US-10-758-165-1	Sequence 1, Appl1
10	48	56.5	426	US-10-214-524-28	Sequence 28, Appl
11	47	55.3	68	US-10-425-115-203123	Sequence 203123
12	47	55.3	84	US-10-474-691-101	Sequence 101, Appl
13	47	55.3	1083	US-10-732-923-13976	Sequence 13976, A
14	46	55.3	2360	US-10-732-923-13960	Sequence 13960, A
15	46	54.1	449	US-11-097-143-9714	Sequence 9714, Ap
16	45	53.9	321	US-09-924-841-8	Sequence 8, Appl1
17	44	51.8	194	US-10-437-963-145550	Sequence 145550
18	44	51.8	673	US-11-097-143-42006	Sequence 42006, A
19	43	50.6	151	US-10-425-115-283053	Sequence 283053
20	43	50.6	425	US-10-425-115-190849	Sequence 190849
21	43	50.6	433	US-10-425-115-189170	Sequence 189170
22	43	50.6	435	US-10-425-115-320857	Sequence 320857
23	43	50.6	459	US-10-425-115-184927	Sequence 184927
24	43	50.6	461	US-10-425-115-320858	Sequence 320858
25	43	50.6	470	US-10-369-493-16930	Sequence 16930, A
26	43	50.6	493	US-10-425-115-190842	Sequence 190842
27	43	50.6	503	US-10-425-115-351700	Sequence 351700

28	43	50.6	505	4	US-10-425-115-184928	Sequence 184928
29	43	50.6	505	4	US-10-425-115-189173	Sequence 189173
30	43	50.6	696	4	US-10-425-114-38018	Sequence 38018, A
31	43	50.6	716	4	US-10-425-115-336115	Sequence 336115
32	42.5	50.0	188	4	US-10-437-963-201785	Sequence 201785
33	42	49.4	68	4	US-10-425-115-233639	Sequence 233639
34	42	49.4	178	4	US-10-104-047-3886	Sequence 3886, Ap
35	42	49.4	197	4	US-10-029-386-34079	Sequence 34079, A
36	42	49.4	262	4	US-10-425-115-220304	Sequence 220304
37	42	49.4	296	4	US-10-094-749-2367	Sequence 2367, Ap
38	42	49.4	537	4	US-10-479-435-15	Sequence 15, Appl
39	41	48.2	152	3	US-09-864-761-37742	Sequence 37742, A
40	41	48.2	473	4	US-10-424-599-153291	Sequence 153291
41	41	48.2	647	3	US-09-738-626-6449	Sequence 6449, Ap
42	41	48.2	671	4	US-10-767-701-45175	Sequence 45175, A
43	41	48.2	750	5	US-10-732-923-11093	Sequence 11093, A
44	41	48.2	812	5	US-10-450-763-49424	Sequence 49424, A
45	41	48.2	1527	5	US-10-450-763-38962	Sequence 38962, A

## ALIGNMENTS

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RESULT 1
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2
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Query Match 100.0%; Score 85; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.3e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HNSDPVTEQQTW 15
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DB 1 HNSDPVTEQQTW 15

RESULT 2
US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14
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Query Match 100.0%; Score 85; DB 3; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATW 15  
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Db 362 HNDSPVTEOQATW 376

RESULT 3  
US-10-409-772-14  
; Sequence 14, Application US/10409772  
; Publication No. US2003021655A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/10/409,772  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/479,614  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-409-772-14

Query Match 100.0%; Score 85; DB 4; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATW 15  
|||  
Db 362 HNDSPVTEOQATW 376

RESULT 4  
US-09-479-614-2  
; Sequence 2, Application US/09479614  
; Publication No. US2003001183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-2

Query Match 100.0%; Score 85; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATW 15  
|||  
Db 427 HNDSPVTEOQATW 441

RESULT 5  
US-09-479-614-29  
; Sequence 29, Application US/09479614  
; Publication No. US2003001183A1

; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-29

Query Match 100.0%; Score 85; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATW 15  
|||  
Db 427 HNDSPVTEOQATW 441

RESULT 6  
US-10-214-524-25  
; Sequence 25, Application US/10214524  
; Publication No. US20030073142A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Swei-Shen Alex  
; APPLICANT: Yang, Yong-Min  
; APPLICANT: Barankiewicz, Theresa J.  
; APPLICANT: Chen, Zhong  
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
; FILE REFERENCE: IGE-00101.P.1.1  
; CURRENT APPLICATION NUMBER: US/10/214,524  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/312,120  
; PRIOR FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 25  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Cat (Felis catus)  
US-10-214-524-25

Query Match 100.0%; Score 85; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATW 15  
|||  
Db 427 HNDSPVTEOQATW 441

RESULT 7  
US-10-409-772-2  
; Sequence 2, Application US/10409772  
; Publication No. US2003021655A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/10/409,772  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/479,614  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin Ver. 2.0



SEQ ID NO 2  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-2

Query Match 100.0%; Score 85; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATTW 15  
|||||  
DB 427 HNDSPVTEQOATTW 441

RESULT 8  
US-10-409-772-29  
Sequence 29, Application US/10409772  
Publication No. US20030216565A1  
GENERAL INFORMATION:  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/10/409,772  
CURRENT FILING DATE: 2003-04-07  
PRIOR APPLICATION NUMBER: US/09/479,614  
PRIOR FILING DATE: 2000-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-29

Query Match 100.0%; Score 85; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATTW 15  
|||||  
DB 427 HNDSPVTEQOATTW 441

RESULT 9  
US-10-758-165-1  
Sequence 1, Application US/10758165  
Publication No. US20050196816A1  
GENERAL INFORMATION:  
APPLICANT: Hammerberg, Bruce  
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
FILE REFERENCE: 5051-661  
CURRENT APPLICATION NUMBER: US/10/758,165  
CURRENT FILING DATE: 2004-01-16  
PRIOR APPLICATION NUMBER: US 60/440,472  
PRIOR FILING DATE: 2003-01-16  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-10-758-165-1

Query Match 56.5%; Score 48; DB 5; Length 15;  
Best Local Similarity 61.5%; Pred. No. 0.23;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPTVTEQOATT 14  
|||||  
DB 2 NDSPTVTEQOATT 14

RESULT 10  
US-10-214-524-28  
Sequence 28, Application US/10214524  
Publication No. US20030073142A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Swei-Shen Alex  
APPLICANT: Yang, Yong-Min  
APPLICANT: Barankiewicz, Theresa J.  
APPLICANT: Chen, Zhong  
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
FILE REFERENCE: IGE-00101.P.1.1  
CURRENT APPLICATION NUMBER: US/10/214,524  
CURRENT FILING DATE: 2002-08-08  
PRIOR APPLICATION NUMBER: 60/312,120  
PRIOR FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 28  
LENGTH: 426  
TYPE: PRT  
ORGANISM: Dog (Canis familiaris)  
US-10-214-524-28

Query Match 56.5%; Score 48; DB 4; Length 426;  
Best Local Similarity 61.5%; Pred. No. 8.9;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPTVTEQOATT 14  
|||||  
DB 358 NDSPTVTEQOATT 370

RESULT 11  
US-10-425-115-203123  
Sequence 203123, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovallik, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 203123  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MHT4577\_116836C.1.pcp  
US-10-425-115-203123

Query Match 55.3%; Score 47; DB 4; Length 68;  
Best Local Similarity 69.2%; Pred. No. 1.8;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPTVTEQOATT 14  
|||||  
DB 38 NDSPTVTEQOATT 50

RESULT 12  
US-10-474-691-101  
Sequence 101, Application US/10474691  
Publication No. US20040221332A1  
GENERAL INFORMATION:  
APPLICANT: Cropdesign N.V.  
TITLE OF INVENTION: Plant growth regulating genes, proteins and uses thereof  
FILE REFERENCE: CROP-028-PCT

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; CURRENT APPLICATION NUMBER: US/10/474,691
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/283,313
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Gossypium arboreum
US-10-474-691-101
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Query Match      55.3%; Score 47; DB 5; Length 84;
Best Local Similarity 61.5%; Pred. No. 2.3;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY      2  HNDSPVTEQOATW 14
Db      32  NDSFAPKTOQOCTT 44
```

```
RESULT 13
US-10-732-923-13976
; Sequence 13976, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13976
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. neoformans
US-10-732-923-13976
```

```
Query Match      55.3%; Score 47; DB 5; Length 1083;
Best Local Similarity 53.3%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY      1  HNDSPVTEQOATW 15
Db      202  HADEPARQEWQROTW 216
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```
RESULT 14
US-10-732-923-13960
; Sequence 13960, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13960
; LENGTH: 2360
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. grubii
US-10-732-923-13960
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Query Match      55.3%; Score 47; DB 5; Length 2360;
Best Local Similarity 53.3%; Pred. No. 87;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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.QY      1  HNDSPVTEQOATW 15
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Db      1479  HADEPARQEWQROTW 1493
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RESULT 15
US-11-097-143-9714
; Sequence 9714, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9714
; LENGTH: 449
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-9714
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Query Match      54.1%; Score 46; DB 6; Length 449;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY      1  HNDSPVTEQOATW 15
Db      133  HNDGFVRCPEALTW 147
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Search completed: December 12, 2005, 20:19:23
Job time : 66.9828 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.4569 Seconds  
(without alignments)  
34.094 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQATTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*

1: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep:.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep:.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep:.\*  
5: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep:.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep:.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep:.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	56.5	312	6 US-10-723-207-2	Sequence 2, Appl1
2	37	43.5	249	6 US-10-793-626-306	Sequence 306, App
3	37	43.5	865	7 US-11-080-991-110	Sequence 110, App
4	36	42.4	339	7 US-11-010-874-3	Sequence 3, Appl1
5	36	42.4	791	7 US-11-056-621-4	Sequence 4, Appl1
6	36	42.4	1275	6 US-10-821-234-1598	Sequence 1598, Ap
7	35	41.2	467	6 US-10-821-234-904	Sequence 904, App
8	35	41.2	737	6 US-10-878-556A-99	Sequence 99, Appl
9	34	40.0	735	6 US-10-467-657-6990	Sequence 6990, Ap
10	34	40.0	7968	7 US-11-186-731-5	Sequence 5, Appl1
11	33	38.8	136	7 US-11-055-822-966	Sequence 966, App
12	33	38.8	136	7 US-11-055-822-994	Sequence 994, App
13	33	38.8	248	6 US-10-467-657-7696	Sequence 7696, Ap
14	33	38.8	252	6 US-10-510-386-104	Sequence 104, App
15	33	38.8	568	7 US-11-055-822-240	Sequence 240, App
16	33	38.8	568	7 US-11-055-822-1134	Sequence 1134, Ap
17	33	38.8	680	6 US-10-467-657-7612	Sequence 7612, Ap
18	33	38.8	716	6 US-10-467-657-8370	Sequence 8370, Ap
19	32.5	38.2	259	6 US-10-510-386-108	Sequence 108, App
20	32	37.6	53	6 US-10-467-657-2814	Sequence 2814, Ap
21	32	37.6	139	6 US-10-485-517-162	Sequence 162, App
22	32	37.6	233	6 US-10-467-657-482	Sequence 482, App
23	32	37.6	233	6 US-10-467-657-5470	Sequence 5470, Ap
24	32	37.6	244	6 US-10-510-386-110	Sequence 110, App
25	32	37.6	353	7 US-11-137-465-44	Sequence 44, Appl

26	32	37.6	448	7 US-11-137-465-45	Sequence 45, Appl
27	32	37.6	505	6 US-10-467-657-6228	Sequence 6228, Ap
28	32	37.6	518	6 US-10-878-556A-156	Sequence 156, App
29	32	37.6	840	7 US-11-108-172-1102	Sequence 1102, Ap
30	32	37.6	886	6 US-10-821-234-1329	Sequence 1329, Ap
31	32	37.6	919	6 US-10-858-730-206	Sequence 206, App
32	32	37.6	1155	6 US-10-793-626-1780	Sequence 1780, Ap
33	32	37.6	1184	6 US-10-131-826A-412	Sequence 412, App
34	31	36.5	146	7 US-11-000-463-881	Sequence 881, App
35	31	36.5	181	7 US-11-000-463-409	Sequence 409, App
36	31	36.5	270	6 US-10-467-657-7100	Sequence 7100, Ap
37	31	36.5	273	6 US-10-467-657-7462	Sequence 7462, Ap
38	31	36.5	278	6 US-10-495-597-9	Sequence 9, Appl1
39	31	36.5	341	6 US-10-515-481-3	Sequence 3, Appl1
40	31	36.5	341	6 US-10-515-481-6	Sequence 6, Appl1
41	31	36.5	341	6 US-10-515-481-9	Sequence 9, Appl1
42	31	36.5	341	6 US-10-515-481-12	Sequence 12, Appl
43	31	36.5	344	6 US-10-567-527A-24	Sequence 24, Appl
44	31	36.5	362	6 US-10-467-657-6880	Sequence 6880, Ap
45	31	36.5	434	6 US-10-467-657-4482	Sequence 4482, Ap

#### ALIGNMENTS

```
RESULT 1
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication NO. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3 of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2
;
Query Match      56.5%   Score 48;   DB 6;   Length 312;
Best Local Similarity 61.5%   Pred. No. 0.063;
Matches      8;   Conservative      3;   Mismatches      2;   Indels      0;   Gaps      0;
QY      2      NDSPIRTDQATT 14
Db      256      NDSPIRTDQATT 268
RESULT 2
US-10-793-626-306
; Sequence 306, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
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; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 306
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-306

Query Match      43.5%; Score 37; DB 6; Length 249;
Best Local Similarity 46.7%; Pred. No. 5.1;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy      1  HNDSPVTEQOATTW 15
Db      54  HNDSTFYKEXQNTGW 68

RESULT 3
US-11-080-991-110
; Sequence 110, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Vealby, Pelter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-080-991-110

Query Match      43.5%; Score 37; DB 7; Length 865;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2  NDSFVTEQOATT 14
Db      365  NDIPRVQRQTT 377

RESULT 4
US-11-010-874-3
; Sequence 3, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820,656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
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; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Version 3.3
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-010-874-3

Query Match      42.4%; Score 36; DB 7; Length 339;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2  NDSFVTEQOATT 14
Db      256  DSSPVSTEQLAPT 268

RESULT 5
US-11-056-621-4
; Sequence 4, Application US/11056621
; Publication No. US20050262592A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; APPLICANT: Dickey, Lynn F.
; APPLICANT: Gasdaeka, John R.
; APPLICANT: Wang, Xiaowei
; APPLICANT: Cox, Kevin M.
; APPLICANT: Peele, Charles G.
; TITLE OF INVENTION: EXPRESSION OF PLASMINOGEN AND
; TITLE OF INVENTION: MICROPLASMINOGEN IN DUCKWEED
; FILE REFERENCE: 40989/274646
; CURRENT APPLICATION NUMBER: US/11/056,621
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,487
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of mature human plasminogen
; US-11-056-621-4

Query Match      42.4%; Score 36; DB 7; Length 791;
Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2  NDSFVTEQOATT 14
Db      334  DSSPVSTEQLAPT 346

RESULT 6
US-10-821-234-1598
; Sequence 1598, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crahn, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
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; SEQ ID NO 1598
; LENGTH: 1275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1598
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```
Query Match          42.4%; Score 36; DB 6; Length 1275;
Best Local Similarity 38.5%; Pred. No. 44;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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```
OY      3 DSPVTEQQTW 15
          ::|||::
Db      1024 ETIRVNRQPTW 1036
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```
RESULT 7
US-10-821-234-904
; Sequence 904, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andaman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL_SEQ_genes Version 1.0
; SEQ ID NO 904
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-904
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```
Query Match          41.2%; Score 35; DB 6; Length 467;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
OY      1 HNDSPVTE 9
          ::|||::
Db      251 YNDSPVKDE 259
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RESULT 8
US-10-878-556A-99
; Sequence 99, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche, Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (98)..(98)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (242)..(242)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC_FEATURE
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; LOCATION: (259)..(259)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
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; NAME/KEY: MISC_FEATURE
; LOCATION: (264)..(264)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (269)..(269)
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; NAME/KEY: MISC_FEATURE
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; NAME/KEY: MISC_FEATURE
; LOCATION: (283)..(283)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (284)..(284)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (337)..(337)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
; LOCATION: (368)..(368)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
; LOCATION: (418)..(418)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
; LOCATION: (419)..(419)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (425)..(425)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (428)..(428)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
; LOCATION: (429)..(429)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
; LOCATION: (430)..(430)
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; NAME/KEY: MISC_FEATURE
; LOCATION: (432)..(432)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
; LOCATION: (439)..(439)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC_FEATURE
; LOCATION: (443)..(443)
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; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (499)..(499)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC FEATURE
; LOCATION: (500)..(500)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC FEATURE
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; NAME/KEY: MISC FEATURE
; LOCATION: (506)..(506)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC FEATURE
; LOCATION: (507)..(507)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC FEATURE
; LOCATION: (511)..(511)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC FEATURE
; LOCATION: (513)..(513)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: haugp/075309-23-0
; DATABASE ENTRY DATE: 2003-02-16
; US-10-878-556A-99
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Query Match          41.2%; Score 35; DB 6; Length 737;
Best Local Similarity 54.5%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      5 PVRTEQATTW 15
Db      322 PLRLRVGATTW 332
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```
RESULT 9
; US-10-467-657-6990
; Sequence 6990, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6990
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-6990
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Query Match          40.0%; Score 34; DB 6; Length 735;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 HNSPVRTEQ 10
Db      11-186-731-5
```

```
Db      275 HIDAPVKLEQ 284
```

```
RESULT 10
; US-11-186-731-5
; Sequence 5, Application US/11186731
; Publication No. US20050255521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Roseana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MP12001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-186-731-5
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```
Query Match          40.0%; Score 34; DB 7; Length 7968;
Best Local Similarity 54.5%; Pred. No. 78;02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 NDSPPRTEQQA 12
Db      4376 DDEPVRTEENA 4386
```

```
RESULT 11
; US-11-055-822-966
; Sequence 966, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schröder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Heberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BG1-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
```

SEQ ID NO 966  
LENGTH: 136  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-11-055-822-966

Query Match 38.8% Score 33; DB 7; Length 136;  
Best Local Similarity 35.7% Pred. No. 14;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 NDSPTREQQATW 15  
DB 119 SDSPEASEREISIW 132

RESULT 12  
US-11-055-822-994  
Sequence 994, Application US/11055822  
Publication No. US20050260707A1  
GENERAL INFORMATION:  
APPLICANT: Pompejus, Markus  
APPLICANT: Krogger, Burkhard  
APPLICANT: Schneider, Hartwig  
APPLICANT: Zeider, Oskar  
APPLICANT: Haberdauer, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
FILE REFERENCE: BGI-121CPN  
CURRENT APPLICATION NUMBER: US/11/055,822  
CURRENT FILING DATE: 2005-02-11  
PRIOR APPLICATION NUMBER: 09/606,740  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: 60/141,031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 60/142,101  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: 60/148,613  
PRIOR FILING DATE: 1999-08-12  
PRIOR APPLICATION NUMBER: 60/187,970  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: DE 19930476.9  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19931415.2  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931418.7  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931419.5  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931420.9  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1158  
SEQ ID NO 994  
LENGTH: 136  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-11-055-822-994

Query Match 38.8% Score 33; DB 7; Length 136;  
Best Local Similarity 35.7% Pred. No. 14;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 NDSPTREQQATW 15  
DB 119 SDSPEASEREISIW 132

RESULT 13  
US-10-467-7696  
Sequence 7696, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 7696  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-7696

Query Match 38.8% Score 33; DB 6; Length 248;  
Best Local Similarity 87.5% Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQQ 11  
DB 144 SPVTEQQ 151

RESULT 14  
US-10-510-386-104  
Sequence 104, Application US/10510386  
Publication No. US20050244922A1  
GENERAL INFORMATION:  
APPLICANT: Andersen, Jens Tonne  
APPLICANT: Jorgensen, Steen Troels  
APPLICANT: Olsen, Peter Bjarke  
APPLICANT: Rasmussen, Michael Dolberg  
TITLE OF INVENTION: Improved Bacillus Host Cell  
FILE REFERENCE: 10294,204-US  
CURRENT APPLICATION NUMBER: US/10/510,386  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 248  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 104  
LENGTH: 252  
TYPE: PRT  
ORGANISM: Bacillus licheniformis  
US-10-510-386-104

Query Match 38.8% Score 33; DB 6; Length 252;  
Best Local Similarity 50.0% Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTREQQATW 15  
DB 174 IRTREQQATW 183

RESULT 15  
US-11-055-822-240  
Sequence 240, Application US/11055822  
Publication No. US20050260707A1  
GENERAL INFORMATION:  
APPLICANT: Pompejus, Markus  
APPLICANT: Krogger, Burkhard  
APPLICANT: Schneider, Hartwig  
APPLICANT: Zeider, Oskar  
APPLICANT: Haberdauer, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING  
FILE REFERENCE: BGI-121CPN  
CURRENT APPLICATION NUMBER: US/11/055,822  
CURRENT FILING DATE: 2005-02-11

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; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 240
; LENGTH: 568
; TYPE: PRF
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-240
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```
Query Match      38.8%; Score 33; DB 7; Length 568;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 DSPVTEQQAAT 14
      : : : : :
Db      398 ETPVTVARSAT 409
```

Search completed: December 12, 2005, 20:19:48  
Job time : 2.4569 secs



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## OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 12.6724 Seconds  
(without alignments)  
113.889 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQOATW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	52.9	321	2	isopenicillin N sy
2	43.5	51.2	403	2	D-galactose-bindin
3	43	50.6	375	2	gag protein - maiz
4	43	50.6	470	2	glutaryl-CRNA synt
5	42	49.4	247	2	hypothetical prote
6	42	49.4	283	2	glucosyltransferas
7	42	49.4	319	2	glucosyltransferas
8	42	49.4	319	2	exon protein - Rhi
9	41	48.2	101	2	hypothetical prote
10	41	48.2	259	2	hypothetical prote
11	41	48.2	1449	2	hypothetical prote
12	41	48.2	1584	2	hypothetical prote
13	41	48.2	1586	2	hypothetical prote
14	40	47.1	151	2	probable exported
15	40	47.1	270	2	glucosamine-6-phos
16	40	47.1	215	2	probable pol polyp
17	40	47.1	410	2	probable integral
18	40	47.1	513	2	probable RNA-dirac
19	40	47.1	557	2	methy-accepting c
20	40	47.1	631	2	hypothetical prote
21	40	47.1	635	2	hypothetical prote
22	39	45.9	88	2	hipb protein - Bac
23	39	45.9	113	2	T-cell receptor de
24	39	45.9	156	2	conserved hypothet
25	39	45.9	161	2	T-cell receptor de
26	39	45.9	166	2	T-cell receptor de
27	39	45.9	295	2	int protein - phag
28	39	45.9	336	2	multidrug resistan
29	39	45.9	514	2	

30	39	45.9	666	2	semaphorin III - m
31	39	45.9	771	2	semaphorin III pre
32	39	45.9	772	2	collapsin - chicke
33	39	45.9	772	2	semaphorin D - mou
34	38	44.7	393	2	gene 16 protein -
35	38	44.7	410	1	cytochrome P450 10
36	38	44.7	437	2	opaque-2 protein -
37	38	44.7	460	2	regulatory protein
38	38	44.7	527	2	glucuronosyltransf
39	38	44.7	528	2	glucuronosyltransf
40	38	44.7	529	2	glucuronosyltransf
41	38	44.7	533	1	methy-accepting c
42	38	44.7	533	2	methy-accepting c
43	38	44.7	533	2	methy-accepting c
44	38	44.7	551	1	serine chemorecept
45	38	44.7	554	2	methy-accepting c

## ALIGNMENTS

RESULT 1  
A58458  
isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces cattleya  
C:Species: Streptomyces cattleya  
C:Date: 30-Sep-1993 #sequence\_revision 21-Jan-1997 #text\_change 09-Jul-2004  
C:Accession: A58458  
R:Wang, Y.G.; Li, R.F.  
Acta Microbiol. Sin. 36, 87-92, 1996  
A:Title: Cloning and sequencing the isopenicillin N synthetase (IPNS) gene from Streptom  
A:Reference number: A58458  
A:Accession: A58458  
A:Molecule type: DNA  
A:Residues: 1-321 <MAN>  
A:Cross-References: UNIPROT:O53932, UNIPARC:UPI000012D7FD  
C:Superfamily: isopenicillin N synthase  
C:Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase  
P:49,213,269/Binding site: iron (His) #status predicted

Query Match 52.9%; Score 45; DB 2; Length 321;  
Best Local Similarity 50.0%; Pred. No. 3.4;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPTVTEQOATW 15  
Db 61 NESTMTDQKSTW 74

RESULT 2  
JCS171  
D-galactose-binding periplasmic protein mglB-2 - syphilis spirochete  
N:Alternate names: carbonhydrate receptor; methylgalactoside transport galactose-binding  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 16-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: JCS171; D71295  
R:Porcella, S.F.; Popova, T.G.; Hagman, K.E.; Penn, C.W.; Radolf, J.D.; Norgard, M.V.  
Gene 177, 115-121, 1996  
A:Title: A mgl-like operon in Treponema pallidum, the syphilis spirochete.  
A:Reference number: JCS171; MUID:97080510; PMID:8921855  
A:Accession: JCS171  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-403 <POB>  
A:Cross-References: UNIPROT:O08255, UNIPARC:UPI000012F062; GB:U46416; MTD:q1230600; PIDN  
R:Fraser, C.W.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
R.; J. Khalek, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Ulfersback, T.; McDo  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770; PMID:9665876  
A:Accession: D71295  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A;Residues: 1-403 <COL>  
A;Cross-references: UNIPARC:UPI0000121062; GB:AE001242; GB:AE000520; NID:G3322976; PIDN:  
A;Experimental source: strain Nichols  
C;Comment: This protein is a component of an ATP-binding cassette operon involved in gal  
C;Genetics:  
A;Gene: mjbB; TP0684  
C;Keywords: calcium binding; chemotaxis; periplasmic space; sugar transport  
F;44,114,116,120,197,220/Binding site: galactose (asn, His, Asp, Arg, Asn, Asp) #status  
F;96,98,100,102,104,191/Binding site: calcium (asp, Asn, Asp, Ile, Gly, Asp) #status pre  
Query Match 51.2%; Score 43.5; DB 2; Length 403;  
Best Local Similarity 55.6%; Pred. No. 8.1;  
Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;  
QY 1 HNDSPVTEQATW 15  
||| ||| |||  
Db 114 HNDKVTREGIRALGTW 131  
||| ||| |||  
RESULT 3  
S58484  
gag protein - maize  
C;Species: Zea mays (maize)  
C;Date: 29-Nov-1995 #sequence\_revision 01-Mar-1996 #text\_change 29-Oct-1999  
C;Accession: S58484  
R;Hu, M.; Das, O. P.; Messing, J.  
Mol. Gen. Genet. 248, 471-480, 1995  
A;Title: Zeon-1, a member of a new maize retrotransposon family.  
A;Reference number: S58484; MUID:96004768; PMID:7565611  
A;Accession: S58484  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-375 <HUM>  
A;Cross-references: UNIPARC:UPI000011DE94; EMBL:U11059; NID:G507844; PIDN:AAA93147.1; PI  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994  
Query Match 50.6%; Score 43; DB 2; Length 375;  
Best Local Similarity 66.7%; Pred. No. 9.2;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 4 SPVTEQATW 15  
||| ||| |||  
Db 61 SPSTELQATPW 72  
||| ||| |||  
RESULT 4  
D87485  
glutamyL-cRNA synthetase [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: D87485  
R;Nierman, W. C.; Felblyum, T. V.; Paulsen, I. T.; Nelson, K. E.; Eissen, J.; Heidelberg, J.  
B.; Laub, M. T.; Deboy, R. T.; Dodson, R. J.; Durkin, A. S.; Gilm, M. L.; Hatt, D. H.; Kolor  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S. L.; Shapiro, L.; Venter, J. C.; Fraser, C. M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11259647  
A;Accession: D87485  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-470 <STO>  
A;Cross-references: UNIPROT:Q9A721; UNIPARC:UPI00000C7547; GB:AE005673; NID:G13423356; F  
C;Genetics:  
A;Gene: CCI1905  
C;Superfamily: glutamate-cRNA ligase; glutamine-cRNA ligase homology  
Query Match 50.6%; Score 43; DB 2; Length 470;  
Best Local Similarity 46.7%; Pred. No. 12;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 HNDSPVTEQATW 15  
||| ||| |||  
Db 274 HGDDVFTDEQALSW 288  
||| ||| |||

RESULT 5  
AF2006  
hypothetical protein alr1604 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AF2006  
R;Kaneoko, T.; Nakamura, Y.; Wolk, C. P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AF2006  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-247 <KIR>  
A;Cross-references: UNIPROT:Q8YWK9; UNIPARC:UPI00000CE143; GB:BA000019; PIDN:BA877970.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr1604  
Query Match 49.4%; Score 42; DB 2; Length 247;  
Best Local Similarity 33.3%; Pred. No. 8.8;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 HNDSPVTEQATW 15  
||| ||| |||  
Db 13 HRAPIEVEKGLTW 27  
||| ||| |||  
RESULT 6  
E49348  
succinoglycan biosynthesis glycosyltransferase (EC 2.4.1.-) exoW [validated] - Rhizobium  
C;Species: Rhizobium meliloti  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: E49348  
R;Glucksmann, M. A.; Reuber, T. L.; Walker, G. C.  
J. Bacteriol. 175, 7033-7044, 1993  
A;Title: Family of glycosyl transferases needed for the synthesis of succinoglycan by Rh  
A;Reference number: A49348; MUID:94042869; PMID:8226645  
A;Accession: E49348  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-283 <GLU>  
A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000016PEBF; GB:L20758; NID:G393240; PIDN:  
C;Genetics:  
A;Gene: exoW  
C;Function:  
A;Description: EC 2.4.1.-; succinoglycan biosynthesis glycosyltransferase [validated, M07  
; exoW and exoW together are responsible for sugar addition to the lipid carrier  
A;Pathway: succinoglycan biosynthesis  
C;Keywords: glycosyltransferase; hexosyltransferase  
Query Match 49.4%; Score 42; DB 2; Length 283;  
Best Local Similarity 57.1%; Pred. No. 10;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 2 NDSPVTEQATW 15  
||| ||| |||  
Db 232 NDSPOFLKQDFNTW 245  
||| ||| |||  
RESULT 7  
A95976  
glucosyltransferase protein (EC 2.4.1.-) [imported] - Sinorhizobium meliloti (strain 102;  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: A95976  
R;Finan, T. M.; Weidner, S.; Wong, K.; Buhrester, J.; Chain, P.; Vorholter, F. J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo;

A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: A95976  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-319 <KUR>  
A;Cross-references: UNIPROT:P33702; UNIPARC:UP1000012A384; GB:AL591985; PIDN:CMC49473.1;  
A;Experimental source: strain 1021, megaplasmid pSymB  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chailin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: exow; SMD21690  
A;Genome: plasmid  
C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase  
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 NDSPVRTQOATW 15  
||| |  
Db 232 NDSPOFLKQOFNTW 245

RESULT 8  
S40175  
Exow protein - Rhizobium meliloti  
C;Species: Rhizobium meliloti  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S40175  
R;Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puhler, A.  
submitted to the EMBL Data Library, April 1993  
A;Description: Analysis of the Rhizobium meliloti genes exuI, exoV, exow, exoT and exoI  
res.  
A;Reference number: S40173  
A;Accession: S40175  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-319 <BEC>  
A;Cross-references: UNIPROT:P33702; UNIPARC:UP1000012A384; EMBL:Z22646; NID:g605659; PID  
C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;  
Best Local Similarity 57.1%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 NDSPVRTQOATW 15  
||| |  
Db 232 NDSPOFLKQOFNTW 245

RESULT 9  
B97851  
hypothetical protein RCI210 [imported] - Rickettsia conorii (strain Malish 7)  
C;Species: Rickettsia conorii  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: B97851  
R;Ogata, H.; Audic, S.; Reneato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro  
Science 293, 2093-2098, 2001  
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A;Reference number: A97700; MUID:21442074; PMID:11557893  
A;Accession: B97851  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-101 <KUR>  
A;Cross-references: UNIPROT:Q92GB3; UNIPARC:UP100000CC02C; GB:AE006914; PIDN:AAL03748.1;

C;Genetics:  
A;Gene: RCI210

Query Match 48.2%; Score 41; DB 2; Length 101;  
Best Local Similarity 60.0%; Pred. No. 4.9;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 HNDSPVRTQO 10  
||| |  
Db 41 HNDDPISRTQO 50

RESULT 10  
B85066  
hypothetical protein AT4G05260 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B85066  
R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin  
Nature 402, 769-777, 1999  
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A;Reference number: A85001; MUID:20083488; PMID:10617198  
A;Accession: B85066  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-259 <STO>  
A;Cross-references: UNIPROT:Q9MOW9; UNIPARC:UP100000A640D; GB:NC\_001268; NID:g7267286; P  
C;Genetics:  
A;Gene: AT4G05260  
A;Map position: 4

Query Match 48.2%; Score 41; DB 2; Length 259;  
Best Local Similarity 63.6%; Pred. No. 14;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 HNDSPVRTQO 11  
||| |  
Db 140 HQDSPVRNNEQ 150

RESULT 11  
T20181  
hypothetical protein C53B4.4c - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Dec-2004  
C;Accession: T20181  
R;Berks, M.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: Z19233  
A;Accession: T20181  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1449 <WIL>  
A;Cross-references: UNIPROT:Q9UJL2; UNIPARC:UP100001641A7; EMBL:Z68215; PIDN:CA54213.1;  
A;Experimental source: clone C53B4  
C;Genetics:  
A;Gene: C53B4.4c  
A;Map position: 4  
A;introns: 15/3; 92/2; 252/3; 306/1; 477/2; 571/1; 605/1; 720/3; 880/3; 1008/2; 1091/1;

Query Match 48.2%; Score 41; DB 2; Length 1449;  
Best Local Similarity 58.3%; Pred. No. 92;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 NDSPVRTQOAT 13  
||| |  
Db 423 NNVPFIRSROAT 434

RESULT 12  
T20180  
hypothetical protein C53B4.4a - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T20180  
R/Berks, M.  
submitted to the EMBL Data Library, December 1995  
A/Reference number: Z19233  
A/Accession: T20180  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1584 <MIL>  
A/Cross-references: UNIPROT:Q18798; UNIPARC:UPI000002A219; EMBL:Z68215; PIDN:CAA92457.1;  
C/Genetics:  
A/Gene: CESP:CS3B4.4a  
A/Map position: 4  
A/Intons: 61/2; 150/3; 227/2; 387/3; 441/1; 612/2; 706/1; 740/1; 855/3; 1015/3; 1143/2;  
C/Superfamily: Caenorhabditis elegans hypothetical protein CS3B4.4c

Query Match 48.2%; Score 41; DB 2; Length 1584;  
Best Local Similarity 58.3%; Pred. No. 1e+02;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSFVTEQOAT 13  
|:|:|:|:|:  
Db 558 NNVPFIRERQAT 569

RESULT 13  
T20179  
hypothetical protein CS3B4.4b - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T20179  
R/Berks, M.  
submitted to the EMBL Data Library, December 1995  
A/Reference number: Z19233  
A/Accession: T20179  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1586 <MIL>  
A/Cross-references: UNIPROT:Q18798; UNIPARC:UPI00000866B7; EMBL:Z68215; PIDN:CAA92456.1;  
C/Genetics:  
A/Gene: CESP:CS3B4.4b  
A/Map position: 4  
A/Intons: 61/2; 150/3; 227/2; 387/3; 441/1; 612/2; 706/1; 740/1; 855/3; 1015/3; 1145/2;  
C/Superfamily: Caenorhabditis elegans hypothetical protein CS3B4.4c

Query Match 48.2%; Score 41; DB 2; Length 1586;  
Best Local Similarity 58.3%; Pred. No. 1e+02;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSFVTEQOAT 13  
|:|:|:|:|:  
Db 558 NNVPFIRERQAT 569

RESULT 14  
AF0931  
probable exported protein [imported] - Salmonella enterica subsp. enterica serovar Typhimurium  
C/Species: Salmonella enterica subsp. enterica serovar Typhimurium  
A/Note: this species has also been called Salmonella typhi  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AF0931  
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulé, S.; O'Gea, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium  
A/Reference number: AB0502; MUID:21534947; PMID:11677608  
A/Accession: AF0931  
A/Status: preliminary  
A/Molecule type: DNA

A/Residues: 1-151 <PAR>  
A/Cross-references: UNIPARC:UPI000013C475; GB:AL513382; PIDN:CAD09472.1; PID:G16504589; C/Genetics:  
A/Gene: STY3713

Query Match 47.1%; Score 40; DB 2; Length 151;  
Best Local Similarity 80.0%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQOAT 13  
|:|:|:|:|:  
Db 42 SPVTEQOAT 51

RESULT 15  
F64050  
glucosamine-6-phosphate deaminase (EC 3.5.99.6) - Haemophilus influenzae (strain Rd KW20)  
C/Species: Haemophilus influenzae  
C/Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C/Accession: F64050  
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehl, A.; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995  
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A/Reference number: A64000; MUID:95350630; PMID:7542800  
A/Accession: F64050  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-270 <TIGR>  
A/Cross-references: UNIPROT:P44538; UNIPARC:UPI000012FD06; GB:U32700; GB:L42023; NID:g323  
C/Superfamily: glucosamine-6-phosphate isomerase  
C/Keywords: hydrolase; isomerase

Query Match 47.1%; Score 40; DB 2; Length 270;  
Best Local Similarity 54.5%; Pred. No. 22;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVTEQOATW 15  
|:|:|:|:|:  
Db 5 PVTEQOATW 15

Search completed: December 12, 2005, 20:42:47  
Job time : 14.6724 secs



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DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Possible ABC transporter with AAA domain and 12 transmembrane
DE domains.
GN ORFNames=cgtd_1390;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_Taxid=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahamte J.E., Zhu G.,
RA Lanco C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Kontorov B.A., Spriggs H.F., Iyer L.,
RA Aantaahtaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum."
RL Science 304:441-445(2004).
DR EMBL; AAEE0100009; EAK87614.1; -; Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016867; F:ATPase activity; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PSS0893; ABC_TRANSPORTER_2; 1.
KW Transmembrane.
SQ SEQUENCE 1522 AA; 176017 MW; 75C04515093B3981 CRC64;

Query Match 58.8%; Score 50; DB 2; Length 1522;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATW 15
DB 72 HNDKQVPESEISTW 86

RESULT 3
Q8XXG1_RALSO
ID Q8XXG1_RALSO PRELIMINARY; PRT; 735 AA.
AC Q8XXG1;
RT "Comparative analysis of PSK peptide growth factor precursor
RT homologs."
RL Plant Sci. 163:321-332(2002).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK00114; DA00278.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008283; P:cell proliferation; IEA.
DR InterPro; IPR009438; PSK.
DR Pfam; PF06404; PSK; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 84 AA; 9242 MW; 6B04F8D05EC36C9B CRC64;

Query Match 55.3%; Score 47; DB 2; Length 84;
Best Local Similarity 61.5%; Pred. No. 2;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATW 14
DB 32 NDSPAKTSQCGIT 44

RESULT 5
O94189_CRYNE
ID O94189_CRYNE PRELIMINARY; PRT; 1083 AA.
AC O94189;
DT 01-MAY-1999 (TReMBLrel. 10, Created)

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DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0015969; P:guanosine tetraphosphate metabolism; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002912; ACT.
DR InterPro; IPR006674; HD_hydro.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR007685; RelA_Spot.
DR InterPro; IPR004811; Spot_rela.
DR InterPro; IPR004095; TGS.
DR Pfam; PF01842; ACT; 1.
DR Pfam; PF01966; HD; 1.
DR Pfam; PF04607; RelA_Spot; 1.
DR Pfam; PF02824; TGS; 1.
DR TIGRFAMs; TIGR00691; spot_rela; 1.
DR SMART; SM00471; HD; 1.
KW Complete proteome; Hydrolase; Transferase.
SQ SEQUENCE 735 AA; 81861 MW; 9A6B0051104FD241 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 735;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATW 15
DB 358 HNDSPVTEQOATW 372

RESULT 4
O7PCB5_GOSAR
ID O7PCB5_GOSAR PRELIMINARY; PRT; 84 AA.
AC O7PCB5;
RT "Comparative analysis of PSK peptide growth factor precursor
RT homologs."
RL Plant Sci. 163:321-332(2002).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK00114; DA00278.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008283; P:cell proliferation; IEA.
DR InterPro; IPR009438; PSK.
DR Pfam; PF06404; PSK; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 84 AA; 9242 MW; 6B04F8D05EC36C9B CRC64;

Query Match 55.3%; Score 47; DB 2; Length 84;
Best Local Similarity 61.5%; Pred. No. 2;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATW 15
DB 358 HNDSPVTEQOATW 372

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DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Phosphatidylinositol 3-kinase TOR1 (Fragment).
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
CX NCBI_TaxId=40410;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=99262981; PubMed=10330150;
RX Cruz M.C., Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heltman J.;
RT "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112(1999).
DR EMBL; AF098973; AAD16274.1; -; mRNA.
DR HSSP; P42345; LAUE.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR InterPro; IPR003151; FAT.
DR InterPro; IPR00403; P13/4_kinase_cat.
DR InterPro; IPR01990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR SMART; SM00454; P13_P14_kinase; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
KW Kinase; Transferase.
FT NON_TER
FT TER
SQ SEQUENCE 1083 AA; 123973 MW; 0C48A17D58353A9 CRC64;

Query Match 55.3%; Score 47; DB 2; Length 1083;
Best Local Similarity 53.3%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15
DB 202 HADEPARQEMORQTW 216

RESULT 6
ID 094188_CRYNE PRELIMINARY; PRT; 2360 AA.
AC 094188;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Phosphatidylinositol 3-kinase TOR1.
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
CX NCBI_TaxId=40410;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H99;
RX MEDLINE=99262981; PubMed=10330150;
RA Cruz M.C., Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heltman J.;
RT "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112(1999).
DR EMBL; AF098972; AAD16273.1; -; Genomic_DNA.
DR HSSP; P42345; LAUE.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR InterPro; IPR011899; ARM-like.

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DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR000357; HEAT.
DR InterPro; IPR000403; P13/4_kinase_cat.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02985; HEAT; 3.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
KW Kinase
SQ SEQUENCE 2360 AA; 267216 MW; ED4A1059B1AA2B2A CRC64;

Query Match 55.3%; Score 47; DB 2; Length 2360;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15
DB 1479 HADEPARQEMORQTW 1493

RESULT 7
ID 055R83_CRYNE PRELIMINARY; PRT; 2360 AA.
AC 055R83;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNBP1080;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
CX NCBI_TaxId=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wicker B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA01000030; BAU20296.1; -; Genomic_DNA.
DR KW Hypothetical protein.
SQ SEQUENCE 2360 AA; 267302 MW; EB7ABF966AB68ADF CRC64;

Query Match 55.3%; Score 47; DB 2; Length 2360;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15
DB 1479 HADEPARQEMORQTW 1493

RESULT 8
ID 05KEY7_CRYNE PRELIMINARY; PRT; 2360 AA.
AC 05KEY7;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Phosphatidylinositol 3-kinase TOR1.
GN ORFNames=CNF03740;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
CX NCBI_TaxId=214684;
RN [1]

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RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=JEC21;  
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Uterback T.,  
RA Van Aken S., Fraser C.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=JEC21;  
RA PubMed=15653466; DOI=10.1126/science.1103773;  
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,  
RA Besder I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
RA D'Souza C.A., Fox D.S., Grindberg V., Fu J., Fukushima M., Haas B.J.,  
RA Huang J.C., Janson G., Jones S.J.M., Koo H.L., Kzysinski M.I.,  
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,  
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,  
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
RA Suh B.B., Tenney A., Uterback T.R., Wickes B.L., Wotman J.R.,  
RA Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,  
RA Fraser C.M., Hyman R.W.;  
RT "The genome of the basidiomycetous yeast and human pathogen  
RT *Cryptococcus neoformans*."  
RL Science 307:1321-1324(2005).  
DR EMBL: AEO17346; AAM44029.1; -, Genomic DNA.  
DR GO: GO:0016301; P:Kinase activity; IEA.  
DR GO: GO:0016773; P:Phosphotransferase activity, alcohol group . . .; IEA.  
DR InterPro: IPR011989; AAM-like.  
DR InterPro: IPR003151; FAT.  
DR InterPro: IPR003152; FAT.  
DR InterPro: IPR000357; HEAT.  
DR InterPro: IPR000403; P13/4\_kinase\_cat.  
DR InterPro: IPR011990; TPR-like\_helical.  
DR Pfam: PF02259; FAT; 1.  
DR Pfam: PF02260; FATC; 1.  
DR Pfam: PF02985; HEAT; 3.  
DR Pfam: PF00454; P13\_P14\_kinase; 1.  
DR SMART: SM00146; P13Kc; 1.  
DR PROSITE: PS00915; P13\_4\_KINASE\_1; 1.  
DR PROSITE: PS50290; P13\_4\_KINASE\_3; 1.  
DR Complete proteome; Kinase.  
SQ SEQUENCE 2360 AA; 267304 MW; EBYABP966A66ADF CRC64;  
QY 1 HNDSPVTEQOATTW 15  
Db 1479 HADEPAKQEMQROTW 1493  
Query Match 55.3%; Score 47; DB 2; Length 2360;  
Best Local Similarity 53.3%; Pred. No. 1.le+02;  
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
RESULT 9  
ID OSVGS4\_DROME PRELIMINARY; PRT; 425 AA.  
AC OSVGS4;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE CG1299-PB, isoform B.  
GN Name=nocutrin; ORNames=CG1299;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscormorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
OC [1]  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wotman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Adiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballwe R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferreira C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jostai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lesko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshell A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasearan D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muny D.M., Nelson C.R.,  
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminke J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celinker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomic perspective."  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Bernan B.P.,  
RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review."  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RG Berkeley *Drosophila* Genome Project;  
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;



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RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003690; AAF54601.2; -; Genomic DNA.
DR Ensemble; CG31299; Drosophila melanogaster.
DR FlyBase; FBgn0037872; CG31299.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 425 AA; 47584 MW; AABF2F74541D29F CRC64;

Query Match          54.1%; Score 46; DB 2; Length 425;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HNDSPVTEQOATW 15
    ||| ||| |||
    109 HNDGFVRCPEALTW 123

RESULT 10
Q8MT26_DROME
ID Q8MT26_DROME PRELIMINARY; PRT; 449 AA.
AC Q8MT26;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nocturnin.
GN Name=nocturnin; ORFNames=CG31299;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=11747467;
RA Dupressoir A., Morel A.-P., Barbot W., Loizeau M.-P., Corbo L.,
RA Heidmann T.;
RT "Identification of four families of YCCR4- and Mg2+-dependent
RT endonuclease-related proteins in higher eukaryotes, and
RT characterization of orthologs of YCCR4 with a conserved leucine-rich
RT repeat essential for hCAFL/hPOP2 binding."
RL BMC Genomics 2:9-9(2001).
DR EMBL; AY043266; AAK85704.1; -; mRNA.
DR Ensemble; CG31299; Drosophila melanogaster.
DR FlyBase; FBgn0037872; CG31299.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 449 AA; 50275 MW; 1607DF25A418A024 CRC64;

Query Match          54.1%; Score 46; DB 2; Length 449;
Best Local Similarity 53.3%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HNDSPVTEQOATW 15
    ||| ||| |||
    133 HNDGFVRCPEALTW 147

RESULT 11
Q6AWF6_DROME
ID Q6AWF6_DROME PRELIMINARY; PRT; 526 AA.
AC Q6AWF6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE GH0334p.
GN Name=nocturnin;

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OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Berkeley;
RC Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celinker S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT015292; AAT94521.1; -; mRNA.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 526 AA; 58950 MW; BDE21244AB110FA CRC64;

Query Match          54.1%; Score 46; DB 2; Length 526;
Best Local Similarity 53.3%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HNDSPVTEQOATW 15
    ||| ||| |||
    210 HNDGFVRCPEALTW 224

RESULT 12
Q9VGS5_DROME
ID Q9VGS5_DROME PRELIMINARY; PRT; 621 AA.
AC Q9VGS5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG31299-PA, isoform A.
GN Name=nocturnin; ORFNames=CG31299;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Aamatsides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jajalji M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RL Science 287:2185-2195(2000).  
 RN  
 RP NOCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Ceolinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Peckol J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*  
 RT melanogaster euchromatic genome sequence,"  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN  
 RP NOCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Ceolinker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomics perspective,"  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
 RN  
 RP NOCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Battencourt B.R., Ceolinker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review,"  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN  
 RP NOCLEOTIDE SEQUENCE.  
 RA Berkeley *Drosophila* Genome Project;  
 RA Ceolinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,  
 RA Yu C., Rubin G.;  
 RT "Protophila melanogaster release 4 sequence,"  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN  
 RP NOCLEOTIDE SEQUENCE.  
 RG FlyBase;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AEO03690; AAF54600.2; -, Genomic DNA.  
 DR Ensembl; CG31299; *Drosophila melanogaster*.  
 DR FlyBase; FBgn0037872; CG31299.  
 DR FlyBase; FBgn0037872; nocturnin.  
 DR InterPro; IPR005135; Exo endo phos.  
 DR Pfam; PF03372; Exo endo phos; 1.  
 SQ SEQUENCE 621 AA; 69511 MW; A775AD0BB776FEF1 CRC64;

Query Match 54.1%; Score 46; DB 2; Length 621;  
 Best Local Similarity 53.3%; Pred. No. 39;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVTEBOATW 15  
 DB 305 HNDGFVRCPEALTW 319

RESULT 13  
 OSOK3\_ENCCU  
 ID OSOK3\_ENCCU PRELIMINARY; PRT; 700 AA.

AC OSOK3;  
 DT 01-JUN-2002 (TEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE VACUOLAR ATP SYNTHASE 95KDA SUBUNIT.  
 GN OrderedLocusNames=ECU09\_1790;  
 OS Encephalitozoon cuniculi.  
 OC Eukaryota; Fungi; Microsporidia; Unikaryoniidae; Encephalitozoon.  
 ON NCBI\_TaxID=6035;  
 RN  
 RP NOCLEOTIDE SEQUENCE.  
 RC STRAIN=GB-M1;  
 RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;  
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomaat F.,  
 RA Prensier G., Barbe V., Peyretallade E., Brotlier P., Wincker P.,  
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
 RA Weissenbach J., Vives C.P.;  
 RT "Genome sequence and gene compaction of the eukaryote parasite  
 RT Encephalitozoon cuniculi,"  
 RL Nature 414:450-453(2001).  
 DR EMBL: AL590451; CAD27151.1; -, Genomic DNA.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
 DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO: GO:0046961; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.  
 DR GO: GO:0015992; P:proton transport; IEA.  
 DR InterPro; IPR00711; ATPeNt OSCP.  
 DR InterPro; IPR002355; Cu ox copper BS.  
 DR InterPro; IPR002490; V\_ATPase\_sub16.  
 DR Pfam; PF01496; V\_ATPase\_1; 1.  
 DR PROSITE; PS00079; MULTICOPPER\_OXIDASE1; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 700 AA; 80781 MW; FD7D9B862373763D CRC64;

Query Match 53.5%; Score 45.5; DB 2; Length 700;  
 Best Local Similarity 45.0%; Pred. No. 54;  
 Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

QY 1 HNDSPVTEBOATW 15  
 DB 233 HNDFAIRKEQKIRHRANTW 252

RESULT 14  
 IPNS\_STRCT  
 ID IPNS\_STRCT STANDARD; PRT; 321 AA.  
 AC Q53932;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin N  
 DE synthase).  
 GN Name-pbc; Synonym=ipns;  
 OS Streptomyces catleya.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycetales; Streptomycetaceae; Streptomycetes.  
 OC NCBI\_TaxID=29303;  
 RN  
 RP NOCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RX MEDLINE=97350503; PubMed=9206271;  
 RA Wang Y., Li R.;  
 RT "Cloning and sequencing the isopenicillin N synthetase (IPNS) gene  
 RT from *Streptomyces catleya*,"  
 RL Wei Sheng Wu Xue Bao 36:87-92(1996).  
 CC -1- FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms  
 CC from delta-L-(alpha-aminoacidipyl)-L-cysteiny-D-valine (ACV) to  
 CC form the azetidinone and thiazolidine rings of isopenicillin.  
 CC -1- CATALYTIC ACTIVITY: N-((5S)-5-amino-5-carboxypentanoyl)-L-  
 CC cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.  
 CC -1- COFACTOR: Iron and ascorbate.  
 CC -1- PATHWAY: Biosynthesis of penicillin and cephalosporin.  
 CC -1- SIMILARITY: Belongs to the iron/ascorbate-dependent oxidoreductase

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CC family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; D78166; BA011234.1; -; Genomic_DNA.
DR PIR; A58458; A58458.
DR HSSP; P05326; 103E.
DR InterPro; IPR005123; 2OG-Fell_Oase.
DR InterPro; IPR002283; IPN_synth.
DR InterPro; IPR002057; Isopen_N_synth.
DR PANTHER; PTHR10209:SF1; Isopen_N_synth; 1.
DR Pfam; PF03171; 2OG-Fell_Oxy; 1.
DR PRINTS; PR00682; IPNSYNTHASE.
DR PROSITE; PS00185; IPNS_1; 1.
DR PROSITE; PS00186; IPNS_2; 1.
DR Antibiotic biosynthesis; Iron; Metal-binding; Oxidoreductase;
KM Vitamin C.
FT METAL 213 213 Iron (By similarity).
FT METAL 215 215 Iron (By similarity).
FT METAL 269 269 Iron (By similarity).
SQ SEQUENCE 321 AA; 36577 MW; BCC0CFECFC07AF1 CRC64;

Query Match 52.9%; Score 45; DB 1; Length 321;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATW 15
Db 61 NESTTMTDQRSTW 74

RESULT 15
Q4WH60 ASPFU PRELIMINARY; PRT; 407 AA.
AC Q4WH60
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE MFS transporter, putative.
GN ORFNames=Afu7G08460;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293.
RA Nierman W., Fain A., Anderson M.J., Wortman J., Kim H., Stanley,
RA Arroya J., Bertrian M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins K., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Rouning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

```

```

CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHP01000009; EAL86731.1; -; Genomic DNA.
SQ SEQUENCE 407 AA; 43375 MW; F249C762E0CA8116 CRC64;

Query Match 52.9%; Score 45; DB 2; Length 407;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATW 15
Db 15 NGSPVMAEQRSTW 28

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Search completed: December 12, 2005, 20:41:05  
Job time : 84.4655 secs

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CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC horse IGE 5.91 recognition site.

XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATTR 15  
 |||||  
 DB 1 RNNVLIQTDOQATTR 15

#### RESULT 2

ID ADC64568  
 ADCC64568 standard; peptide; 15 AA.

AC ADC64568;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide PA.

XX Horse; immunoglobulin E, IGE; heavy chain; immunogen; allergy.

XX Equus caballus.

OS US2003087314-A1.

XX  
 PN 08-MAY-2003.

PD 08-NOV-2001; 2001US-00052788.

PF 08-NOV-2001; 2001US-00052788.

PR 08-NOV-2001; 2001US-00052788.

XX (REGC ) UNIV CALIFORNIA.

XX Gerstwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

XX Immunogenic composition comprising an isolated equine immunoglobulin E  
 PT polypeptide that induces production of antibodies which specifically bind  
 PT to equine immunoglobulin E.

XX Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (SI-86). 15 amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (IgE), the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (SI)-(86), an antibody that  
 CC specifically binds to equine IGE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (SI)-(86), making an  
 CC antibody that specifically binds to equine IGE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-  
 CC (86)), and collecting antiserum from the animal) and a kit for detection  
 CC of equine IGE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IGE. The  
 CC antibody is useful for detecting equine IGE protein in a biological  
 CC sample (serum) which involves contacting the sample with the antibody/  
 CC thus forming an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the  
 CC complex can be detected. The complex is detected using a second labelled

CC antibody. The peptides are useful for generating antibodies specific for  
 CC IGE which can serve as a diagnostic test for allergy. The present  
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic  
 CC peptide from the early portion of the C4 region.

XX  
 SQ Sequence 15 AA;

Query Match 66.2%; Score 49; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.071;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IOTDQATTR 15  
 |||||  
 DB 1 IOTDQATTR 10

#### RESULT 3

ID ADR10601  
 ADR10601 standard; peptide; 15 AA.

AC ADR10601;

DT 21-OCT-2004 (first entry)

DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

XX WO2004065936-A2.

XX 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

XX (VUNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.

XX  
 SQ Sequence 15 AA;

Query Match 55.4%; Score 41; DB 8; Length 15;  
 Best Local Similarity 64.3%; Pred. No. 2;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDQOATT 14  
 ||: |||||  
 DB 1 RNDSPVRIQTDQYTTT 14

## RESULT 4

ADRI0607  
 ID ADRI0607 standard; peptide; 15 AA.

AC ADRI0607;

XX 21-OCT-2004 (first entry)

DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KM pig.

XX Sue scrofa.

OS WO2004065936-A2.

PN 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

PF 16-JAN-2003; 2003US-0440472P.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC pig IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 54.1%; Score 40; DB 8; Length 15;

Best Local Similarity 46.7%; Pred. No. 3.1;  
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDQOATT 15  
 ||: |||||

DB 1 RNDAPVQADRHSTTR 15

## RESULT 5

ADRI0602  
 ID ADRI0602 standard; peptide; 15 AA.

AC ADRI0602;  
 XX 21-OCT-2004 (first entry)  
 XX

DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KM cat.

XX Felis catus.

OS WO2004065936-A2.

PN 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

PF 16-JAN-2003; 2003US-0440472P.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC cat IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 50.0%; Score 37; DB 8; Length 15;

Best Local Similarity 53.8%; Pred. No. 11;  
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 RNNVLIQTDQOATT 14  
 ||: |||||

DB 2 RNDSPVRIQTDQATT 14

## RESULT 6

ADDA4095  
 ID ADDA4095 standard; peptide; 15 AA.

AC ADDA4095;

XX 15-JAN-2004 (first entry)

DE CPG2 peptide #1 able to stimulate human T-cells in vitro.

XX bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;  
 KW immunogenic; T-cell epitope; MHC class II binding ligand;  
 KW immunostimulant; enzyme therapy; immune response;

XX	gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.
XX	Pseudomonas sp. RS-16.
XX	WO2003045426-A1.
XX	05-JUN-2003.
XX	27-NOV-2002; 2002WO-EP013351.
XX	29-NOV-2001; 2001EP-00128519.
XX	PR 25-JAN-2002; 2002EP-00001778.
XX	PR 13-SEP-2002; 2002EP-00020634.
XX	(MERE ) MERCK PATENT GMBH.
XX	Hellendoorn K, Baker M, Williams S, Carr FJ;
XX	WPI; 2003-513617/48.
XX	New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
XX	PT substantially non-immunogenic or less immunogenic than any non-modified
XX	PT CPG2, useful for inducing an immune response in a human host.
XX	Claim 3; Page 14; 52pp; English.
XX	The invention relates to a novel modified bacterial enzyme
XX	CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
XX	CC proteins that are substantially non-immunogenic or less immunogenic than
XX	CC any non-modified CPG2 having essentially the same biological specificity
XX	CC when used in vivo, and comprising specific amino acid residues having
XX	CC alterations compared with the non-modified parental enzyme. The
XX	CC alterations cause a reduction or an elimination of one or more of T-cell
XX	CC epitope sequences, which act in the parental enzyme as MHC class II
XX	CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
XX	CC CPG2 proteins have immunostimulant activity and may be used in enzyme
XX	CC therapy. The modified CPG2 enzyme may be used to induce an immune
XX	CC response in a human host, or as a therapeutic entity such as the gene
XX	CC directed enzyme prodng strategy. The peptide is useful for the
XX	CC manufacture of a modified CPG2 enzyme having substantially no or less
XX	CC immunogenicity than any non-modified parental enzyme when used in vivo,
XX	CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
XX	CC This sequence represents a CPG2 enzyme peptide able to stimulate human T-
XX	CC cells in vitro of the invention.
XX	SQ Sequence 15 AA;
XX	Query Match 43.2%; Score 32; DB 7; Length 15;
XX	Best Local Similarity 61.5%; Pred. No. 89;
XX	Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
OY	1 RNNVLIO--TDQQ 11
OY	:           :   :
Dd	3 KDNVLFPQATPDEQ 15
RESULT 7	
ID ADD44240	standard; peptide; 15 AA.
XX AC ADD44240;	
XX DT 15-JAN-2004	(first entry)
XX DE Carboxypeptidase G2 (CPG2) enzyme immunogenic peptide #1.	
XX bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;	
KW immunogenic; T-cell epitope; MHC class II binding ligand;	
KW immunostimulant; enzyme therapy; immune response;	
KW gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.	
OS Pseudomonas sp. RS-16.	

PN	WO2003045426-A1.
XX	
PD	05-JUN-2003.
XX	
PF	27-NOV-2002; 2002WO-EP013351.
XX	
PR	29-NOV-2001; 2001EP-00128519.
PR	25-JAN-2002; 2002EP-00001778.
XX	
PR	13-SEP-2002; 2002EP-00020634.
XX	
PA	(MERE ) MERCK PATENT GMBH.
XX	
PI	Hellendoorn K, Baker M, Williams S, Carr FT;
XX	
DR	WPI; 2003-513617/48.
XX	
PT	New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
PT	substantially non-immunogenic or less immunogenic than any non-modified
PT	CPG2, useful for inducing an immune response in a human host.
XX	
PS	Example 2; Fig 1; 52pp; English.
XX	
CC	The invention relates to a novel modified bacterial enzyme
CC	carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
CC	proteins that are substantially non-immunogenic or less immunogenic than
CC	any non-modified CPG2 having essentially the same biological specificity
CC	when used in vivo, and comprising specific amino acid residues having
CC	alterations compared with the non-modified paracatal enzyme. The
CC	alterations cause a reduction or an elimination of one or more of T-cell
CC	epitope sequences, which act in the parental enzyme as MHC class II
CC	binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
CC	CPG2 proteins have immunostimulant activity and may be used in enzyme
CC	therapy. The modified CPG2 enzyme may be used to induce an immune
CC	response in a human host, or as a therapeutic entity such as the gene
CC	directed enzyme proding strategy. The peptide is useful for the
CC	manufacture of a modified CPG2 enzyme having substantially no or less
CC	immunogenicity than any non-modified parental enzyme when used in vivo,
CC	and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
CC	This sequence represents an immunogenic peptide of the CPG2 enzyme of the
CC	invention.
CC	
XX	
SQ	Sequence 15 AA:
	Query Match                      43.2%; Score 32; DB 7; Length 15;
	Best Local Similarity        61.5%; Pred. No. 89;
	Matches     8; Conservative     2; Mismatches     1; Indels     2; Gaps     1;
OY	1 RNNVLIQ--TDQQ 11
	:               :
DB	3 RDNVLFQMATEDQ 15
RESULT 8	
AECL1192	ID AECL1192 standard; peptide; 12 AA.
AC	AECL1192;
DT	20-OCT-2005 (first entry)
DE	Pseudomonas aeruginosa phosphoglucosamine mutase peptide.
XX	
KW	protein purification; antibacterial; antimicrobial; infection;
XX	drug screening; phosphoglucoisomerase mutase.
OS	Pseudomonas aeruginosa.
PN	US2005181388-A1.
XX	
PD	18-AUG-2005.
XX	
PF	04-OCT-2004; 2004US-00958216.
XX	



PR 02-APR-2002; 2002US-0369511P.  
 PR 04-APR-2002; 2002US-0369817P.  
 PR 04-APR-2002; 2002US-0370102P.  
 PR 08-APR-2002; 2002US-0370778P.  
 PR 08-APR-2002; 2002US-0370792P.  
 PR 08-APR-2002; 2002US-0370820P.  
 PR 08-APR-2002; 2002US-0370859P.  
 PR 08-APR-2002; 2002US-0370899P.  
 PR 08-APR-2002; 2002US-0370915P.  
 PR 09-APR-2002; 2002US-0371107P.  
 PR 09-APR-2002; 2002US-0371140P.  
 PR 09-APR-2002; 2002US-0371185P.  
 PR 31-MAY-2002; 2002US-0385089P.  
 PR 31-MAY-2002; 2002US-0385426P.  
 PR 04-JUN-2002; 2002US-0386018P.  
 PR 05-JUN-2002; 2002US-0386367P.  
 PR 05-JUN-2002; 2002US-0386549P.  
 PR 05-JUN-2002; 2002US-0386553P.  
 PR 05-JUN-2002; 2002US-0386566P.  
 PR 05-JUN-2002; 2002US-0386577P.  
 PR 06-JUN-2002; 2002US-0386283P.  
 PR 06-JUN-2002; 2002US-0386390P.  
 PR 06-JUN-2002; 2002US-0386430P.  
 PR 06-JUN-2002; 2002US-0386601P.  
 PR 06-JUN-2002; 2002US-0386826P.  
 PR 06-JUN-2002; 2002US-0386869P.  
 PR 31-JUL-2002; 2002US-0398972P.  
 PR 01-AUG-2002; 2002US-0400348P.  
 PR 05-NOV-2002; 2002US-0424053P.  
 PR 06-NOV-2002; 2002US-0424380P.  
 PR 08-NOV-2002; 2002US-0425395P.  
 PR 08-NOV-2002; 2002US-0425086P.  
 PR 24-DEC-2002; 2002US-0436243P.  
 PR 24-DEC-2002; 2002US-0436288P.  
 PR 24-DEC-2002; 2002US-0436345P.  
 PR 24-DEC-2002; 2002US-0436349P.  
 PR 26-DEC-2002; 2002US-0436566P.  
 PR 26-DEC-2002; 2002US-0436567P.  
 PR 26-DEC-2002; 2002US-0436568P.  
 PR 27-DEC-2002; 2002US-0436675P.  
 PR 27-DEC-2002; 2002US-0436708P.  
 PR 27-DEC-2002; 2002US-0436734P.  
 PR 27-DEC-2002; 2002US-0436804P.  
 PR 27-DEC-2002; 2002US-0436834P.  
 PR 27-DEC-2002; 2002US-0436842P.  
 PR 27-DEC-2002; 2002US-0436861P.  
 PR 27-DEC-2002; 2002US-0436885P.  
 PR 27-DEC-2002; 2002US-0436889P.  
 PR 27-DEC-2002; 2002US-0436893P.  
 PR 27-DEC-2002; 2002US-0436900P.  
 PR 30-DEC-2002; 2002US-0436947P.  
 PR 30-DEC-2002; 2002US-0436971P.  
 PR 30-DEC-2002; 2002US-0436987P.  
 PR 30-DEC-2002; 2002US-0437013P.  
 PR 30-DEC-2002; 2002US-0437038P.  
 PR 30-DEC-2002; 2002US-0437141P.  
 PR 31-DEC-2002; 2002US-0437281P.  
 PR 31-DEC-2002; 2002US-0437527P.  
 PR 31-DEC-2002; 2002US-0437620P.  
 PR 02-APR-2003; 2003US-CA000462.  
 PR 04-APR-2003; 2003US-CA000464.  
 PR 08-APR-2003; 2003US-CA000481.  
 PR 08-APR-2003; 2003US-CA000485.

(AFFI-) AFFINUM PHARM INC.

XX Edwards A, Dharmas A, Vedadi M, Alam MZ, Arrowsmith C, Awrey DE;  
 PI Beattie B, Buzadzija K, Canadien V, Domagala M, Houston S;  
 PI Kanagarajah D, Li Q, Mansoury K, McDonald M, Nethery-Brooks K, Ng I;

PI Ouyang H, Pinder B, Richards D, Tai M, Thalakada R, Vallee F;  
 PI Virag C;  
 XX WPI; 2005-628189/64.  
 DR  
 XX  
 PT New composition comprising purified polypeptides from bacteria (e.g.  
 PT Escherichia coli), useful for diagnosing, preventing or treating  
 PT microbial infections, or in pharmacogenomic or drug screening procedures.  
 XX  
 PS Example 1; Fig 219; 667pp; English.  
 CC The invention relates to a composition (I) comprising purified  
 CC polypeptides from bacteria. Also described: (1) a crystallized,  
 CC recombinant polypeptide comprising an amino acid sequence of (I), where  
 CC the polypeptide is in crystal form; (2) a crystallized complex comprising  
 CC the crystallized, recombinant polypeptide and a co-factor or a small  
 CC organic molecule, where the complex is in crystal form; and (3) a host  
 CC cell comprising a nucleic acid encoding a polypeptide of (I), where a  
 CC culture of the host cell produces at least about 1 mg of the polypeptide  
 CC per liter of culture and the polypeptide is at least about one-third  
 CC soluble as measured by gel electrophoresis. The composition and methods  
 CC are useful for diagnosing, preventing or treating diseases, such as  
 CC microbial infections. These may also be used in pharmacogenomic or drug  
 CC screening procedures. The present sequence represents a pseudomonas  
 CC aeruginosa phosphoglucosamine mutase peptide, which is used in an example  
 CC from the present invention.  
 XX  
 SQ Sequence 12 AA;

Query Match 39.2%; Score 29; DB 9; Length 12;  
 Best Local Similarity 33.3%; Pred. No. 2.4e+02;  
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 VLQTDQQTTR 15  
 DB 1 VMVSGDERASVR 12

RESULT 9  
 AAY65622  
 ID AAY65622 standard; peptide, 15 AA.  
 XX  
 AC AAY65622;  
 XX

DT 01-FEB-2000 (first entry)

DE Oestrogen receptor beta ERB binding peptide 17E-beta.

KW Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERE;  
 KW binding; biological activity; fingerprint; molecular braille;  
 KW cellular braille; modulation; tamoxifen; breast cancer; ovarian cancer;  
 KW menopause; osteoporosis; selective oestrogen receptor modulator;  
 KW identification; characterisation; classification.

OS Synthetic.  
 OS Homo sapiens.

PN W09954728-A2.

PD 28-OCT-1999.

PF 26-MAR-1999; 99WO-US006664.

PR 23-APR-1998; 98US-0082756P.

PR 09-SEP-1998; 98US-0099656P.

PR 08-JAN-1999; 99US-0115345P.

PA (NOVA-) NOVAFON PHARM CORP.

PI Paige LA, Hamilton PT, Fowlkes DM, Buehrer B, Barnett T;  
 PI McDonnell DP, Christensen DJ;  
 XX WPI; 2000-013281/01.

XX Methods for identifying new receptor modulators, especially estrogen  
PT modulators to treat tamoxifen refractory breast cancer.  
XX  
PS Example 2.2; Page 164; 219pp; English.  
XX  
CC The present invention describes a method for predicting the biological  
CC activity of new receptor modulating compounds (I) using novel oligomeric  
CC peptides (blokeys) which have differential abilities to bind to 2  
CC different receptor conformations. The method is used to identify new  
CC drugs that are physiological or pharmacological agonists/antagonists and  
CC that target various receptors, which are involved in certain disease  
CC conditions. The system may be used as a primary screening tool to  
CC identify hits, to classify lead compounds from a drug screen to,  
CC characterise selective oestrogen receptor modulators (SERMs) in terms of  
CC agonist and antagonist function and to predict possible clinical effects  
CC of SERMs such as tissue and receptor specificity. The method can also be  
CC applied to the fractionation of mixtures of SERMs to determine which  
CC components are producing agonistic and antagonistic activity. The method  
CC may be used with other receptors (e.g. progesterone, androgen,  
CC glucocorticoid, thyroid, vitamin D, beta-adrenergic, dopamine and  
CC epidermal growth factor, to identify, characterise and classify  
CC modulators of receptor activity. Peptides comprising a LXXLL motif may be  
CC used to modulate the oestrogen receptor in treating e.g. breast and  
CC ovarian cancer and ameliorating the effects of menopause, including  
CC oestroporosis. AAY65439 to AAY65652 represent oestrogen receptor,  
CC estradiol receptor and oestrogen response element binding peptides given  
CC in the exemplification of the present invention. AA235740 to AA235745  
CC represent oligonucleotides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 39.2%; Score 29; DB 3; Length 15;  
Best Local Similarity 46.2%; Pred. No. 3.1e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 3 NVLIQTDQQAATR 15  
|:| |::| |:  
Db 3 NLCLLDQEAACSR 15  
  
RESULT 10  
AAY6359 standard; peptide; 15 AA.  
XX  
AC AAY6359;  
XX  
XX 21-MAY-2002 (first entry)  
XX  
DE Oestrogen receptor beta binding peptide 17B-beta.  
XX  
KM Oestrogen receptor; breast cancer; combinatorial peptide library;  
XX receptor modulating compound.  
OS Synthetic.  
XX  
XX WO200204956-A2.  
XX  
XX 17-JAN-2002.  
XX  
XX 11-JUL-2001; 2001WO-US021867.  
XX  
XX 12-JUL-2000; 2000US-00614865.  
XX  
XX 21-MAY-2001; 2001US-00860688.  
XX  
XX (KARO-) KARO BIO USA INC.  
XX  
XX Fowlkes DM, Barnett TR, Buehrer B;  
XX  
XX WPI; 2002-154969/20.  
XX  
XX Identifying receptor-binding peptides comprises screening combinatorial  
XX  
XX  
XX

PT peptide library presented in form of cells each of which coexpress one  
PT peptide member and receptor with signal producing system for reporting  
PT binding.  
XX  
XX Disclosure; Page 146; 175pp; English.  
XX  
XX The invention relates to identifying a binding peptide which binds a  
CC receptor and which is a member of a combinatorial library of peptides,  
CC comprising screening a combinatorial peptide library presented in the  
CC form of cells which coexpress the receptor or its ligand-binding receptor  
CC moiety and one member of the library, together with a signal producing  
CC system for reporting binding of the peptide to the receptor. Also  
CC included is a method for predicting the receptor-modulating activity of a  
CC compound which modulates the biological activity of a receptor comprising  
CC (a) identifying peptides which bind the receptor by the method above, (b)  
CC using a number of the peptides to predict the receptor-modulating  
CC activity of a compound by (i) providing a panel of identified peptides,  
CC where the members differ in their ability to bind to the receptor  
CC depending on reference conformations known to modulate the biological  
CC activity of the receptor on the binding of each member of the panel is  
CC known and is characterised as a reference fingerprint for each reference  
CC substance, (ii) screening a test substance of unknown activity relative  
CC to the receptor to determine its effect on the binding of each member of  
CC the panel to the receptor, thereby obtaining a test fingerprint for the  
CC test substance, (iii) comparing the test fingerprint to the reference  
CC fingerprints and (iv) predicting the biological activity of the test  
CC substance based on the assumption that its biological activity will be  
CC similar to that of reference substances with similar fingerprints. The  
CC method is useful for identifying a binding peptide which binds a  
CC vertebrate, mammalian, preferably human receptor, an intracellular,  
CC nuclear, oestrogen or androgen receptor. The identified peptides which  
CC bind to the receptor are useful for predicting the receptor-modulating  
CC activity of a compound (e.g. ant/agonists). The receptor-binding library  
CC members are useful in the prediction of the ability of small organic  
CC molecules, suitable for pharmaceutical use (e.g. in the case of oestrogen  
CC receptors, for breast cancer treatment), to interact with the receptor.  
CC The analyte-binding molecules can also be used for in vivo imaging. The  
CC method has several advantages over whole animal-based assay systems in  
CC that the same technology can be applied to a variety of different  
CC receptors, the system can be used for high throughput screening and  
CC compound characterisation, and gives very distinct patterns for agonists  
CC and antagonists of receptor activity using very much less protein. The  
CC present sequence is an oestrogen receptor binding peptide from a  
CC combinatorial peptide library  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 39.2%; Score 29; DB 5; Length 15;  
Best Local Similarity 46.2%; Pred. No. 3.1e+02;  
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 3 NVLIQTDQQAATR 15  
|:| |::| |:  
Db 3 NLCLLDQEAACSR 15  
  
RESULT 11  
ADM79070 standard; peptide; 15 AA.  
XX  
XX ADM79070;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Oestrogen receptor beta binding peptide #57.  
XX  
XX Oestrogen receptor; drug identification; in vivo imaging;  
XX binding peptide; drug identification; in vivo imaging;  
XX oestrogen receptor beta.  
XX  
XX Unidentified.  
XX  
XX US2003224390-A1.  
XX  
XX  
XX  
XX

XX 04-DEC-2003.  
 PD 17-JAN-2003; 2003US-00346162.  
 XX  
 PF 12-JUL-2000; 2000US-00614865.  
 XX 21-MAY-2001; 2001US-00860688.  
 PR 11-JUL-2001; 2001WO-US021867.  
 XX  
 PA (KARO-) KARO BIO AB.  
 XX  
 PI Fowlkes DM, Barnett TR, Buehrer B;  
 XX WPI; 2004-060539/06.  
 DR  
 XX  
 PT Identifying a binding peptide that binds a receptor, for use as a  
 PT therapeutic or diagnostic agent, comprises screening a combinatorial  
 PT peptide library presented in cells co-expressing a peptide, a receptor  
 PT and a signal producing system.  
 XX  
 PS Example; SEQ ID NO 192; 66pp; English.  
 XX  
 CC The invention relates to a method of identifying a binding peptide which  
 CC binds a receptor comprising screening a combinatorial peptide library  
 CC presented in cells which co-expresses one member peptide and the  
 CC receptor, together with a signal producing system for reporting binding.  
 CC The method is useful in identifying drugs which can mediate the  
 CC biological activity of a target protein. The receptor-binding library  
 CC members may be used as therapeutic or diagnostic reagents, for in vivo  
 CC imaging, or to purify target from a fluid, e.g. blood. The present  
 CC sequence represents an oestrogen receptor beta binding peptide.  
 XX  
 SQ Sequence 15 AA;

Query Match 39.2%; Score 29; DB 8; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 NVLIOTDQOATTR 15  
 |||::|::|::|  
 Db 3 NVLCILDQECRSR 15

RESULT 12  
 ADR10604  
 ID ADR10604 standard; peptide; 15 AA.  
 XX  
 AC ADR10604;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Sheep IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 4.  
 KW Antiasthmatic; Antiallergic; Immunosuppressive; IGF; dog; asthma;  
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 XX sheep.  
 XX  
 OS Ovis aries.  
 XX  
 PN WO2004065936-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 15-JAN-2004; 2004WO-US003566.  
 XX  
 PR 16-JAN-2003; 2003US-0440472P.  
 XX  
 PA (UNNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 PI Hammerberg B;  
 XX  
 DR WPI; 2004-593545/57.  
 XX

PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.  
 XX  
 PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (1) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (1) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC sheep IGE 5.91 recognition site.

XX  
 SQ Sequence 15 AA;

Query Match 39.2%; Score 29; DB 8; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 RNNVLIOTDQOATTR 15  
 |||::|::|::|  
 Db 1 RNNKELMREGQHTTQ 15

RESULT 13  
 AAG95534  
 ID AAG95534 standard; peptide; 10 AA.  
 XX  
 AC AAG95534;  
 XX  
 DT 18-SEP-2001 (first entry)  
 XX  
 DE Human complementary peptide, SEQ ID NO: 1728.  
 XX  
 DE Human complementary peptide; ligand; drug discovery; drug design.  
 XX  
 KM Human; complementary peptide; ligand; drug discovery; drug design.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200142277-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 13-DEC-2000; 2000WO-GB004776.  
 XX  
 PR 13-DEC-1999; 99GB-00029464.  
 XX  
 PA (PROT-) PROTEOM LTD.  
 XX  
 PI Roberts GW, Heal JR;  
 XX  
 DR WPI; 2001-408419/43.  
 XX  
 PT A set of peptide ligands consisting of specific complementary peptides to  
 PT proteins encoded by genes of the human genome, useful in an assay for  
 PT screening and identifying of one or more novel peptides which are drug  
 PT candidates or pro-drugs.  
 XX  
 PS Example 4; Page 290; 646pp; English.  
 XX  
 CC The invention relates to a set of complementary peptide ligands generated  
 CC from the human genome. The complementary peptides interact with their  
 CC relevant target proteins encoded in the human genome. They can be used as  
 CC reagents in drug discovery and as lead ligands to facilitate drug design

CC and development. The present sequence is a complementary peptide provided  
CC in the specification  
XX  
SQ Sequence 10 AA;  
Query Match 36.5%; Score 27; DB 4; Length 10;  
Best Local Similarity 71.4%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 8 TDQOATT 14  
: ||| |  
1 SDQQT 7  
Db  
RESULT 14  
ADV57215  
ID ADV57215 standard; peptide; 11 AA.  
XX  
AC ADV57215;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE G protein coupled receptor peptide SEQ ID NO 4719.  
XX  
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
XX  
OS Unidentified.  
XX  
PN W02004111636-A2.  
XX  
PD 23-DEC-2004.  
XX  
PF 17-JUN-2004; 2004WO-EP051158.  
XX  
PR 17-JUN-2003; 2003EP-00101775.  
PR 17-JUN-2003; 2003US-0479061P.  
PA (VIBV-) VIB VZW.  
PA (UYGE-) UNIV GENT.  
XX  
PI Kas K, Vandekerckhove J, Krols L;  
XX  
DR WPI; 2005-057893/06.  
XX  
PT Identifying a peptide combo which corresponds with a family of proteins,  
PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the  
PT family of protein.  
XX  
PS Example; SEQ ID NO 4719; 265pp; English.  
XX  
CC The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide

CC combo.  
XX  
SQ Sequence 11 AA;  
Query Match 36.5%; Score 27; DB 9; Length 11;  
Best Local Similarity 54.5%; Pred. No. 5.1e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 5 LIOTDQOATTR 15  
: | : ||| |  
1 LMHTVEQATLR 11  
Db  
RESULT 15  
ADV54438  
ID ADV54438 standard; peptide; 11 AA.  
XX  
AC ADV54438;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE G protein coupled receptor peptide SEQ ID NO 1935.  
XX  
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.  
XX  
OS Unidentified.  
XX  
PN W02004111636-A2.  
XX  
PD 23-DEC-2004.  
XX  
PF 17-JUN-2004; 2004WO-EP051158.  
XX  
PR 17-JUN-2003; 2003EP-00101775.  
PR 17-JUN-2003; 2003US-0479061P.  
PA (VIBV-) VIB VZW.  
PA (UYGE-) UNIV GENT.  
XX  
PI Kas K, Vandekerckhove J, Krols L;  
XX  
DR WPI; 2005-057893/06.  
XX  
PT Identifying a peptide combo which corresponds with a family of proteins,  
PT useful for diagnosing a variety of diseases, drug development or in  
PT agriculture, comprises generating peptides by applying a digest on the  
PT family of protein.  
XX  
PS Example; SEQ ID NO 1935; 265pp; English.  
XX  
CC The invention relates to a method of identifying a peptide combo which  
CC corresponds with a family of proteins where each of the members of the  
CC peptide combo is derived from a unique protein from the family. The  
CC peptide combo is useful for quantifying specific known splice variants of  
CC one or more particular proteins in a sample, for diagnosing complex  
CC genetic diseases such as cancer, obesity, diabetes, asthma and  
CC inflammation, neuropsychiatric disorders such as depression, for  
CC quantifying one to several hundreds of protein disease markers  
CC simultaneously leading to a more accurate diagnostic sub-classification,  
CC for determining the extent of protein modification in a particular sample  
CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
CC the presence of a congenital disease or for quantitating protein levels  
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
CC or neurological diseases, as biomarkers preclinical drug development,  
CC development of improved animal models, biomarkers related with  
CC toxicology, clinical drug development, guidance marketed drugs,  
CC prognostic or diagnostic disease markers, drug target validation and  
CC selection, monitoring protein splicing, drug lead profiling, pathway  
CC analysis, answering basic disease biology questions, and in the fields of  
CC food and feed, cosmetics, agriculture and animal breeding. The present  
CC sequence represents a peptide from a G-protein coupled receptor peptide  
CC combo.

XX Sequence 11 AA;

Query Match 36.5%; Score 27; DB 9; Length 11;  
 Best Local Similarity 54.5%; Pred No. 5.1e+02;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LIOTDQATTR 15  
 | : | : | : |  
 Db 1 LMHTVEQATLR 11

Search completed: December 12, 2005, 21:11:38  
 Job time : 114.667 secs

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## OM protein - protein search, using sw model

Run on: December 12, 2005, 20:20:00 ; Search time 27 Seconds  
(without alignments)  
45.931 Million cell updates/sec

Title: US-10-758-165A-3

Perfect score: 74

Sequence: 1 RNNVLQTDQQA1TR 15

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents, AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	25	33.8	14	2	US-09-236-415-6 Sequence 6, Appli
2	25	33.8	15	1	US-08-221-583-42 Sequence 42, Appl
3	25	33.8	15	4	PCR-US93-04018-42 Sequence 42, Appl
4	24	32.4	11	1	US-08-456-6708-38 Sequence 38, Appl
5	24	32.4	11	2	US-09-372-036-38 Sequence 38, Appl
6	24	32.4	15	1	US-08-403-3788-7 Sequence 7, Appli
7	23	31.1	10	2	US-08-485-324-4 Sequence 4, Appli
8	23	31.1	10	2	US-08-485-324-30 Sequence 30, Appl
9	23	31.1	10	2	US-08-447-506-4 Sequence 4, Appli
10	23	31.1	10	2	US-08-447-506-30 Sequence 30, Appl
11	23	31.1	10	2	US-08-235-437-4 Sequence 4, Appli
12	23	31.1	10	2	US-08-235-437-30 Sequence 30, Appl
13	23	31.1	10	2	US-08-447-515-4 Sequence 4, Appli
14	23	31.1	10	2	US-08-447-515-30 Sequence 30, Appl
15	23	31.1	10	2	US-09-462-645C-29 Sequence 29, Appl
16	23	31.1	10	2	US-09-573-830-4 Sequence 4, Appli
17	23	31.1	10	2	US-09-573-830-30 Sequence 30, Appl
18	23	31.1	12	1	US-08-479-233-8 Sequence 8, Appli
19	23	31.1	12	2	US-09-392-812A-7 Sequence 7, Appli
20	23	31.1	12	4	PCR-US93-00643-8 Sequence 8, Appli
21	23	31.1	14	2	US-10-394-980-55 Sequence 55, Appli
22	23	31.1	15	2	US-09-700-993-6 Sequence 6, Appli
23	22	29.7	5	1	US-08-762-106-19 Sequence 19, Appl
24	22	29.7	5	2	US-09-320-774-19 Sequence 19, Appl
25	22	29.7	6	1	US-08-762-106-17 Sequence 17, Appl
26	22	29.7	6	1	US-08-762-106-18 Sequence 18, Appl
27	22	29.7	6	2	US-09-320-774-17 Sequence 17, Appl

28	22	29.7	6	2	US-09-320-774-18 Sequence 18, Appl
29	22	29.7	8	1	US-08-762-106-15 Sequence 15, Appl
30	22	29.7	8	2	US-09-320-774-15 Sequence 15, Appl
31	22	29.7	9	1	US-08-456-6708-25 Sequence 25, Appl
32	22	29.7	9	1	US-08-762-106-13 Sequence 13, Appl
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35	22	29.7	9	2	US-09-320-774-14 Sequence 14, Appl
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38	22	29.7	10	2	US-09-908-392-53 Sequence 53, Appl
39	22	29.7	11	2	US-09-194-285-54 Sequence 54, Appl
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42	22	29.7	13	1	US-07-920-519-12 Sequence 12, Appl
43	22	29.7	13	1	US-08-086-410-9 Sequence 9, Appli
44	22	29.7	13	1	US-08-148-106-33 Sequence 33, Appl
45	22	29.7	13	1	US-08-298-021-33 Sequence 33, Appl

## ALIGNMENTS

```
RESULT 1
US-09-236-415-6
; Sequence 6, Application US/09236415
; Patent No. 6309863
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Appella, Ettore
; APPLICANT: Sakaguchi, Kazuyaau
; TITLE OF INVENTION: METHODS FOR GENERATING PHOSPHORYLATION SITE-SPECIFIC
; FILE REFERENCE: U.S. Application 09/236,415
; CURRENT APPLICATION NUMBER: US/09/236,415
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
; OTHER INFORMATION: ANTIGEN
; FEATURE:
; OTHER INFORMATION: Residue Xaa is a phosphoserine mimetic
US-09-236-415-6
Query Match      33.8% Score 25; DB 2; Length 14;
Best Local Similarity 54.5% Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 NNVLIQTDOQA 12
      |||||
Db      3 NNVLIQTDOQA 13

RESULT 2
US-08-221-583-42
; Sequence 42, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5486595r1s
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
```

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25,mdctcm0d.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,583  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: CCOR-0185  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-221-583-42

Query Match 33.8%; Score 25; DB 1; Length 15;  
Best Local Similarity 55.6%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QTDQATTR 15  
Db 4 QVETQATR 12

RESULT 3  
PCT-US95-04018-42  
Sequence 42, Application PC/TUS9504018  
GENERAL INFORMATION:  
APPLICANT: Heaven, George A.  
APPLICANT: Kruszynski, Marian  
APPLICANT: Meriv, Miljenko  
APPLICANT: Weber, Robert W.  
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSEE: Norris  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04018  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,580  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,583  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,581  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: CCOR-0232

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-04018-42

Query Match 33.8%; Score 25; DB 4; Length 15;  
Best Local Similarity 55.6%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QTDQATTR 15  
Db 4 QVETQATR 12

RESULT 4  
US-08-456-670B-38  
Sequence 38, Application US/08456670B  
Patent No. 5932415  
GENERAL INFORMATION:  
APPLICANT: SCHUBERT, PETER  
APPLICANT: NEUMANN, SIEGFRIED  
APPLICANT: PAMELZIK, MARTINA  
APPLICANT: LINXWEILER, WINFRIED  
APPLICANT: BURGER, CHRISTA  
APPLICANT: HORMANN, GOTTFRIED  
APPLICANT: BUBERT, ANDREAS  
APPLICANT: GOEBEL, WERNER  
APPLICANT: KOHLER, STEFAN  
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD., SUITE 1400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,670B  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/412,227  
FILING DATE: 27-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/075,248  
FILING DATE: 11-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4239567.4  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4219111.4  
FILING DATE: 11-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1694D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
TELEX: 64191



;/ INFORMATION FOR SEQ ID NO: 38:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 11 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ ORIGINAL SOURCE:  
;/ ORGANISM: Listeria innocua  
;/ US-08-456-670B-38

Query Match 32.4%; Score 24; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 9 DQOATTR 15  
: ||| :  
Db 1 EQOTTTK 7

RESULT 5  
US-09-372-036-38  
; Sequence 38, Application US/09372036  
; Patent No. 6951925  
; GENERAL INFORMATION:  
; APPLICANT: SCHUBERT, PETER  
; APPLICANT: NEUMANN, SIEGFRIED  
; APPLICANT: PAWELZIK, MARTINA  
; APPLICANT: LINKELEIR, WINFRIED  
; APPLICANT: BURGER, CHRISTA  
; APPLICANT: HOFMANN, GOTTFRIED  
; APPLICANT: BUBERT, ANDREAS  
; APPLICANT: GOEBEL, WERNER  
; APPLICANT: KOHLER, STEFAN  
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING  
; TITLE OF INVENTION: LISTERIAS  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.  
; STREET: 2200 CLARENDON BLVD., SUITE 1400  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: US  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/372,036  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/456,670  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/075,248  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4239567.4  
; FILING DATE: 25-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4219111.4  
; FILING DATE: 11-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HAMLET-KING, DIANA  
; REGISTRATION NUMBER: 33,302  
; REFERENCE/DOCKET NUMBER: MERCK 1694D1  
; TELEPHONE: 703-243-6333  
; TELEFAX: 703-243-6410  
; TELEX: 64191  
; INFORMATION FOR SEQ ID NO: 38:

;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 11 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ ORIGINAL SOURCE:  
;/ ORGANISM: Listeria innocua  
;/ US-09-372-036-38

Query Match 32.4%; Score 24; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 9 DQOATTR 15  
: ||| :  
Db 1 EQOTTTK 7

RESULT 6  
US-08-403-378B-7  
; Sequence 7, Application US/08403378B  
; Patent No. 5759991  
; GENERAL INFORMATION:  
; APPLICANT: TOHDOH, MAOKI  
; APPLICANT: TOJO, SHIN-ICHIRO  
; APPLICANT: KOJIMA, SHIN-ICHI  
; APPLICANT: Ueki, YASUYUKI  
; APPLICANT: NISHIHARA, TOSHIO  
; APPLICANT: FUKUSHIMA, NOBUYUKI  
; APPLICANT: IRIE, TSUNEMASA  
; APPLICANT: ONO, KEIICHI  
; APPLICANT: AGUI, HIDEO  
; APPLICANT: OIYKA, KOSEI  
; TITLE OF INVENTION: NEUROTROPHIC PEPTIDE DERIVATIVES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 PENNSYLVANIA AVENUE, NW  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,378B  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-124668  
; FILING DATE: 27-APR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 1-080398  
; FILING DATE: 30-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 1-280590  
; FILING DATE: 27-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 1-333241  
; FILING DATE: 21-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-243003  
; FILING DATE: 12-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/758,043  
; FILING DATE: 12-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/873,764  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/01214  
FILING DATE: 27-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGART, WADELL A  
REGISTRATION NUMBER: 24,861  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: rattus norvegicus  
STRAIN: mistar  
TISSUE TYPE: hippocampal tissue of brain  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..15  
US-08-403-378B-7

Query Match 32.4%; Score 24; DB 1; Length 15;  
Best Local Similarity 45.5%; Pred. No. 5.5e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIOTDQATTR 15

Db 4 LVLTDPAPSR 14

RESULT 7  
US-08-485-324-4  
Sequence 4, Application US/08485324  
Patent No. 6043093  
GENERAL INFORMATION:  
APPLICANT: Mohlstader, Jacob  
TITLE OF INVENTION: SELECTION METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris, & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,324  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,437  
FILING DATE: 29-APR-1994  
APPLICATION NUMBER: US 07/852,412  
FILING DATE: 16-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370132-2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-324-4

Query Match 31.1%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDOQATT 14

Db 1 TDOEQTS 7

RESULT 8  
US-08-485-324-30  
Sequence 30, Application US/08485324  
Patent No. 6043093  
GENERAL INFORMATION:  
APPLICANT: Mohlstader, Jacob  
TITLE OF INVENTION: SELECTION METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris, & Safford  
ADDRESSEE: c/o Barry Evans  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,324  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,437  
FILING DATE: 29-APR-1994  
APPLICATION NUMBER: US 07/852,412  
FILING DATE: 16-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Evans, Barry  
REGISTRATION NUMBER: 22,802  
REFERENCE/DOCKET NUMBER: 370132-2000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-0712  
TELEFAX: (212) 840-3333  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-324-30

Query Match 31.1%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDOQATT 14

Db 1 TDOEQTS 7

RESULT 9  
US-08-447-506-4  
Sequence 4, Application US/08447506

```
Patent No. 6066499
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,506
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
TELEFAX: (212) 840-3333
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-506-4

Query Match      31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 TDQOATT 14
      |||:|:
      1 TDQOETS 7

RESULT 10
US-08-447-506-30
Sequence 30, Application US/08447506
Patent No. 6066499
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/447,506
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-506-30

Query Match      31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 TDQOATT 14
      |||:|:
      1 TDQOETS 7

RESULT 11
US-08-235-437-4
Sequence 4, Application US/08235437
Patent No. 6087177
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,437
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
```

US-08-235-437-4

Query Match 31.1%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TDOQATT 14  
Db 1 TDOEQTS 7

RESULT 12

US-08-235-437-30

; Sequence 30, Application US/08235437  
; Patent No. 6087177  
; GENERAL INFORMATION:  
; APPLICANT: Wohlstadter, Jacob  
; TITLE OF INVENTION: SELECTION METHODS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Curtis, Morris, & Safford  
; ADDRESSEE: C/O Barry Evans  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,437  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/852,412  
; FILING DATE: 16-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, Barry  
; REGISTRATION NUMBER: 22,802  
; REFERENCE/DOCKET NUMBER: 370132-2000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-235-437-30

Query Match 31.1%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TDOQATT 14  
Db 1 TDOEQTS 7

RESULT 13

US-08-447-515-4

; Sequence 4, Application US/08447515  
; Patent No. 6162640  
; GENERAL INFORMATION:  
; APPLICANT: Wohlstadter, Jacob  
; TITLE OF INVENTION: SELECTION METHODS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Curtis, Morris, & Safford

; ADDRESSEE: C/O Barry Evans  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,515  
; FILING DATE: 23-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,437  
; FILING DATE: 29-APR-1994  
; APPLICATION NUMBER: US 07/852,412  
; FILING DATE: 16-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, Barry  
; REGISTRATION NUMBER: 22,802  
; REFERENCE/DOCKET NUMBER: 370132-2000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-447-515-4

Query Match 31.1%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TDOQATT 14  
Db 1 TDOEQTS 7

RESULT 14

US-08-447-515-30

; Sequence 30, Application US/08447515  
; Patent No. 6162640  
; GENERAL INFORMATION:  
; APPLICANT: Wohlstadter, Jacob  
; TITLE OF INVENTION: SELECTION METHODS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Curtis, Morris, & Safford  
; ADDRESSEE: C/O Barry Evans  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/447,515  
; FILING DATE: 23-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,437  
; FILING DATE: 29-APR-1994  
; APPLICATION NUMBER: US 07/852,412

FILING DATE: 16-MAR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Evans, Barry  
 REGISTRATION NUMBER: 22,802  
 REFERENCE/DOCKET NUMBER: 370132-2000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 INFORMATION FOR SEQ ID NO: 30:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-447-515-30

Query Match 31.1%; Score 23; DB 2; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDQOATT 14  
 |||:  
 Db 1 TDQOETS 7

RESULT 15  
 US-09-462-645C-29  
 ; Sequence 29, Application US/09462645C  
 ; Patent No. 6436681  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schroeder, Hartwig  
 ; APPLICANT: Hauser, Bernhard  
 ; TITLE OF INVENTION: The preparation of biotin  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/09/462,645C  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/04097  
 ; PRIOR FILING DATE: 1998-02-07  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: WordPerfect version 6.1  
 ; SEQ ID NO 29  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: A. vinelandii  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 7..7  
 ; OTHER INFORMATION: Xaa is unknown. Amino acid sequence is a typical N-terminal  
 ; OTHER INFORMATION: sequence of proteins of the Nifs family.  
 US-09-462-645C-29

Query Match 31.1%; Score 23; DB 2; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 5.2e+02;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIOTDQOATT 14  
 :|||  
 Db 1 MIYLDNXXATT 10

Search completed: December 12, 2005, 21:00:46  
 Job time : 28 secs

THIS PAGE BEGINS  
(USPTO)

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:30:45 ; Search time 92.6667 Seconds  
(without alignments)  
67.634 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBSCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBSCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBSCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBSCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBSCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBSCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	74	100.0	15	US-10-758-165-3	Sequence 3, Appli
2	49	66.2	15	US-10-052-788-4	Sequence 4, Appli
3	41	55.4	15	US-10-758-165-1	Sequence 1, Appli
4	40	54.1	15	US-10-758-165-7	Sequence 2, Appli
5	37	50.0	15	US-10-758-165-2	Sequence 128, App
6	32	43.2	15	US-10-497-091-128	Sequence 713, App
7	29	39.2	15	US-10-958-216-713	Sequence 192, App
8	29	39.2	15	US-10-346-162-192	Sequence 4, Appli
9	29	39.2	15	US-10-758-165-4	Sequence 1728, Ap
10	27	36.5	13	US-09-572-404B-1728	Sequence 14, Appl
11	27	36.5	13	US-10-497-091-14	Sequence 37, Appl
12	27	36.5	14	US-10-172-425B-37	Sequence 129, App
13	27	36.5	15	US-10-497-091-119	Sequence 48, Appl
14	26	35.1	12	US-10-935-642-48	Sequence 15, Appl
15	26	35.1	12	US-11-074-473-48	Sequence 1243, Ap
16	26	35.1	12	US-10-497-091-15	Sequence 123, App
17	25	33.8	12	US-09-764-868-1243	Sequence 1, Appli
18	25	33.8	12	US-09-955-999-123	Sequence 796, App
19	25	33.8	14	US-10-221-125-1	Sequence 1123, Ap
20	25	33.8	15	US-10-014-340-796	Sequence 94, Appl
21	25	33.8	15	US-10-225-567A-1123	Sequence 560, App
22	25	33.8	15	US-11-004-270-94	Sequence 560, App
23	25	33.8	15	US-11-004-270-94	Sequence 560, App
24	24	32.4	9	US-10-117-937-560	Sequence 560, App
25	24	32.4	9	US-11-067-064-560	Sequence 560, App
26	24	32.4	9	US-11-067-159-560	Sequence 561, App
27	24	32.4	10	US-10-117-937-561	

28	24	32.4	10	6	US-11-067-064-561	Sequence 561, App
29	24	32.4	10	6	US-11-067-159-561	Sequence 561, App
30	24	32.4	12	4	US-10-097-175-66	Sequence 289, App
31	24	32.4	12	5	US-10-264-309-289	Sequence 584, App
32	24	32.4	12	5	US-10-264-309-289	Sequence 584, App
33	24	32.4	13	3	US-09-791-378-584	Sequence 568, App
34	24	32.4	13	3	US-09-791-378-584	Sequence 568, App
35	24	32.4	13	4	US-10-014-340-569	Sequence 569, App
36	24	32.4	13	4	US-10-014-340-569	Sequence 31, Appli
37	24	32.4	13	4	US-10-369-736-31	Sequence 31, Appli
38	24	32.4	13	4	US-10-112-582-31	Sequence 11, Appli
39	24	32.4	13	4	US-10-369-738-31	Sequence 706, App
40	24	32.4	13	5	US-10-807-807-706	Sequence 706, App
41	24	32.4	13	5	US-10-807-807-706	Sequence 31, Appli
42	24	32.4	13	6	US-11-028-058-31	Sequence 135, App
43	24	32.4	14	3	US-09-791-378-135	Sequence 587, App
44	24	32.4	14	3	US-09-791-378-587	
45	24	32.4				

ALIGNMENTS

```
RESULT 1
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match      100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2,2e+06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQATTR 15
      |||||
Db      1 RNNVLIQTDOQATTR 15

RESULT 2
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US2003008731A1
; GENERAL INFORMATION:
; APPLICANT: Gerethwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kallina, Warren V.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence:epitope peptide  
; OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon  
; OTHER INFORMATION: heavy chain  
US-10-052-788-4

Query Match 66.2%; Score 49; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.07;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IQTDQOATTR 15  
|:|:|:|:|:|  
Db 1 IQTDQOATTR 10

RESULT 3  
US-10-758-165-1  
; Sequence 1, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamnerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-758-165-1

Query Match 55.4%; Score 41; DB 5; Length 15;  
Best Local Similarity 64.3%; Pred. No. 1.9;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDQOATT 14  
|:|:|:|:|:|  
Db 1 RNDSPFIQTDQYTTT 14

RESULT 4  
US-10-758-165-7  
; Sequence 7, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamnerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-7

Query Match 54.1%; Score 40; DB 5; Length 15;  
Best Local Similarity 46.7%; Pred. No. 2.9;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDQOATTR 15  
|:|:|:|:|:|  
Db 1 RNDAPVQADRHSTR 15

RESULT 5

US-10-758-165-2  
; Sequence 2, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamnerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-2

Query Match 50.0%; Score 37; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 10;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RNNVLIQTDQOATT 14  
|:|:|:|:|:|  
Db 2 RNDSPFIQTDQOATT 14

RESULT 6  
US-10-497-091-128  
; Sequence 128, Application US/10497091  
; Publication No. US20050074863A1  
; GENERAL INFORMATION:  
; APPLICANT: HELLEDOORN, Koen  
; APPLICANT: BAKER, Matthew  
; APPLICANT: MILLIAMS, Steven  
; APPLICANT: CARB, Francis J.  
; TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2  
; FILE REFERENCE: MER-130  
; CURRENT APPLICATION NUMBER: US/10/497,091  
; PRIOR FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: PCT/EP02/13351  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: EP02020634.8  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: EP02001778.6  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: EP01128519.4  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 312  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-497-091-128

Query Match 43.2%; Score 32; DB 5; Length 15;  
Best Local Similarity 61.5%; Pred. No. 81;  
Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 RNNVLIQ-TDQ 11  
|:|:|:|:|:|  
Db 3 RDNVLFOATDQ 15

RESULT 7  
US-10-958-216-713  
; Sequence 713, Application US/10958216  
; Publication No. US20050181388A1  
; GENERAL INFORMATION:  
; APPLICANT: EDWARDS, ALED  
; APPLICANT: DHARMSI, AKIL



```
APPLICANT: VEDADI, MASOUD
APPLICANT: ALAM, MUHAMMAD ZAHoor
APPLICANT: ARROWSMITH, CHERYL
APPLICANT: AMREY, DONALD E.
APPLICANT: BEATTIE, BRYAN
APPLICANT: BUHADZIOJA, KRISTINA
APPLICANT: CANADIEN, VERONICA
APPLICANT: DOMAGALA, MEGAN
APPLICANT: HOUSTON, SIMON
APPLICANT: KANAGARAJAH, DHUSHY
APPLICANT: LI, QIN
APPLICANT: MANSOURY, KAMRAN
APPLICANT: McDONALD, MERRY-LYNN
APPLICANT: NETHERY, KATHLEEN
APPLICANT: NG, IVY
APPLICANT: OUYANG, HUI
APPLICANT: PINDER, BENJAMIN
APPLICANT: RICHARDS, DAMN
APPLICANT: TAI, MATTHEW
APPLICANT: THALAKADA, ROSANNE
APPLICANT: VALLEE, FRANCOIS
APPLICANT: VIRAG, CRISTINA
TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
FILE REFERENCE: IFT-205.01
CURRENT FILING DATE: US/10/958,216
PRIOR APPLICATION NUMBER: PCT/CA03/00462
PRIOR FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 60/369,511
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/385,089
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/385,751
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/386,553
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,577
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,367
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,566
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,390
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 60/386,601
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1132
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 713
LENGTH: 12
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-958-216-713

Query Match          39.2% Score 29; DB 5; Length 12;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 VLIQTDOQATTR 15
|::|::|::|
DB 1 VMEGDEEASVR 12
```

```
RESULT 8
US-10-346-162-192
; Sequence 192, Application US/10346162
; Publication No. US20030224390A1
; GENERAL INFORMATION:
; APPLICANT: KARO BIO USA, INC.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: BARNETT, Thomas R.
; APPLICANT: BUEHRER, Benjamin
```

```
TITLE OF INVENTION: METHOD OF IDENTIFYING CONFORMATION-SENSITIVE BINDING PEPTIDES AND
FILE REFERENCE: THEREOF
FILE REFERENCE: PAIGE=1H
CURRENT APPLICATION NUMBER: US/10/346,162
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: US 09/614,865
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 09/860,688
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn version 3.1
SEQ ID NO 192
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-346-162-192
```

```
Query Match          39.2% Score 29; DB 4; Length 15;
Best Local Similarity 46.2%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 3 NVLIQTDOQATTR 15
|::|::|::|
DB 3 NLICLIDQDEACSR 15
```

```
RESULT 9
US-10-758-165-4
; Sequence 4, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-758-165-4
```

```
Query Match          39.2% Score 29; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 RNNVLIQTDOQATTR 15
|::|::|::|
DB 1 RNKEIMREGQHTTQ 15
```

```
RESULT 10
US-09-572-404B-1728
; Sequence 1728, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1728
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
```

```
FEATURE:
OTHER INFORMATION: sequence located in TPP2 at 1925-1934 and may interact with Sequ
OTHER INFORMATION: 1727 in this patent.
US-09-572-404B-1728
```

```
Query Match      36.5%; Score 27; DB 3; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      8 TDQOATT 14
      :|||:|
Db      1 SDQOTT 7
```

```
RESULT 11
US-10-497-091-14
Sequence 14, Application US/10497091
Publication No. US20050074863A1
GENERAL INFORMATION:
APPLICANT: HELLENDORN, Koen
APPLICANT: BAKER, Matthew
APPLICANT: WILLIAMS, Steven
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
FILE REFERENCE: MER-130
CURRENT APPLICATION NUMBER: US/10/497,091
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: PCT/EP02/13351
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP02020634.8
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: EP02001778.6
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP01128519.4
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 13
TYPE: PRT
ORGANISM: homo sapiens
US-10-497-091-14
```

```
Query Match      36.5%; Score 27; DB 5; Length 13;
Best Local Similarity 58.3%; Pred. No. 5.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
```

```
QY      2 NNVLIQ--TDQO 11
      :|||:|
Db      1 DNVLFOAATDEQ 12
```

```
RESULT 12
US-10-172-425B-37
Sequence 37, Application US/10172425B
Publication No. US20030147908A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Arad, Gila
TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
DIRECTED AGAINST PYROGENIC EXOTOXINS
FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
CURRENT APPLICATION NUMBER: US/10/172,425B
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 09/150,947
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
```

```
LENGTH: 14
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-172-425B-37
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```
Query Match      36.5%; Score 27; DB 4; Length 14;
Best Local Similarity 44.4%; Pred. No. 6e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY      6 IOTDOATT 14
      :|||:|
Db      1 VOTDKSVT 9
```

```
RESULT 13
US-10-497-091-129
Sequence 129, Application US/10497091
Publication No. US20050074863A1
GENERAL INFORMATION:
APPLICANT: HELLENDORN, Koen
APPLICANT: BAKER, Matthew
APPLICANT: WILLIAMS, Steven
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
FILE REFERENCE: MER-130
CURRENT APPLICATION NUMBER: US/10/497,091
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: PCT/EP02/13351
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP02020634.8
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: EP02001778.6
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP01128519.4
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 129
LENGTH: 15
TYPE: PRT
ORGANISM: homo sapiens
US-10-497-091-129
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```
Query Match      36.5%; Score 27; DB 5; Length 15;
Best Local Similarity 58.3%; Pred. No. 6.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
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```
QY      2 NNVLIQ--TDQO 11
      :|||:|
Db      1 DNVLFOAATDEQ 12
```

```
RESULT 14
US-10-935-642-48
Sequence 48, Application US/10935642
Publication No. US20050050656A1
GENERAL INFORMATION:
APPLICANT: Huang, Xueying
APPLICANT: Wang, Hong
APPLICANT: Wu, Ying
TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and
FILE REFERENCE: C12296 US NA
CURRENT APPLICATION NUMBER: US/10/935,642
CURRENT FILING DATE: 2004-09-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Hair-binding peptide
```

US-10-935-642-48

Query Match 35.1%; Score 26; DB 5; Length 12;  
Best Local Similarity 62.5%; Pred. No. 7.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQATTR 15  
|||  
|:  
Db 1 TDMQAPRK 8

RESULT 15

US-11-074-473-48  
; Sequence 48, Application US/11074473  
; Publication No. US20050226839A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Xueying  
; APPLICANT: Wang, Hong  
; APPLICANT: Wu, Ying  
; TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and  
; TITLE OF INVENTION: Nails  
; FILE REFERENCE: CL2296 US NA  
; CURRENT APPLICATION NUMBER: US/11/074,473  
; PRIOR APPLICATION NUMBER: 2005-03-08  
; PRIOR FILING DATE: 2004-09-07  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 48  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hair-binding peptide  
US-11-074-473-48

Query Match 35.1%; Score 26; DB 6; Length 12;  
Best Local Similarity 62.5%; Pred. No. 7.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQATTR 15  
|||  
|:  
Db 1 TDMQAPRK 8

Search completed: December 12, 2005, 21:05:29  
Job time : 92.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:00:56 ; Search time 4.66667 Seconds  
(without alignments)  
17.950 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 8641

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications\_AA\_New:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	22	29.7	15	7	US-11-072-170A-21
2	21	28.4	11	6	US-10-467-657-8862
3	21	28.4	13	6	US-10-511-559-802
4	21	28.4	13	6	US-10-511-559-803
5	20	27.0	10	7	US-11-053-076-242
6	20	27.0	10	7	US-11-053-076-242
7	20	27.0	13	6	US-10-511-559-177
8	20	27.0	13	6	US-10-511-559-861
9	20	27.0	13	6	US-10-511-559-862
10	20	27.0	13	6	US-10-511-559-1096
11	20	27.0	13	6	US-10-511-559-1097
12	20	27.0	13	6	US-10-511-559-1098
13	20	27.0	14	6	US-10-939-890-60
14	19	25.7	12	7	US-10-507-662-49
15	19	25.7	12	7	US-11-016-706-5
16	19	25.7	13	6	US-10-511-559-264
17	19	25.7	13	6	US-10-511-559-265
18	19	25.7	13	6	US-10-511-559-266
19	19	25.7	13	6	US-10-511-559-267
20	19	25.7	13	6	US-10-511-559-725
21	19	25.7	13	6	US-10-511-559-725
22	19	25.7	14	6	US-10-467-657-8907
23	18	24.3	7	7	US-11-096-706-192
24	18	24.3	9	6	US-10-491-096-94
25	18	24.3	10	6	US-10-491-096-95

26	18	24.3	12	7	US-11-016-706-26	Sequence 26, Appl
27	18	24.3	13	6	US-10-511-559-199	Sequence 199, App
28	18	24.3	13	6	US-10-511-559-200	Sequence 200, App
29	18	24.3	13	6	US-10-511-559-201	Sequence 201, App
30	18	24.3	13	6	US-10-511-559-202	Sequence 202, App
31	18	24.3	13	6	US-10-511-559-608	Sequence 608, App
32	18	24.3	13	6	US-10-511-559-609	Sequence 609, App
33	18	24.3	13	6	US-10-511-559-610	Sequence 610, App
34	18	24.3	14	6	US-10-511-559-611	Sequence 611, App
35	18	24.3	14	6	US-10-467-657-8804	Sequence 8804, Ap
36	18	24.3	14	6	US-10-524-643-51	Sequence 51, Appl
37	18	24.3	14	7	US-11-054-515-2537	Sequence 2537, Ap
38	18	24.3	14	7	US-11-054-515-2539	Sequence 2539, Ap
39	18	24.3	14	7	US-11-054-515-2622	Sequence 2622, Ap
40	18	24.3	15	6	US-10-467-657-8918	Sequence 8918, Ap
41	17.5	23.6	8	7	US-11-058-727-107	Sequence 107, App
42	17.5	23.6	8	7	US-11-108-389-107	Sequence 107, App
43	17	23.0	4	7	US-11-032-794-58	Sequence 58, Appl
44	17	23.0	6	6	US-10-467-657-9114	Sequence 9114, Ap
45	17	23.0	7	7	US-11-096-706-30	Sequence 30, Appl

#### ALIGNMENTS

```
RESULT 1
US-11-072-170A-21
; Sequence 21, Application US/11072170A
; Publication No. US20050260159A1
; GENERAL INFORMATION:
; APPLICANT: Hasey, Karen
; APPLICANT: Postlethwait, Arnold
; APPLICANT: Kanangat, Sivadasan
; TITLE OF INVENTION: Intracellular Interleukin-1 Receptor Antagonist and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: D6564
; CURRENT APPLICATION NUMBER: US/11/072.170A
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: US 60/550,108
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Macintosh OS 10
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: IL-1ra peptides
US-11-072-170A-21
Query Match      29.7%  Score 22;  DB 7;  Length 15;
Best Local Similarity 66.7%  Pred. No. 62;
Matches 4;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;
QY      1 RNNVLI 6
DB      4 RNNQLV 9
RESULT 2
US-10-467-657-8862
; Sequence 8862, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467.657
; CURRENT FILING DATE: 2003-08-11
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; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 8862
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8862

Query Match
Best Local Similarity 57.1%; Score 21; DB 6; Length 11;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 QTDQAT 13
   :|||:
Db 1 KTDQYT 7

RESULT 3
US-10-511-559-802
; Sequence 802, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 802
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-802

Query Match
Best Local Similarity 28.4%; Score 21; DB 6; Length 13;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 IQTDOQ 11
   :|||:
Db 8 LQSDQE 13

RESULT 4
US-10-511-559-803
; Sequence 803, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
```

```
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 803
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-803

Query Match
Best Local Similarity 28.4%; Score 21; DB 6; Length 13;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 IQTDOQ 11
   :|||:
Db 3 LQSDQE 8

RESULT 5
US-11-053-076-242
; Sequence 242, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 242
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-242

Query Match
Best Local Similarity 27.0%; Score 20; DB 7; Length 10;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDOQAT 13
   :|||:
Db 1 TSDQAT 6

RESULT 6
US-11-053-076-247
```

```
; Sequence 247, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Schwelzer, Johannes
; APPLICANT: Lu, Peter S.
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-247

Query Match      27.0%; Score 20; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 TDOQAT 13
      |||||
Db      1 TSOQAT 6

RESULT 7
US-10-511-559-177
; Sequence 177, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-177

Query Match      27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 38.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 NVLIQTDOQATTR 15
      |||||
Db      1 NSIMQDRDAASAR 13

RESULT 8
US-10-511-559-861
; Sequence 861, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 861
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-861

Query Match      27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 25.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 NVNLIQTDOQAT 13
      :|||:
Db      2 DNIMVTFRNQAS 13

RESULT 9
US-10-511-559-862
; Sequence 862, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 862
; LENGTH: 13
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-862
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 25.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 NNVLIGTDOQAT 13
      :|::||:
Db      1 DNIMVTFRNQAS 12
```

```
RESULT 10
US-10-511-559-1096
; Sequence 1096, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1096
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1096
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      6 IOTDQATTR 15
      :|::||:
Db      4 LQVDFQKTMK 13
```

```
RESULT 11
US-10-511-559-1097
; Sequence 1097, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1097
; LENGTH: 13
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1097
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      6 IOTDQATTR 15
      :|::||:
Db      3 LQVDFQKTMK 12
```

```
RESULT 12
US-10-511-559-1098
; Sequence 1098, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1098
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1098
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      6 IOTDQATTR 15
      :|::||:
Db      1 LQVDFQKTMK 10
```

```
RESULT 13
US-10-939-890-60
; Sequence 60, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappa, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondaredidhar
; APPLICANT: Shrivastava, Ajay
```



```
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617, 70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 60
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-939-890-60
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Query Match      27.0%; Score 20; DB 6; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      6 IOTDQA 12
      |||:|
      2 IQCDKA 8
```

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RESULT 14
US-10-507-662-49
; Sequence 49, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: THE REAGENTS OF THE UNIVERSITY OF CALIFORNIA
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-507-662-49
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Query Match      25.7%; Score 19; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 NNVLIO 7
      |||:|
      5 NNDLIE 10
```

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RESULT 15
US-11-016-706-5
; Sequence 5, Application US/11016706
; Publication No. US2005024434A1
; GENERAL INFORMATION:
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```
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO: 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-706-5
```

```
Query Match      25.7%; Score 19; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 NNVLIO 7
      |||:|
      2 SNVFOQ 7
```

```
Search completed: December 12, 2005, 21:17:41
Job time : 5.66667 secs
```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 12, 2005, 21:05:42 ; Search time 18 seconds  
(without alignments)  
80.181 Million cell updates/sec

Title: US-10-758-165a-3

Perfect score: 74  
Sequence: 1 RNNVLIQDQQTTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	25	33.8	15	2	nitrogenase cofact
2	21	28.4	13	2	Ig kappa chain V-I
3	21	28.4	13	2	Ig kappa chain V-I
4	20	28.4	15	2	Ig heavy chain DJ
5	20	27.0	10	2	cytochrome-c oxida
6	19	25.7	10	2	proteoglycan core
7	19	25.7	13	2	urinary tract ston
8	19	25.7	14	2	synaptoosomal-asso
9	18	24.3	9	2	alpha-2-macroglobu
10	18	24.3	13	2	cytochrome-c oxida
11	18	24.3	15	2	epithelial dog all
12	18	24.3	15	2	insulin-like growt
13	18	24.3	15	2	epoxypropion isomer
14	17	23.0	10	2	carnitine medium/l
15	17	23.0	10	2	T-cell receptor be
16	17	23.0	11	4	proteasome endopep
17	17	23.0	11	4	hypothetical prote
18	17	23.0	12	2	sucrose-6-phosphat
19	17	23.0	13	2	ribosomal protein
20	17	23.0	13	2	proteasome endopep
21	17	23.0	13	2	40K extracellular
22	17	23.0	13	2	deoxynucleotidyltr
23	17	23.0	14	2	Ig heavy chain V r
24	17	23.0	14	2	T-cell receptor be
25	17	23.0	14	2	T-cell receptor de
26	17	23.0	15	2	protein QP200022 -
27	17	23.0	15	2	nitrophorin 4 - Rh
28	17	23.0	15	2	porphobilinogen sy
29	17	23.0	15	2	phospholipase C-be

30	16	21.6	10	2	D54823	olfactory receptor
31	16	21.6	10	2	C54823	olfactory receptor
32	16	21.6	11	2	S70720	trigger factor hom
33	16	21.6	12	2	A33099	163K exoantigen -
34	16	21.6	13	2	S28425	20K protein - rape
35	16	21.6	14	2	B81280	probable proteolys
36	16	21.6	15	2	PQ0681	photosystem I 19.0
37	16	21.6	15	2	PS0452	32K protein 3306 -
38	16	21.6	15	2	PH1631	Ig H chain V-D-J r
39	16	21.6	15	2	A45096	thyrotropin-releas
40	16	21.6	15	2	A36527	juvenile-hormone e
41	16	21.6	15	2	A53594	calnexin - mouse
42	15	20.3	8	2	S71919	alcohol dehydrogen
43	15	20.3	8	2	T48890	hypothetical prote
44	15	20.3	10	2	PQ0788	NADH2 dehydrogenas
45	15	20.3	11	2	PQ0682	photosystem I 17.5

## ALIGNMENTS

## RESULT 1

S32677  
nitrogenase cofactor synthesis protein nifs - Anabaena variabilis (fragment)  
N:Contains: L-cysteine sulfuryltransferase (EC 2.8.1.-)  
C:Species: Anabaena variabilis  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S32677  
R:Monmerjahn, U.; Boehme, H.  
submitted to the EMBL Data Library, December 1992  
A:Description: Cloning and expression in E. coli of the Anabaena.  
A:Reference number: S32675  
A/Accession: S32677  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <MON>  
A:Cross-references: UNIPROT:Q44507; UNIPARC:UPI00001301CC; EMBL:X69898; NID:G296503; PID  
C:Superfamily: nitrogen fixation protein nifs  
C:Keywords: sulfurtransferase

Query Match 33.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LIQTDQQTTR 15  
Db 3 VLYDNNATTK 13

## RESULT 2

B61458  
Ig kappa chain V-I region (BLA) - human (fragment)  
C:Species: Homo sapiens (man)  
C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
C/Accession: B61458  
R:Brown, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A:title: Expression of a public idiootype by human monoclonal IGM directed to myelin-asso  
A:Reference number: A61458; MUID:90039128; PMID:2478651  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <BRO>  
A/Cross-references: UNIPARC:UPI000017C2SD  
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;  
Best Local Similarity 55.6%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 IQTDQQTTR 14  
Db 2 IQTOSPTT 10

RESULT 3  
A61458  
Ig kappa chain V-I region (BOU) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
C/Accession: A61458; P10156  
R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mhaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A/Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-assc  
A/Reference number: A61458; MUID:90035126; PMID:2478651  
A/Accession: A61458  
A/Molecule type: protein  
A/Residues: 1-13 <BRO>  
A/Cross-references: UNIPARC:UPI000017C25E  
C/Comment: This protein is one of monoclonal IgM reactive with myeloma-associated glycop  
C/Keywords: heterotrimer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;  
Best Local Similarity 55.6%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 IOTDQATT 14  
Db 2 IOWTQSPPT 10

RESULT 4  
PH1329  
Ig heavy chain DJ region (clone C552-104) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1329  
R/Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1329  
A/Molecule type: DNA  
A/Residues: 1-15 <MAS>  
A/Cross-references: UNIPARC:UPI000017C245  
C/Keywords: heterotrimer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNNVLI 6  
Db 4 RNEVMI 9

RESULT 5  
S43625  
cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)  
C/Species: Oncorhynchus mykiss (rainbow trout)  
C/Date: 20-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: S43625  
R/Freund, R.; Kadenbach, B.  
Eur. J. Biochem. 221, 1111-1116, 1994  
A/Title: Identification of tissue-specific isoforms for subunits Vb and V1A of cytochr  
A/Reference number: S43624; MUID:94237150; PMID:8181469  
A/Accession: S43625  
A/Molecule type: protein  
A/Residues: 1-10 <FRK>  
A/Cross-references: UNIPROT:P80328; UNIPARC:UPI0000128131  
A/Note: the source is designated as Salmo gairdneri  
C/Genetics:  
A/Genome: nuclear  
C/Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 27.0%; Score 20; DB 2; Length 10;

Best Local Similarity 33.3%; Pred. No. 1.2e+03;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 6 IOTDQ 11  
Db 5 VERDEE 10

RESULT 6  
A55695  
proteoglycan core protein - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 17-Mar-1999  
C/Accession: A55695  
R/Lark, M.W.; Gordy, J.T.; Weidner, J.R.; Ayala, J.; Kimura, J.H.; Williams, H.R.; Mumfo  
J. Biol. Chem. 270, 2550-2556, 1995  
A/Title: Cell-mediated catabolism of aggrecan. Evidence that cleavage at the "aggrecanase  
A/Reference number: A55695; MUID:9515314; PMID:7852317  
A/Accession: A55695  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <LAR>  
A/Cross-references: UNIPARC:UPI000017C9A9

Query Match 25.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNNVLI 6  
Db 2 RNNVIL 7

RESULT 7  
H56046  
urinary tract stone matrix protein 10, 42K - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 09-Jul-2004  
C/Accession: H56046  
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.  
submitted to the Protein Sequence Database, February 1995  
A/Description: Isolation, characterization and sequence of stone proteins.  
A/Reference number: A56046  
A/Accession: H56046  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <BIN>  
A/Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.7%; Score 19; DB 2; Length 13;  
Best Local Similarity 37.5%; Pred. No. 2.5e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NNVLITD 9  
Db 6 NDLAETD 13

RESULT 8  
C44823  
synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)  
N/Alternate names: superprotein peptide 8  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C/Accession: C44823  
R/Lowey, A.; Liu, W.S.; Battinger, C.; Willard, M.B.  
J. Neurosci. 11, 3412-3421, 1991  
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
A/Reference number: A44823; MUID:92044785; PMID:1941090  
A/Accession: C44823  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <LOB>

A:Cross-references: UNIPARC:UPI000017C5E7  
A:Experimental source: Visual tissue  
A>Note: sequence extracted from NCBI backbone (NCBIP:64253)  
C:Keywords: membrane trafficking

Query Match 25.7%; Score 19; DB 2; Length 14;  
Best Local Similarity 42.9%; Pred. No. 2.7e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Db 5 LIQTDQ 11  
2 LVMLDEQ 8

RESULT 9  
S6636  
alpha-2-macroglobulin isoform 2 - bovine (fragment)  
C:Species: Bos primigenius indicus (zebu cattle)  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S6636  
R:Dommer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup  
FEB5 Lett. 372, 93-95, 1995  
A>Title: Crystallization and preliminary X-ray analysis of the receptor-binding domain c  
A:Reference number: S6634; MUID:96032553; PMID:7556651  
A:Accession: S6636  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <DB>  
A:Cross-references: UNIPROT:Q7M2N7; UNIPARC:UPI000017C480

Query Match 24.3%; Score 18; DB 2; Length 9;  
Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Db 3 NVLIQTDQ 10  
2 NILPKDE 9

RESULT 10  
S43626  
cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)  
C:Species: Salmo sp. (trout)  
C>Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 02-Jul-1998  
C:Accession: S43626  
R:Freund, R.; Kadenbach, B.  
Eur. J. Biochem. 221, 1111-1116, 1994  
A>Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochr  
A:Reference number: S43624; MUID:94237150; PMID:8181469  
A:Accession: S43626  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <FRE>  
A:Cross-references: UNIPARC:UPI000017BF62  
C:Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory

Query Match 24.3%; Score 18; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 6 IQTDQ 11  
6 IPTDE 11

RESULT 11  
A59491  
epithelial dog allergen - Canis familiaris (fragment)  
C:Species: Canis familiaris  
C>Date: 27-Oct-2003 #sequence\_revision 27-Oct-2003 #text\_change 27-Oct-2003  
C:Accession: A59491  
R:Saarelainen, S.; Taitvaanen, A.; Ryckm-vnen-Missinen, M.; Auriola, S.; Immonen, A.; MM-  
submitted to the Protein Sequence Database, October 2003

A>Description: Diagnosis of dog allergy with recombinant allergens.  
A:Reference number: A59491  
A:Accession: A59491  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <VIR>  
A>Note: IGE-binding protein; allergen

Query Match 24.3%; Score 18; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 3.8e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 3 NVLIQ 7  
3 NVLTQ 7

RESULT 12  
PT0205  
insulin-like growth factor-binding protein, bone - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 08-Dec-1994  
C:Accession: PT0205; A33175  
R:Bautista, C.M.; Baylink, D.J.; Mohan, S.  
Biochem. Biophys. Res. Commun. 176, 756-763, 1991  
A>Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from huma  
A:Reference number: PT0205; MUID:9122244; PMID:1709017  
A:Accession: PT0205  
A:Molecule type: protein  
A:Residues: 1-15 <BAU>  
A:Cross-references: UNIPARC:UPI000017C275

Query Match 24.3%; Score 18; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. No. 4.5e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 4 VLIQTDQA 12  
5 VVVEPDKA 13

RESULT 13  
S72432  
epoxypropen isomerase component B - Xanthobacter sp. (strain Py2) (fragment)  
C:Species: Xanthobacter sp.  
A:Variety: strain Py2  
C>Date: 14-Apr-1998 #sequence\_revision 08-May-1998 #text\_change 07-May-1999  
C:Accession: S72432  
R:Chan Kwo Chion, C.K.N.; Leak, D.J.  
Biochem. J. 319, 499-506, 1996  
A>Title: Purification and characterization of two components of epoxypropene isomerase/c  
A:Reference number: S72431; MUID:97069704; PMID:8912687  
A:Accession: S72432  
A:Molecule type: protein  
A:Residues: 1-15 <CHA>  
A:Cross-references: UNIPARC:UPI000017CA9F  
A>Note: 3-Met and 13-Leu were also found  
C:Complex: homodimer  
C:Function:  
A>Description: NADP-dependent lipamide reductase  
A:Pathway: epoxypropene degradation  
A>Note: sensitive to N-ethyl-maleimide and p-chloromercuribenzoate  
C:Keywords: PAD

Query Match 24.3%; Score 18; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 4.5e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 RNVLIQTD 9  
7 RNDHLIXD 15

## RESULT 14

A61354  
carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)  
N:Alternate names: endoplasmic reticulum protein ERp61; glucose regulated protein GRP58;  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C/Accession: A61354  
R/Murthy, M.S.R.; Pande, S.V.  
Mol. Cell. Biochem. 122, 133-138, 1993  
A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the prev  
A/Reference number: A61354; MUID:94049728; PMID:8232244  
A/Accession: A61354  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <MUR>  
A/Cross-references: UNIPARC:UPI000017C8DE  
C/Keywords: acyltransferase

Query Match 23.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.4e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 NVLIQTDO 10  
|||  
Db 2 DVLEITDE 9

## RESULT 15

PH0933  
T-cell receptor beta chain V-D-J region (clone 4) - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C/Accession: PH0933  
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A/Reference number: PH0931; MUID:92078857; PMID:1836012  
A/Accession: PH0933  
A/Molecule type: mRNA  
A/Residues: 1-10 <GOL>  
A/Cross-references: UNIPARC:UPI000017C9E5  
A/Experimental source: complete Freund's adjuvant-immunized lymph node  
A/Note: the authors translated the codon CAG for residue 9 as Glu  
C/Keywords: T-cell receptor

Query Match 23.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNN 3  
|||  
Db 6 RNN 8

Search completed: December 12, 2005, 21:18:42  
Job time : 18 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 12, 2005, 20:59:31 ; Search time 114 Seconds

(without alignments)  
92.833 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
Sequence: 1 RNNVLIQDQQTTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	33.8	15	1 NIFS1 ANAVA	Q44507 anabaena va
2	24	32.4	15	2 Q38B05 CYNCA	Q45812 plasmodium
3	23	31.1	14	2 Q4X512 PLACH	P70740 alcaligenes
4	22	29.7	12	2 Q70740 ALCEU	Q9WZS4 canis fam1
5	22	29.7	12	2 Q9WZS4 CANFA	Q9CTRQ bos taurus
6	22	29.7	14	2 Q9TRQ7 BOVIN	Q9CTRQ bos taurus
7	22	29.7	15	2 Q9TRH1 BOVIN	Q6IDM9 canis fam1
8	21	28.4	10	2 Q6IDM9 CANFA	Q7SMV9 homo sapien
9	21	28.4	13	2 Q7SMV9 HUMAN	P83330 streptococc
10	21	28.4	14	2 P83330 STRTR	Q23622 oryctolagus
11	21	28.4	15	2 Q23622 RABIT	Q9CTRQ oryctolagus
12	21	28.4	15	2 Q9TR62 RABIT	P80328 oncomychnu
13	20	27.0	10	1 COX5A ONCMY	Q9UJ48 homo sapien
14	20	27.0	10	2 Q9UJ48 HUMAN	Q6WZ21 homo sapien
15	20	27.0	15	2 Q6WZ21 HUMAN	Q5GJ62 coxiella bu
16	20	27.0	15	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
17	20	27.0	15	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
18	19	25.7	8	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
19	19	25.7	8	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
20	19	25.7	10	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
21	19	25.7	10	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
22	19	25.7	10	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
23	19	25.7	10	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
24	19	25.7	10	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
25	19	25.7	11	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
26	19	25.7	11	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
27	19	25.7	13	1 Q5GJ62 COXBU	Q5GJ62 coxiella bu
28	19	25.7	13	1 Q5GJ62 COXBU	Q5GJ62 coxiella bu
29	19	25.7	13	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
30	19	25.7	13	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu
31	19	25.7	14	2 Q5GJ62 COXBU	Q5GJ62 coxiella bu

32	19	25.7	14	2	Q714T6_9EUKA	Q714T6 pyrmesium
33	19	25.7	14	2	Q8L1Y9_9CYAN	Q8L1Y9 chroococcid
34	19	25.7	15	1	TX11B_BUNCA	P84471 bungarus ca
35	19	25.7	15	2	Q9UR90_YEAST	Q9UR90 saccharomyc
36	19	25.7	15	2	P82936_HORVU	P82936 hordeum vul
37	19	25.7	15	2	Q8WK21_5STRA	Q8WK21 bolldomonas
38	18	24.3	9	2	Q7M2N7_BOSIN	Q7M2N7 bos indicus
39	18	24.3	9	2	Q4QWV3_9MARC	Q4QWV3 pallavicini
40	18	24.3	9	2	Q4QWV9_9MARC	Q4QWV9 jenssenia sp
41	18	24.3	9	2	Q9JH81_9GAMA	Q9JH81 retroperito
42	18	24.3	10	2	Q5C1M9_SCHUA	Q5C1M9 schistosoma
43	18	24.3	10	2	Q4QWV8_9MARC	Q4QWV8 jenssenia di
44	18	24.3	12	1	NCP3_COPCM	P83454 coprinus co
45	18	24.3	13	2	Q5BTL6_SCHUA	Q5BTL6 schistosoma

## ALIGNMENTS

RESULT 1  
NIFS1 ANAVA STANDARD, PRT, 15 AA.

AC Q44507, 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Cysteine desulfurase 1 (EC 2.8.1.7) (Nitrogenase metalloclusters  
DE biosynthesis protein nifs1) (fragment).  
GN Name=nifs1; Synonyms=nifs;  
OS Anabaena variabilis.  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
OX NCBI\_TaxId=1172;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PCC 7937 / ATCC 29413;  
RA Monnerjahn U., Boehme H.;  
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.  
[2]  
RP EXPRESSION PATTERN.  
RC STRAIN=PCC 7937 / ATCC 29413;  
RX MEDLINE=96016168; PubMed=7568132;  
RA Thiel T., Lyons E.M., Erker J.C., Ernst A.;  
RT "A second nitrogenase in vegetative cells of a heterocyst-forming  
RT cyanobacterium.";  
RL Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).  
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur atoms from  
CC cysteine to produce alanine. Seems to participate in the  
CC biosynthesis of the nitrogenase metalloclusters by providing the  
CC inorganic sulfur required for the Fe-S core formation (By  
CC similarity).  
CC -!- CATALYTIC ACTIVITY: L-cysteine + [enzyme]-cysteine = L-alanine +  
CC [enzyme]-S-sulfanylcysteine.  
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- MISCELLANEOUS: Belongs to the Nif1 gene cluster which is expressed  
CC in heterocysts under anaerobic and aerobic conditions.  
CC -!- SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent  
CC aminotransferase family. Nifs1/iscs subfamily.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: X69898; CAA49523.1; -; Genomic\_DNA.  
CC PIR: S32677; S32677.  
CC InterPro: IPR000192; Aminoacids V.  
CC PROSITE: PS00595; AA\_TRANSFERR CLASS\_5; PARTIAL.  
CC Nitrogen fixation; Pyridoxal phosphate; Transferase.  
CC NON\_TER 15  
CC SEQUENCE 15 AA; 1684 MW; 0888F106DE65547D CRC64;

Query Match 33.8%; Score 25; DB 1; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIOTDOQATR 15  
 :|:|:|:  
 Db 3 VITYDNNATTK 13

## RESULT 2

Q9S8D5\_CYNCA PRELIMINARY; PRT; 15 AA.  
 AC Q9S8D5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE CARDOSIN A (Fragment).  
 OS Cynara cardunculus (Cardoon).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Campanulids; Asterales; Asteraceae; Carduoideae; Cardueae; Cynara.  
 NCBI\_TaxID=4265;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=96073661; PubMed=8540346;  
 RA Faro C., Verissimo P., Lin Y., Tang J., Pires E.;  
 RT "Cardosin A and B, aspartic proteases from the flowers of cardoon,";  
 RL Adv. Exp. Med. Biol. 362:373-377(1995).  
 SQ SEQUENCE 15 AA; 1555 MW; CC95D9155C97325B CRC64;

Query Match 32.4%; Score 24; DB 2; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 NVLIQTQOAT 13  
 :|:|:|:  
 Db 4 SALVATDNQNT 14

## RESULT 3

Q4XS12\_PLACH PRELIMINARY; PRT; 14 AA.  
 AC Q4XS12;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC106890.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=5825;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Brittan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jense C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01003511; CAH80130.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 14 AA; 1781 MW; 989A795983FA9A51 CRC64;

Query Match 31.1%; Score 23; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNVLIO 7  
 :|:|:|:  
 Db 8 NNVLIFQ 13

## RESULT 4

P70740\_ALCEU PRELIMINARY; PRT; 9 AA.  
 ID P70740;  
 AC P70740;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hoxa protein (Fragment).  
 GN Name=hoxa;  
 OS Alcaligenes eutrophus (Ralstonia eutropha).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Cupriavidus.  
 NCBI\_TaxID=106590;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=H16;  
 RX MEDLINE=94292469; PubMed=8021224;  
 RA Lenz O., Schwartz E., Derrnede J., Bitinger M., Friedrich B.;  
 RT "The Alcaligenes eutrophus H16 hoxa gene participates in hydrogenase  
 RT regulation.";  
 RL J. Bacteriol. 176:4385-4393(1994).  
 DR EMBL; X74670; CAAS2736.1; -; Genomic\_DNA.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 992 MW; 970BD1ADC6D3A85 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 TDOQAT 13  
 :|:|:|:  
 Db 2 SDRQAT 7

## RESULT 5

Q9WZS4\_CANFA PRELIMINARY; PRT; 12 AA.  
 AC Q9WZS4;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Growth hormone (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22319383; PubMed=12431806; DOI=10.1016/S0303-7207(02)00257-5;  
 RA Lantinga-van Leeuwen I.S., Timmermans-Sprang E.A., Mol J.A.;  
 RT "Cloning and characterization of the 5'-flanking region of the canine  
 RT growth hormone gene.";  
 RL Mol. Cell. Endocrinol. 197:133-141(2002).  
 DR EMBL; AF166119; AAF89582.1; -; Genomic\_DNA.  
 FT NON TER 12  
 SQ SEQUENCE 12 AA; 1229 MW; 2B587268ECB45417 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 4.1e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLI 6  
 :|:|:|:  
 Db 6 RNSVLL 11



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RESULT 6
Q9TRQ7 BOVIN PRELIMINARY; PRT; 14 AA.
ID Q9TRQ7 BOVIN PRELIMINARY; PRT; 14 AA.
AC Q9TRQ7 BOVIN PRELIMINARY; PRT; 14 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Calyculin-associated protein peptide L-8, CAP-50=ANNEXIN
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92317074; PubMed=1618851;
RA Mitutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Hidaka H.;
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3T1 cells."
RL J. Biol. Chem. 267:13498-13504(1992).
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1446 MW; C8322EB36DD9C6C6 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TDQQA 12
DB 4 TDEQA 8

RESULT 7
Q9TRH1 BOVIN PRELIMINARY; PRT; 15 AA.
ID Q9TRH1 BOVIN PRELIMINARY; PRT; 15 AA.
AC Q9TRH1 BOVIN PRELIMINARY; PRT; 15 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Alkaline phosphodiesterase I (EC 3.1.4.1) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93250579; PubMed=8387370;
RA Maruyama E., Iwamatsu A., Takashima S.;
RA Blochem. Mol. Biol. Int. 29:579-586(1993).
RL GO:0004528; F:phosphodiesterase I activity; IEA.
SQ SEQUENCE 15 AA; 1678 MW; BE31498EAB87071 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 VLIOQDQAT 13
DB 2 VLATQMOST 11

RESULT 8
Q6JDM9 CANFA PRELIMINARY; PRT; 10 AA.
ID Q6JDM9 CANFA PRELIMINARY; PRT; 10 AA.
AC Q6JDM9 CANFA PRELIMINARY; PRT; 10 AA.
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Mitochondrial H+ transporting ATP synthase F1 (Fragment).

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GN Name=ATP5A1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15233990; DOI=10.1016/j.ygeno.2004.04.001;
RA Housley D.J.E., Ritzert E., Venta P.J.;
RT "Comparative radiation hybrid map of canine chromosome 1 (CFA1)
RT incorporating SNP and indel polymorphisms."
RL Genomics 84:248-264(2004).
DR EMBL: AY514688; AAT44872.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1059 MW; C47457B1A045B042 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 5.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 NVLIQTDQ 11
DB 2 NVISITDQ 10

RESULT 9
Q75MW9 HUMAN PRELIMINARY; PRT; 13 AA.
ID Q75MW9 HUMAN PRELIMINARY; PRT; 13 AA.
AC Q75MW9;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein SSBP1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.E.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., DeLahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harting R., Harris A.,
RA Strong C.W., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Stromwater C.,
RA Latreille P., Miller N., Johnson D., Murray J., Moesener J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowitz N., Wohldmann P.E., Cook L.L.,
RA Hickmonotham M.T., Biedel J., Williams D., Bedell J.A., Mardis E.R.,
RA Cifton S.W., Chisoe S.L., Maier M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bock P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7."
RL Nature 424:157-164(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.

```

```
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004979; AAS02037.1; -; GenomC_DNA.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 13 AA; 1565 MW; 9A39BF645040DAB5 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 7e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVLIQTQDQ 10
Db 1 NITFLSDQ 8

RESULT 10
P83330 STRTR PRELIMINARY; PRT; 14 AA.
ID P83330 STRTR PRELIMINARY;
AC P83330;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE M protein, serotype 32 (Fragment).
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ITG82;
RA Guimont C., Chopard M.A., Galliard J.L., Chamba J.F.;
RT "Comparative study of the protein composition of three strains of
RL Streptococcus thermophilus grown either in M17 medium or in milk.";
RL Lait 0:0-0(2002).
CC -1- FUNCTION: This protein is one of the different antigenic serotypes
CC of protein M. Protein M is closely associated with virulence of
CC the bacterium and can render the organism resistant to
CC phagocytosis (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall (By
CC similarity).
CC -1- SIMILARITY: TO OTHER M PROTEINS.
CC -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN
CC THE REGION OF THE MEMBRANE ANCHOR.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006909; P:phagocytosis; IEA.
KW Antigen; Cell wall; Phagocytosis; Transmembrane; Virulence.
FT NON TER
SQ SEQUENCE 14 AA; 1739 MW; 66339B9F3A3FE24B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
Best Local Similarity 28.6%; Pred. No. 7.7e+03;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NVVLIQTQDQATT 15
Db 1 NHOULTENERLTK 14

RESULT 11
Q29622_RABIT PRELIMINARY; PRT; 15 AA.
ID Q29622_RABIT PRELIMINARY;
AC Q29622;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2004 (Tremblrel. 26, Last annotation update)
```

```
DE Recombination activating protein (Fragment).
GN Name=RAG-2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIM/fgm; TISSUE=Thymus;
RX MEDLINE=93354283; Pubmed=8350872; DOI=10.1016/0161-5890(93)90127-W;
RA Puschiotti P., Harindranath N., Mage R.G., McCormack W.T.,
RA Dhanarajan P., Roux K.H.;
RT "Recombination activating genes-1 and -2 of the rabbit: cloning and
RT characterization of germ-line and expressed genes.";
RL MOL. Immunol. 30:1021-1032(1993).
DR EMBL; M99310; AAA03028.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON TER
SQ SEQUENCE 15 AA; 1717 MW; CE095FAD5FED42B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RNNVLI 6
Db 9 RNNIAL 14

RESULT 12
Q9TR62_RABIT PRELIMINARY; PRT; 15 AA.
ID Q9TR62_RABIT PRELIMINARY;
AC Q9TR62;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE Apolipoprotein A-IV (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95329112; Pubmed=7605356; DOI=10.1016/0021-9150(94)05444-N;
RA Mezdour H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low
RT apolipoprotein A-IV level in rabbit sera.";
RL Atherosclerosis 113:171-178(1995).
SQ SEQUENCE 15 AA; 1761 MW; DE115B7351F0ABC CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 IQTDDQAT 13
Db 2 VSADQVAT 9

RESULT 13
COX5A_ONCMY STANDARD; PRT; 10 AA.
ID COX5A_ONCMY
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1)
```

```

DE (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; S43625; S43625.
KW Direct protein sequencing; Heme; Inner membrane; Iron; Membrane;
KW Metal-binding; Mitochondrion; Oxidoreductase.
FT NON TER
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 27.0%; Score 20; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 8.1e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 6 IQTDOQ 11
DB 5 VETDER 10

RESULT 14
O9U48 HUMAN
ID O9U48_HUMAN PRELIMINARY; PRT; 10 AA.
AC O9U48_2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Lactophillin-2 (Fragment).
GN Name=LPHN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99153747; PubMed=10030676; DOI=10.1038/sj.onc.1202487;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterisation of a human homologue of the
RT lactophillin gene from a region of 1p31.1 implicated in breast
RT cancer.";
RL Oncogene 17:3513-3519(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20225451; PubMed=10760572; DOI=10.1016/S0167-4781(00)00020-8;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Genomic structure and expression profile of LPHN1, a 7TM gene
RT variably expressed in breast cancer cell lines.";
RL Biochim. Biophys. Acta 1491:75-92(2000).
DR EMBL; AJ244514; CAB60206.1; -; Genomic_DNA.
FT NON_TER 1

```

```

SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 NVLIQ 7
DB 5 NILLQ 9

RESULT 15
O6MZZ1 HUMAN
ID O6MZZ1_HUMAN PRELIMINARY; PRT; 15 AA.
AC O6MZZ1_1
DT 05-JUN-2004 (TRENBLrel. 27, Created)
DT 05-JUN-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686J2076.
DE Name=DKFZp686J2076;
GN Name=sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human endometrium carcinoma cell line;
RG The German Human CDNA Consortium;
RA Ansgore W., Krieger S., Regiert T., Ritzmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amld C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640801; CA645884.1; -, mRNA.
SQ SEQUENCE 15 AA; 1715 MW; 91F5CE0118445CE3 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.3e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 LIQTDQ 11
DB 4 LKVDQ 10

```

Search completed: December 12, 2005, 21:17:25  
Job time : 116 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 81.3362 Seconds  
(without alignments)  
81.030 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
Sequence: 1 RNNVLIQTDQATTR 15

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*
9:	Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	ADRI0603	Adri0603 Horse IGE
2	74	100.0	424	AAW50103	AAW50103 Equine IGE
3	74	100.0	424	AAW50104	AAW50104 Equine IGE
4	74	100.0	569	ABP96585	ABP96585 Horse IGE
5	49	66.2	15	ADC64568	ADC64568 Horse Imm
6	43	58.1	417	AEBS39722	AEBS39722 L. pneumo
7	43	58.1	452	AEBS39722	AEBS39722 L. pneumo
8	43	58.1	580	ABG32001	ABG32001 O. intest
9	43	58.1	580	ADP79623	ADP79623 Giardia i
10	41	55.4	15	ADRI0601	Adri0601 Dog IGE
11	41	55.4	312	AAV79995	AAV79995 Dog Immun
12	41	55.4	312	ADN24060	ADN24060 Bacteri
13	41	55.4	417	AAW23067	AAW23067 Canine IGE
14	41	55.4	426	AAW23067	AAW23067 Canine IGE
15	41	55.4	426	ABP96583	ABP96583 Dog IGE
16	41	55.4	2000	ABRS2669	ABRS2669 Protein s
17	41	55.4	2000	ADK61774	ADK61774 Disease t
18	40	54.1	15	ADRI0607	Adri0607 Pig IGE
19	40	54.1	567	ABP96588	ABP96588 Pig IGE
20	38	51.4	613	AAW73009	AAW73009 Cobra ven
21	38	51.4	621	AAW73013	AAW73013 Cobra ven
22	38	51.4	703	ABU44458	ABU44458 Protein e
23	38	51.4	814	ABJ26042	ABJ26042 Aspergill
24	37	50.0	15	ADRI0602	Adri0602 Cat IGE

25	37	50.0	66	4	AAU62291	AAU62291 Propionib
26	37	50.0	66	6	ABM58810	ABM58810 Propionib
27	37	50.0	223	6	ADJ48583	ADJ48583 Oil-aseoc
28	37	50.0	285	2	AAV17498	AAV17498 Zoota prot
29	37	50.0	370	6	ADA34539	ADA34539 Acinetoba
30	37	50.0	431	8	ADG73237	ADG73237 Cat immun
31	37	50.0	496	6	ABP96580	ABP96580 Cat IGE
32	37	50.0	496	6	ABU09338	ABU09338 Feline IGE
33	37	50.0	496	6	ABU09336	ABU09336 Feline IGE
34	37	50.0	496	6	ADG73251	ADG73251 Cat parti
35	37	50.0	496	8	ADG73225	ADG73225 Cat parti
36	37	50.0	663	8	ADJ49049	ADJ49049 Oil-aseoc
37	37	50.0	1320	4	AAU48101	AAU48101 Propionib
38	37	50.0	1320	6	ABM44620	ABM44620 Propionib
39	36	48.6	21	7	ADM66490	ADM66490 Peptide f
40	36	48.6	75	8	ADV87747	ADV87747 Streptoco
41	36	48.6	75	8	ADV79000	ADV79000 Streptoco
42	36	48.6	143	6	ABJ26246	ABJ26246 Aspergill
43	36	48.6	199	8	ADR94119	ADR94119 Novel S.
44	36	48.6	199	9	AEA57989	AEA57989 Streptoco
45	36	48.6	210	8	ADU47057	ADU47057 Corn Dice

## ALIGNMENTS

RESULT 1  
ID ADRI0603 standard; peptide, 15 AA.  
XX  
XX ADRI0603;  
AC  
XX  
XX 21-OCT-2004 (first entry)  
DT  
XX  
XX  
DE Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.  
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW horse.  
XX  
XX OS Equus caballus.  
XX  
XX PN WO2004065936-A2.  
XX  
XX PD 05-AUG-2004.  
XX  
XX PF 15-JAN-2004; 2004WO-US003566.  
XX  
XX PR 16-JAN-2003; 2003US-0440472P.  
XX  
XX (UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hammerberg B;  
XX  
XX WPI, 2004-593545/57.  
XX  
XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
XX or treating asthma or anaphylactic shock.  
XX  
XX Example 6; Page 9; 14pp; English.  
XX  
XX The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine IGE corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
CC either pig or human epsilon-chains of IgE. The present sequence is the  
CC horse IgE 5.91 recognition site.

XX  
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIOTDQOATTR 15  
| | | | | | | | | | | | | | |  
Db 1 RNNVLIOTDQOATTR 15

## RESULT 2

AAM50103  
ID AAM50103 standard; protein; 424 AA.

XX  
AC AAM50103;

XX  
DT 02-SEP-2002 (first entry)

XX  
DE Equine IgE heavy chain constant region C-epsilon allotype A.

XX  
KM Cea; equine; horse; heavy chain; constant region; allotype a; IgE;  
XX C-epsilon a; immunoglobulin E; anti-allergic; allergy.

XX  
OS Equus caballus.

XX  
FH Key Location/Qualifiers

FT Domain 1..97  
/note= "CH1 domain"  
FT Domain 98..205  
/note= "CH2 domain"  
FT Domain 206..312  
/note= "CH3 domain"  
FT Domain 313..424  
/note= "CH4 domain"

XX  
PN W0200250280-A2.

XX  
PD 27-JUN-2002.

XX  
PF 20-DEC-2001; 2001WO-DE004810.

XX  
PR 21-DEC-2000; 2000DE-01064415.

XX  
PA (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

XX  
PI Leibold W, Wagner B, Radbruch A;

XX  
DR WPI; 2002-508803/54.

XX  
N-PSDB; ABL61246.

XX  
PT DNA sequence encoding part of an equine immunoglobulin G, useful for  
PT preparing isotype-specific antibodies for diagnosis and treatment of  
PT allergy in horses.

XX  
PS Claim 1; Page 31-32; 37pp; German.

XX  
CC This invention describes a novel DNA (I) encoding the constant region  
CC (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The  
CC products of the invention are capable of neutralising IgE activity and  
CC have anti-allergic activity. The polynucleotides of the invention are used  
CC to produce recombinant IgE (II), and this is used to raise specific  
CC monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,  
CC particularly of allergy in horses, and Mab can also be used for treatment  
CC of allergies. (I) make possible production of isotype-specific  
CC antibodies, important for precise evaluation of the immune response. This  
CC sequence represents a fragment of the equine IgE heavy chain constant

CC region C-epsilon allotype a (Cea), used in the method of the invention  
CC for IgE-isotype recombinant immunoglobulin production

XX  
SQ Sequence 424 AA;

Query Match 100.0%; Score 74; DB 5; Length 424;  
Best Local Similarity 100.0%; Pred. No. 8.2e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIOTDQOATTR 15  
| | | | | | | | | | | | | | |  
Db 356 RNNVLIOTDQOATTR 370

## RESULT 3

AAM50104  
ID AAM50104 standard; protein; 424 AA.

XX  
AC AAM50104;

XX  
DT 02-SEP-2002 (first entry)

XX  
DE Equine IgE heavy chain constant region C-epsilon allotype b.

XX  
KM Ceb; equine; horse; heavy chain; constant region; allotype b; IgE;  
XX C-epsilon b; immunoglobulin E; anti-allergic; allergy.

XX  
OS Equus caballus.

XX  
FH Key Location/Qualifiers  
FT Domain 1..97  
/note= "CH1 domain"  
FT Domain 98..205  
/note= "CH2 domain"  
FT Domain 206..312  
/note= "CH3 domain"  
FT Domain 313..424  
/note= "CH4 domain"

XX  
PN W0200250280-A2.

XX  
PD 27-JUN-2002.

XX  
PF 20-DEC-2001; 2001WO-DE004810.

XX  
PR 21-DEC-2000; 2000DE-01064415.

XX  
PA (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

XX  
PI Leibold W, Wagner B, Radbruch A;

XX  
DR WPI; 2002-508803/54.

XX  
N-PSDB; ABL61247.

XX  
PT DNA sequence encoding part of an equine immunoglobulin G, useful for  
PT preparing isotype-specific antibodies for diagnosis and treatment of  
PT allergy in horses.

XX  
PS Claim 1; Page 34-36; 37pp; German.

XX  
CC This invention describes a novel DNA (I) encoding the constant region  
CC (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The  
CC products of the invention are capable of neutralising IgE activity and  
CC have anti-allergic activity. The polynucleotides of the invention are used  
CC to produce recombinant IgE (II), and this is used to raise specific  
CC monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,  
CC particularly of allergy in horses, and Mab can also be used for treatment  
CC of allergies. (I) make possible production of isotype-specific  
CC antibodies, important for precise evaluation of the immune response. This  
CC sequence represents a fragment of the equine IgE heavy chain constant  
CC region C-epsilon allotype b (Ceb), used in the method of the invention  
CC for IgE-isotype recombinant immunoglobulin production

SQ Sequence 424 AA;  
 Query Match 100.0%; Score 74; DB 5; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 8,2e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATTR 15  
 |||||  
 Db 356 RNNVLIQTDOQATTR 370

RESULT 4  
 ABP96585  
 ID ABP96585 standard; protein; 569 AA.  
 XX  
 AC ABP96585;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Horse IGE heavy chain amino acid sequence SEQ ID NO:30.  
 XX  
 KM Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
 KM immune response; major histocompatibility complex; MHC; immunogenic;  
 KM antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;  
 KM dermatological; antiinflammatory; IGE-mediated condition; food allergy;  
 KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KM urticaria hives.  
 KM  
 OS Equus caballus.  
 XX  
 PN MO2003015716-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 08-AUG-2002; 2002WO-US026986.  
 XX  
 PR 13-AUG-2001; 2001US-0312120P.  
 XX  
 PA (IGET-) IGE THERAPEUTICS INC.  
 XX  
 PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 XX  
 DR WPI; 2003-268242/26.  
 XX  
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IGE, by identifying peptide eliciting CTL response to IGE  
 PT peptides naturally presented by major histocompatibility complex class I  
 PT protein.  
 XX  
 PS Example 7; Page 157-160; 187pp; English.  
 XX  
 CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IGE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IGE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IGE peptides. C1-3 have antiallergic, antiaesthetic, immunosuppressive,  
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IGE, and in  
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-

CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an IGE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention  
 XX

SQ Sequence 569 AA;  
 Query Match 100.0%; Score 74; DB 6; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATTR 15  
 |||||  
 Db 501 RNNVLIQTDOQATTR 515

RESULT 5  
 ADC64568  
 ID ADC64568 standard; peptide; 15 AA.  
 XX  
 AC ADC64568;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.  
 XX  
 KM Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.  
 XX  
 OS Equus caballus.  
 XX  
 PN US2003087314-A1.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 08-NOV-2001; 2001US-00052788.  
 XX  
 PR 08-NOV-2001; 2001US-00052788.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Gerhwin LJ, Pettigrew HD, Kalina WV;  
 XX  
 DR WPI; 2003-765437/72.  
 XX  
 PT Immunogenic composition comprising an isolated equine immunoglobulin E  
 PT polypeptide that induces production of antibodies which specifically bind  
 PT to equine immunoglobulin E.  
 XX  
 PS Example 1; Page 8; 14pp; English.  
 XX  
 CC The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that  
 CC specifically binds to equine IGE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an  
 CC antibody that specifically binds to equine IGE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-  
 CC (S6)), and collecting antiserum from the animal) and a kit for detection  
 CC of equine IGE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IGE. The  
 CC antibody is useful for detecting equine IGE protein in a biological  
 CC sample (serum) which involves contacting the sample with the antibody,  
 CC thus forming an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the  
 CC complex can be detected. The complex is detected using a second labelled  
 CC antibody. The peptides are useful for generating antibodies specific for  
 CC IGE which can serve as a diagnostic test for allergy. The present

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

ID ABG32001 standard; protein; 580 AA.



AC ABG32001;  
XX  
DT 06-AUG-2003 (revised)  
DT 15-NOV-2002 (first entry)  
XX  
DE Q. intestinalis arginine deiminase gene, QIAD1INT.  
XX  
KM Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine;  
KM citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;  
KM auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.  
XX  
OS Giardia intestinalis.  
XX  
PN WO200244360-A2.  
XX  
PD 06-JUN-2002.  
XX  
PP 19-SEP-2001; 2001WO-US029184.  
XX  
PR 28-NOV-2000; 2000US-00723546.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Clark MA;  
XX  
PT WPI; 2002-619003/66.  
XX  
DR  
XX  
PT Compound for treating tumor such as melanoma, hepatoma or sarcoma in a  
PT patient, comprises arginine deiminase covalently bonded by a linking  
PT group such as succinimide to polyethylene glycol.  
XX  
PS Disclosure; Fig 12; 59pp; English.  
XX  
XX The invention discloses a compound comprising arginine deiminase (ADI)  
CC covalently bonded by a linking group to polyethylene glycol (PEG) having  
CC a total weight average molecular weight of about 1000-50000. Also  
CC disclosed is a method for enhancing the circulating half life or the  
CC tumoricidal activity of arginine deiminase by modifying the arginine  
CC deiminase by covalently bonding the arginine deiminase by a linking group  
CC to PEG. Normal cells can synthesize arginine from citrulline in a 2 step  
CC process catalysed by argininosuccinate synthase and argininosuccinate  
CC lyase. In contrast, many cancerous cells do not express argininosuccinate  
CC synthase and are, therefore, auxotrophic for arginine. Arginine deiminase  
CC catalyses the conversion of arginine to citrulline and can be used to  
CC eliminate arginine from the cancerous cells. The compound is useful for  
CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or  
CC for treating and inhibiting metastases in a patient. When compared to  
CC native arginine deiminase the compound retains most of its enzymatic  
CC activity, is far less antigenic, has a greatly extended circulating half-  
CC life, and is much more efficacious in the treatment of tumours. The  
CC sequence presented is the Giardia intestinalis arginine deiminase gene,  
CC QIAD1INT. (updated on 06-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 580 AA;  
XX  
Query Match 58.1%; Score 43; DB 5; Length 580;  
Best Local Similarity 57.1%; Pred. No. 52;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 NNVLIQTDQDQATTR 15  
||: ||| |||  
Db 168 NNMVFMRDQQTTR 181  
XX  
RESULT 9  
ADP79623  
ID ADP79623 standard; protein; 580 AA.  
XX  
AC ADP79623;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
XX Giardia intestinalis arginine deaminase.

XX  
KM Arginine deaminase; cytosolic; virucide; viral replication;  
KM nitric oxide synthesis; tumour; liver function; enzyme.  
XX  
OS Giardia intestinalis.  
XX  
PN WO2004046309-A2.  
XX  
PD 03-JUN-2004.  
XX  
PP 29-SEP-2003; 2003WO-US030770.  
XX  
PR 18-NOV-2002; 2002US-0427497P.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Clark MA;  
XX  
PT WPI; 2004-431965/40.  
XX  
DR  
XX  
PT Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
PS Claim 18; SEQ ID NO 17; 89pp; English.  
XX  
XX The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deaminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritidis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Giardia intestinalis arginine deaminase.  
XX  
SQ Sequence 580 AA;  
XX  
Query Match 58.1%; Score 43; DB 8; Length 580;  
Best Local Similarity 57.1%; Pred. No. 52;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 NNVLIQTDQDQATTR 15  
||: ||| |||  
Db 168 NNMVFMRDQQTTR 181  
XX  
RESULT 10  
ADRI0601  
ID ADRI0601 standard; peptide; 15 AA.  
XX  
AC ADRI0601;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.  
XX  
KM Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
OS Canis familiaris.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.

```
XX 16-JAN-2003; 2003US-0440472P.
PR (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0603) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE.
XX
XX Sequence 15 AA;
SQ
XX
XX Query Match 55.4%; Score 41; DB 8; Length 15;
XX Best Local Similarity 64.3%; Pred. No. 2;
XX Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 RNNVLITQDQATT 14
XX ||:|||||
XX 1 RNDSPITQDQYTT 14
XX
XX RESULT 11
XX AAY79995
XX ID AAY79995 standard; protein; 312 AA.
XX
XX AAY79995;
XX
XX 15-MAY-2000 (first entry)
XX
XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
XX
XX Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;
XX immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX antibody; allergy; allergic disease; immunisation; anti-allergic;
XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX Canis sp.
XX
XX WO9967293-A1.
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-US013959.
XX
XX 20-JUN-1998; 98US-00100287.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY, Walfield AM;
XX
XX WPI; 2000-160578/14.
XX
```

```
PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy.
XX
XX Example 1; Page 66-68; 155pp; English.
XX
XX The present invention describes immunoglobulin E (IGE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC a target effector site on the epsilon-heavy chain of IGE, and so
CC preventing triggering and activation of mast cells and basophils and
CC downregulation of IGE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IGE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe (non-
CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
CC sequences used in the exemplification of the present invention
XX
XX Sequence 312 AA;
SQ
XX
XX Query Match 55.4%; Score 41; DB 3; Length 312;
XX Best Local Similarity 64.3%; Pred. No. 60;
XX Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 RNNVLITQDQATT 14
XX ||:|||||
XX 255 RNDSPITQDQYTT 268
XX
XX RESULT 12
XX ADN24060
XX ID ADN24060 standard; protein; 312 AA.
XX
XX ADN24060;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #6713.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT
```



XX WPI, 1996-277321/28.  
 DR N-PSDB; AAT29824.  
 XX  
 PT New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense  
 PT therapy, assays, drug screening, etc.  
 XX  
 PS Claim 11; Page 29-30; 49pp; English.  
 XX  
 CC The canine IGE amino acid sequence (AAR97753) was deduced from an  
 CC isolated gene (AAT29824) obd. from a canine liver DNA library. The  
 CC cloning of the IGE gene allows produ. of large quantities of recombinant  
 CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE  
 CC can be used in drug development (e.g. small molecule screening, assay  
 CC development and anti-IGE antibody generation). Fragments of IGE can be  
 CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new  
 CC sequence information permits targeted modulation of IGE-mediated immune  
 CC responses  
 XX  
 SQ Sequence 426 AA;  
 Query Match 55.4%; Score 41; DB 2; Length 426;  
 Best Local Similarity 64.3%; Pred. No. 85;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RNNVLIQTDOQATT 14  
 Db 357 RNDSPITQTDQYTTT 370  
 RESULT 15  
 ABB96583  
 ID ABB96583 standard; protein; 426 AA.  
 XX  
 AC ABB96583;  
 XX  
 DT 28-MAY-2003 (first entry)  
 DE Dog IGE heavy chain amino acid sequence SEQ ID NO:28.  
 XX  
 KM Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
 KM immune response; major histocompatibility complex; MHC; immunogenic;  
 KM antiallergic; antisthmatic; immunosuppressive; vasotropic; cytostatic;  
 KM dermatological; antiinflammatory; IGE-mediated condition; food allergy;  
 KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KM urticaria hives.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO2003015716-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 08-AUG-2002; 2002WO-US026986.  
 XX  
 PR 13-AUG-2001; 2001US-0312120P.  
 XX  
 PA (IGET-) IGE THERAPEUTICS INC.  
 XX  
 PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 XX  
 DR WPI, 2003-268242/26.  
 XX  
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL, response  
 PT against IGE, by identifying peptide eliciting CTL response to IGE  
 PT peptides naturally presented by major histocompatibility complex class I  
 PT protein.  
 XX  
 XX Example 7; Page 152-154; 187pp; English.  
 CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin

CC E (IGE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IGE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (c1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (c2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (c3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IGE peptides. C1-3 have antiallergic, antisthmatic, immunosuppressive,  
 CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IGE, and in  
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an IGE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention  
 XX  
 SQ Sequence 426 AA;  
 Query Match 55.4%; Score 41; DB 6; Length 426;  
 Best Local Similarity 64.3%; Pred. No. 85;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RNNVLIQTDOQATT 14  
 Db 357 RNDSPITQTDQYTTT 370

Search completed: December 12, 2005, 20:30:29  
 Job time : 83.3362 secs

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## OM protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 20.431 Seconds  
(without alignments)  
60.699 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
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Scoring table: BLOSUM62  
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*

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- 3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/PCITUS\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	58.1	580	2	US-09-723-546-10 Sequence 10, Appl
2	41	55.4	108	2	US-09-281-760E-37 Sequence 37, Appl
3	41	55.4	312	2	US-09-701-623C-2 Sequence 2, Appl
4	41	55.4	426	1	US-08-336-583-2 Sequence 2, Appl
5	41	55.4	426	4	PCR-US95-13795-2 Sequence 2, Appl
6	38	51.4	345	2	US-09-270-767-41480 Sequence 41480, A
7	38	51.4	613	2	US-09-026-001A-10 Sequence 10, Appl
8	38	51.4	613	2	US-09-996-620-10 Sequence 10, Appl
9	38	51.4	621	2	US-09-026-001A-18 Sequence 18, Appl
10	38	51.4	621	2	US-09-996-620-18 Sequence 18, Appl
11	37	50.0	370	2	US-09-328-352-5826 Sequence 5826, Ap
12	37	50.0	431	2	US-09-479-614-14 Sequence 14, Appl
13	37	50.0	496	2	US-09-479-614-2 Sequence 2, Appl
14	37	50.0	496	2	US-09-479-614-29 Sequence 29, Appl
15	36	48.6	153	2	US-09-248-796A-22366 Sequence 22366, A
16	36	48.6	199	2	US-09-107-433-2754 Sequence 2754, Ap
17	36	48.6	383	2	US-09-328-352-5969 Sequence 5969, Ap
18	36	48.6	441	2	US-09-583-110-4400 Sequence 4400, Ap
19	36	48.6	445	2	US-09-107-433-5039 Sequence 5039, Ap
20	36	48.6	447	2	US-09-205-258-408 Sequence 408, App
21	36	48.6	461	2	US-10-004-860-408 Sequence 408, App
22	36	48.6	461	2	US-09-991-181-301 Sequence 301, App
23	36	48.6	461	2	US-09-990-444-301 Sequence 301, App
24	36	48.6	461	2	US-09-997-333-301 Sequence 301, App
25	36	48.6	601	2	US-09-992-598-301 Sequence 301, App
26	36	48.6	601	2	US-09-489-039A-8499 Sequence 8499, Ap
27	35	47.3	75	2	US-09-248-796A-24803 Sequence 24803, A

28	35	47.3	138	2	US-09-540-236-1974 Sequence 1974, Ap
29	35	47.3	213	2	US-09-270-767-46161 Sequence 46161, A
30	35	47.3	286	2	US-09-107-532A-4821 Sequence 4821, A
31	35	47.3	406	2	US-09-134-001C-3544 Sequence 3544, Ap
32	35	47.3	418	2	US-08-630-172-18 Sequence 18, Appl
33	35	47.3	418	2	US-09-375-419-18 Sequence 18, Appl
34	35	47.3	434	2	US-09-198-452A-118 Sequence 118, App
35	35	47.3	434	2	US-09-438-185A-102 Sequence 102, App
36	35	47.3	551	2	US-08-886-886-15 Sequence 15, Appl
37	35	47.3	570	2	US-09-489-039A-12964 Sequence 12964, A
38	35	47.3	650	2	US-09-107-532A-5521 Sequence 5521, Ap
39	35	47.3	695	2	US-09-902-540-10055 Sequence 10055, A
40	35	47.3	1061	2	US-09-489-039A-12740 Sequence 12740, A
41	35	47.3	5024	2	US-09-710-279-2964 Sequence 2964, Ap
42	35	47.3	10182	2	US-09-134-001C-3159 Sequence 3159, Ap
43	34	45.9	92	2	US-09-134-001C-4864 Sequence 4864, Ap
44	34	45.9	135	2	US-09-293-395-2 Sequence 2, Appl
45	34	45.9	135	2	US-09-668-648-2 Sequence 2, Appl

## ALIGNMENTS

```
RESULT 1
US-09-723-546-10
; Sequence 10, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHE00059
; CURRENT APPLICATION NUMBER: US/09/723,546
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-09-723-546-10

Query Match      58.1% Score 43; DB 2; Length 580;
Best Local Similarity 57.1% Pred. No. 13;
Matches      8; Conservative      2; Mismatches      4; Indels      0; Gaps      0;

QY      2 NNNLVIQTDQQTTR 15
      |||: ||| |||
DB      168 NNNVFMRDQQTTR 181

RESULT 2
US-09-281-760E-37
; Sequence 37, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Warner, Brian
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
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```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (530)..(530)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (847)..(849)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
; US-09-281-760E-37

Query Match          55.4%; Score 41; DB 2; Length 108;
Best Local Similarity 64.3%; Pred. No. 4.3;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 14
Db 43 RNDSPITQDQYTTT 56

RESULT 3
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
```

```

; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2

Query Match          55.4%; Score 41; DB 2; Length 312;
Best Local Similarity 64.3%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 14
Db 255 RNDSPITQDQYTTT 268

RESULT 4
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match          55.4%; Score 41; DB 1; Length 426;
Best Local Similarity 64.3%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 14
Db 357 RNDSPITQDQYTTT 370

RESULT 5
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PCT-US95-13795-2  
; Sequence 2, Application PC/TUS9513795  
; GENERAL INFORMATION:  
; APPLICANT: HOLLIS, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13795  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E.  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19211Y  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-6734  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-13795-2

Query Match 55.4%; Score 41; DB 4; Length 426;  
Best Local Similarity 64.3%; Pred. No. 21;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATY 14  
||:|||||  
Db 357 RNDSPITQDQYTT 370

RESULT 6  
US-09-270-767-41480  
; Sequence 41480, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7325-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 41480  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-41480

Query Match 51.4%; Score 38; DB 2; Length 345;  
Best Local Similarity 57.1%; Pred. No. 57;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNVLITDQATTR 15

Db 77 NQKLIRKXQQTTR 90  
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RESULT 7  
US-09-026-001A-10  
; Sequence 10, Application US/09026001A  
; Patent No. 6413760  
; GENERAL INFORMATION:  
; APPLICANT: Boodhoo, Amechand  
; APPLICANT: Seehra, Jaabir  
; APPLICANT: Shaw, Gray  
; APPLICANT: Sako, Dianne  
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,001A  
; FILING DATE: 18-FEB-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: G15293B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 876-5851  
; TELEFAX: (617) 876-5824  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 613 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-026-001A-10

Query Match 51.4%; Score 38; DB 2; Length 613;  
Best Local Similarity 53.8%; Pred. No. 1.1e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQAT 13  
||:|||||  
Db 261 RNEINVOQSDVQAT 273

RESULT 8  
US-09-996-620-10  
; Sequence 10, Application US/09996620  
; Patent No. 6881404  
; GENERAL INFORMATION:  
; APPLICANT: Boodhoo, Amechand  
; APPLICANT: Seehra, Jaabir  
; APPLICANT: Saw, Gray  
; APPLICANT: Sako, Dianne  
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM  
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive

```

; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,620
; FILING DATE: 27-Feb. 6881404-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,001
; FILING DATE: 18-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 613 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-996-620-10

Query Match      51.4%; Score 38; DB 2; Length 613;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQAT 13
Db      261 RNEINVSQSDVQAT 273

RESULT 9
US-09-026-001A-18
; Sequence 18, Application US/09026001A
; Patent No. 6413760
; GENERAL INFORMATION:
; APPLICANT: Boonhoo, Amechand
; APPLICANT: Seehra, Jaabir
; APPLICANT: Shaw, Dianne
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,001A
; FILING DATE: 18-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
```

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; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 621 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-026-001A-18

Query Match      51.4%; Score 38; DB 2; Length 621;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQAT 13
Db      269 RNEINVSQSDVQAT 281

RESULT 10
US-09-996-620-18
; Sequence 18, Application US/09996620
; Patent No. 6881404
; GENERAL INFORMATION:
; APPLICANT: Boonhoo, Amechand
; APPLICANT: Seehra, Jaabir
; APPLICANT: Shaw, Dianne
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,620
; FILING DATE: 27-Feb. 6881404-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,001
; FILING DATE: 18-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 621 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-996-620-18

Query Match      51.4%; Score 38; DB 2; Length 621;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
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Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RNNVLIOQTDOQAT 13
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Db 269 RNEINOSDVQAT 281

RESULT 11
US-09-328-352-5826
; Sequence 5826, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5826
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5826

Query Match 50.0%; Score 37; DB 2; Length 370;
Best Local Similarity 42.9%; Pred. No. 95;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIOQTDOQAT 14
   ||:|:|:|
Db 175 KNNIYTTDNSATS 188

RESULT 12
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 50.0%; Score 37; DB 2; Length 431;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNNVLIOQTDOQAT 14
   ||:|:|:|
Db 363 NDSPVRTQOQAT 375

RESULT 13
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
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; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNNVLIOQTDOQAT 14
   ||:|:|:|
Db 428 NDSPVRTQOQAT 440

RESULT 14
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNNVLIOQTDOQAT 14
   ||:|:|:|
Db 428 NDSPVRTQOQAT 440

RESULT 15
US-09-248-796A-22386
; Sequence 22386, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22386
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22386
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Query Match 48.6%; Score 36; DB 2; Length 153;  
Best Local Similarity 77.8%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNNVLIQTD 9  
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Db 21 RNNYFIQTD 29

Search completed: December 12, 2005, 19:37:05  
Job time : 21.431 secs

GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: December 12, 2005, 19:33:42 ; Search time 66.9828 Seconds  
(without alignments)  
93.568 Million cell updates/sec

Title: US-10-758-165a-3  
Perfect score: 74  
Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBSCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBSCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBSCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBSCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBSCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	US-10-758-165-3	Sequence 3, Appli
2	74	100.0	424	US-10-451-078-2	Sequence 2, Appli
3	74	100.0	424	US-10-451-078-4	Sequence 4, Appli
4	74	100.0	569	US-10-214-524-30	Sequence 40, Appli
5	49	66.2	15	US-10-052-788-4	Sequence 4, Appli
6	43	58.1	580	US-10-674-666-17	Sequence 17, Appli
7	43	58.1	580	US-10-757-845-10	Sequence 10, Appli
8	41.5	56.1	854	US-10-732-923-23294	Sequence 23294, A
9	41	55.4	15	US-10-758-165-1	Sequence 1, Appli
10	41	55.4	105	US-10-437-963-129557	Sequence 129557,
11	41	55.4	312	US-10-369-493-6713	Sequence 6713, Ap
12	41	55.4	426	US-10-214-524-28	Sequence 28, Appli
13	41	55.4	917	US-10-437-963-181484	Sequence 181484,
14	40	54.1	15	US-10-758-165-7	Sequence 7, Appli
15	40	54.1	567	US-10-214-524-33	Sequence 33, Appli
16	38	51.4	558	US-10-437-963-185049	Sequence 185049,
17	38	51.4	613	US-09-996-620-10	Sequence 10, Appli
18	38	51.4	613	US-11-066-236-10	Sequence 10, Appli
19	38	51.4	621	US-09-996-620-18	Sequence 18, Appli
20	38	51.4	621	US-11-066-236-18	Sequence 18, Appli
21	38	51.4	703	US-10-282-122A-72382	Sequence 72382, A
22	38	51.4	814	US-10-128-714-8100	Sequence 8100, Ap
23	37	50.0	15	US-10-758-165-2	Sequence 2, Appli
24	37	50.0	67	US-10-437-963-138338	Sequence 138338,
25	37	50.0	223	US-10-389-566-587	Sequence 587, App
26	37	50.0	431	US-09-479-614-14	Sequence 14, Appli
27	37	50.0	431	US-10-409-772-14	Sequence 14, Appli

28	37	50.0	496	3	US-09-479-614-2	Sequence 2, Appli
29	37	50.0	496	3	US-09-479-614-29	Sequence 29, Appli
30	37	50.0	496	4	US-10-214-524-25	Sequence 25, Appli
31	37	50.0	496	4	US-10-409-772-2	Sequence 2, Appli
32	37	50.0	496	4	US-10-409-772-29	Sequence 29, Appli
33	37	50.0	663	4	US-10-389-566-1053	Sequence 1053, Ap
34	37	50.0	663	5	US-10-732-923-2730	Sequence 9730, Ap
35	37	50.0	750	4	US-10-425-115-351098	Sequence 351098,
36	36.5	49.3	272	4	US-10-425-115-233903	Sequence 233903,
37	36	48.6	21	4	US-10-340-288-37	Sequence 37, Appli
38	36	48.6	143	4	US-10-128-714-8304	Sequence 8304, Ap
39	36	48.6	199	4	US-10-425-115-29967	Sequence 29967,
40	36	48.6	199	5	US-10-617-320-2754	Sequence 2754, Ap
41	36	48.6	309	4	US-10-264-237-2751	Sequence 2751, Ap
42	36	48.6	318	4	US-10-128-714-3304	Sequence 3304, Ap
43	36	48.6	343	5	US-10-450-763-45557	Sequence 45557, A
44	36	48.6	333	5	US-09-731-872-247	Sequence 247, App
45	36	48.6	348	3	US-09-876-997-247	Sequence 247, App

## ALIGNMENTS

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RESULT 1
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match      100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2,2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQATTR 15
      |||||
Db      1 RNNVLIQTDOQATTR 15

RESULT 2
US-10-451-078-2
; Sequence 2, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bettina, Wagner
; APPLICANT: Radbruch, Andreas
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
; TITLE OF INVENTION: Heavy Chain of an Equine IGE Allotype, Recombinant
; TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 03100177aa
; CURRENT APPLICATION NUMBER: US/10/451,078
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 100 64 415.5
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Equus caballus
; FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (1)..(97)
;   OTHER INFORMATION: CH1 domain, IGE allotype a
;   FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (98)..(205)
;   OTHER INFORMATION: CH2 domain, IGE allotype a
;   FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (206)..(312)
;   OTHER INFORMATION: CH3 domain, IGE allotype a
;   FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (313)..(424)
;   OTHER INFORMATION: CH4 domain, IGE allotype a
US-10-451-078-2
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Query Match          100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 RNNVLIQTDOQATTR 15
Db      356 RNNVLIQTDOQATTR 370
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RESULT 3
US-10-451-078-4
; Sequence 4, Application US/10451078
; Publication No. US2004015764A1
; GENERAL INFORMATION:
;   APPLICANT: Leibold, Wolfgang
;   APPLICANT: Bettina, Wagner
;   TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
;   TITLE OF INVENTION: Heavy Chain of an Equine IGE Allotype, Recombinant
;   TITLE OF INVENTION: Immunoglobulin Obtained Using Them, and Corresponding
;   FILE REFERENCE: 03100177a
;   CURRENT APPLICATION NUMBER: US/10/451,078
;   CURRENT FILING DATE: 2003-12-24
;   PRIOR APPLICATION NUMBER: PCT/DE01/04810
;   PRIOR FILING DATE: 2001-12-20
;   PRIOR APPLICATION NUMBER: DE 100 64 415.5
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 4
;   LENGTH: 424
;   TYPE: PRT
;   ORGANISM: Equus caballus
;   FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (1)..(97)
;   OTHER INFORMATION: CH1 domain, IGE allotype b
;   FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (98)..(205)
;   OTHER INFORMATION: CH2 domain, IGE allotype b
;   FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (206)..(312)
;   OTHER INFORMATION: CH3 domain, IGE allotype b
;   FEATURE:
;   NAME/KEY: Domain
;   LOCATION: (313)..(424)
;   OTHER INFORMATION: CH4 domain, IGE allotype b
US-10-451-078-4
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Query Match          100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 RNNVLIQTDOQATTR 15
Db      356 RNNVLIQTDOQATTR 370
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RESULT 4
US-10-214-524-30
; Sequence 30, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
;   APPLICANT: Chen, Swey-Shen Alex
;   APPLICANT: Yang, Yong-Min
;   APPLICANT: Barankiewicz, Theresa J.
;   APPLICANT: Chen, Zhong
;   TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
;   FILE REFERENCE: IGE-00101.P.1.1
;   CURRENT APPLICATION NUMBER: US/10/214,524
;   CURRENT FILING DATE: 2002-08-08
;   PRIOR APPLICATION NUMBER: 60/312,120
;   PRIOR FILING DATE: 2001-08-13
;   NUMBER OF SEQ ID NOS: 61
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 30
;   LENGTH: 569
;   TYPE: PRT
;   ORGANISM: Horse (Equus caballus)
US-10-214-524-30
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Query Match          100.0%; Score 74; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 RNNVLIQTDOQATTR 15
Db      501 RNNVLIQTDOQATTR 515
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RESULT 5
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
;   APPLICANT: Gershwin, Laurel J.
;   APPLICANT: Pettigrew, Howard David
;   APPLICANT: Kalina, Warren V.
;   TITLE OF INVENTION: The Regents of the University of California
;   TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
;   TITLE OF INVENTION: Induction of Anti-IGE Antibodies
;   FILE REFERENCE: 023070-121000US
;   CURRENT APPLICATION NUMBER: US/10/052,788
;   CURRENT FILING DATE: 2001-11-08
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 4
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
;   OTHER INFORMATION: P4, early portion of C4 of equine Ige epsilon
;   OTHER INFORMATION: heavy chain
US-10-052-788-4
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Query Match          66.2%; Score 49; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      6 IOTDQATTR 15
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Db      1 10TDOQATTR 10
|||||
RESULT 6
US-10-674-666-17
; Sequence 17, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-674-666-17

Query Match      58.1%; Score 43; DB 4; Length 580;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2  NNVL1QTDQOATTR 15
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Db      168  NNWVFMRDQOITTR 181

RESULT 7
US-10-757-843-10
; Sequence 10, Application US/10757843
; Publication No. US20050129706A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHE00059
; CURRENT APPLICATION NUMBER: US/10/757,843
; PRIOR FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/723,546
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-757-843-10

Query Match      58.1%; Score 43; DB 5; Length 580;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2  NNVL1QTDQOATTR 15
|||||
Db      168  NNWVFMRDQOITTR 181

RESULT 8
US-10-732-923-23294
; Sequence 23294, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgettson, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
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; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 23294
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-23294

Query Match      56.1%; Score 41.5; DB 5; Length 854;
Best Local Similarity 78.6%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      2  NNVL1Q-TDQOATT 14
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Db      483  NNVL1QKDQOATT 496

RESULT 9
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      55.4%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  RNNVL1QTDQOATT 14
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Db      1  RNDSP1QTDQYTTT 14

RESULT 10
US-10-437-963-129557
; Sequence 129557, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 129557
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31803C.1.pcp
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US-10-437-963-129557

Query Match 55.4%; Score 41; DB 4; Length 105;  
Best Local Similarity 46.7%; Pred. No. 18;  
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 15  
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DB 10 RNNGMVELEQATSR 24

RESULT 11

US-10-369-493-6713  
; Sequence 6713, Application US/10369493  
; Publication No. US2003023675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianning  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6713  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6713

Query Match 55.4%; Score 41; DB 4; Length 312;  
Best Local Similarity 57.1%; Pred. No. 60;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RNNVLIOTDQOATTR 15  
|||:::|||||  
DB 159 DNVLIQKDEENTAR 172

RESULT 12

US-10-214-524-28  
; Sequence 28, Application US/10214524  
; Publication No. US20030073142A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Swei-Shen Alex  
; APPLICANT: Yang, Yong-Min  
; APPLICANT: Barankiewicz, Theresa J.  
; APPLICANT: Chen, Zhong  
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
; FILE REFERENCE: IGE-00101.P.1.1  
; CURRENT APPLICATION NUMBER: US/10/214,524  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: 60/312,120  
; PRIOR FILING DATE: 2001-08-13  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Dog (Canis familiaris)  
US-10-214-524-28

Query Match 55.4%; Score 41; DB 4; Length 426;  
Best Local Similarity 64.3%; Pred. No. 86;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 14  
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DB 357 RNDSPLOTQOYTTT 370

RESULT 13  
US-10-437-963-181484  
; Sequence 181484, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 181484  
; LENGTH: 917  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(917)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_78753C.1.pep  
US-10-437-963-181484

Query Match 55.4%; Score 41; DB 4; Length 917;  
Best Local Similarity 50.0%; Pred. No. 28+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 14  
|||:::|||||  
DB 143 RNNIMVLDNQMTT 156

RESULT 14

US-10-758-165-7  
; Sequence 7, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-7

Query Match 54.1%; Score 40; DB 5; Length 15;  
Best Local Similarity 46.7%; Pred. No. 2.9;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 15  
|||:::|||||  
DB 1 RNDAPVQADRHSTTR 15

RESULT 15



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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.4569 Seconds  
(without alignments)  
34.094 Million cell updates/sec

Title: US-10-758-165A-3

Perfect score: 74  
Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_New:\*  
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3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	55.4	312	6	US-10-723-207-2
2	38	51.4	1827	7	US-11-057-058-62
3	36	48.6	461	6	US-10-131-826A-454
4	36	48.6	943	6	US-10-467-657-5508
5	35	47.3	5024	6	US-10-793-626-2564
6	34	45.9	310	7	US-10-131-826A-538
7	34	45.9	310	7	US-11-025-834A-13
8	34	45.9	310	7	US-11-025-834A-15
9	34	45.9	362	6	US-10-821-234-1148
10	34	45.9	377	6	US-10-821-234-1148
11	33.5	45.3	522	6	US-10-793-626-2526
12	33.5	45.3	522	6	US-10-793-626-456
13	33	44.6	114	6	US-10-793-626-2042
14	33	44.6	1095	6	US-10-793-626-2252
15	33	44.6	1095	6	US-10-793-626-3154
16	32	43.2	2725	7	US-11-113-424-52
17	32	43.2	409	6	US-10-467-657-5732
18	32	43.2	409	6	US-10-467-657-7450
19	32	43.2	592	6	US-10-467-657-4888
20	32	43.2	2314	7	US-11-097-728-2
21	32	43.2	2353	7	US-11-097-728-6
22	31.5	42.6	197	6	US-11-186-284-26
23	31	41.9	106	7	US-10-467-657-2812
24	31	41.9	238	7	US-11-008-727-12
25	31	41.9	270	7	US-11-008-727-26
					Sequence 2, Appli
					Sequence 62, Appl
					Sequence 454, App
					Sequence 5508, Ap
					Sequence 2964, Ap
					Sequence 538, App
					Sequence 15, Appl
					Sequence 1148, Ap
					Sequence 2926, Ap
					Sequence 456, App
					Sequence 2042, Ap
					Sequence 2252, Ap
					Sequence 3154, Ap
					Sequence 52, Appl
					Sequence 5732, Ap
					Sequence 7450, Ap
					Sequence 4888, Ap
					Sequence 2, Appli
					Sequence 6, Appli
					Sequence 26, Appl
					Sequence 2412, Ap
					Sequence 12, Appl
					Sequence 26, Appl
					Sequence 24, Appl

26	31	41.9	416	6	US-10-793-626-2	Sequence 2, Appli
27	31	41.9	476	7	US-11-008-727-22	Sequence 22, Appl
28	31	41.9	492	6	US-10-793-626-1276	Sequence 1276, Ap
29	31	41.9	509	7	US-11-008-727-16	Sequence 16, Appl
30	31	41.9	531	7	US-11-008-727-18	Sequence 18, Appl
31	31	41.9	543	6	US-10-689-742-78	Sequence 78, Appl
32	31	41.9	703	6	US-10-467-657-7158	Sequence 7158, Ap
33	31	41.9	740	7	US-11-110-837-2	Sequence 2, Appli
34	31	41.9	740	7	US-11-110-837-4	Sequence 4, Appli
35	31	41.9	1189	7	US-11-074-176-134	Sequence 134, App
36	31	41.9	1279	6	US-10-793-626-3188	Sequence 3188, Ap
37	31	41.9	104	6	US-10-467-657-138	Sequence 138, App
38	30	40.5	104	6	US-10-467-657-6972	Sequence 6972, Ap
39	30	40.5	208	6	US-10-878-556A-133	Sequence 133, App
40	30	40.5	226	6	US-10-878-556A-106	Sequence 106, App
41	30	40.5	236	7	US-11-008-727-4	Sequence 4, Appli
42	30	40.5	257	6	US-10-467-962B-73	Sequence 73, Appl
43	30	40.5	263	6	US-10-821-234-1312	Sequence 1312, Ap
44	30	40.5	369	7	US-11-055-822-32	Sequence 32, Appl
45	30	40.5	394	6	US-10-510-386-208	Sequence 208, App

#### ALIGNMENTS

RESULT 1  
US-10-723-207-2  
; Sequence 2, Application US/10723207  
; Publication No. US20050250934A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Y1  
; APPLICANT: Walfield, Alan M.  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; TITLE OF INVENTION: ALLERGY  
; FILE REFERENCE: 1151-4153US2  
; CURRENT APPLICATION NUMBER: US/10/723, 207  
; PRIOR FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: 09/701, 623  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100, 287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Dog  
; FEATURE:  
; OTHER INFORMATION: CH2CH3n of dog IGE  
; PUBLICATION INFORMATION:  
; AUTHORS: Patel,  
; JOURNAL: Immunogenetics  
; VOLUME: 41  
; PAGES: 282-286  
; DATE: 1995  
; US-10-723-207-2  
Query Match 55.4%; Score 41; DB 6; Length 312;  
Best Local Similarity 64.3%; Pred. No. 0.53;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 RNNVLIQTDOQATTT 14  
DB 255 RNDSPRIQDQYTTT 268  
RESULT 2  
US-11-057-058-62  
; Sequence 62, Application US/11057058  
; Publication No. US20050244400A1  
; GENERAL INFORMATION:

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; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Mega, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 1827
; TYPE: PRT
; ORGANISM: Rabbit sp.
; US-11-057-058-62

Query Match      51.4%; Score 38; DB 7; Length 1827;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 NNVLIQTDQATTR 15
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Db      144 NNVLTTESQTPANR 157

RESULT 3
; Sequence 454, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACTIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 454
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-131-826A-454

Query Match      48.6%; Score 36; DB 6; Length 461;
Best Local Similarity 53.8%; Pred. No. 7.6;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 NNVLIQTDQATTR 15
      |||:|:|:|
Db      175 NNVLITDMQIMVR 187

RESULT 4
; Sequence 5508, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 5508
; LENGTH: 943
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-5508

Query Match      48.6%; Score 36; DB 6; Length 943;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLIQTDQATTR 15
      |||:|:|:|
Db      886 RNNVHTGELSLX 900

RESULT 5
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P33480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5024)
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OTHER INFORMATION: variable amino acid  
US-10-793-626-2964

Query Match 47.3%; Score 35; DB 6; Length 5024;  
Best Local Similarity 46.7%; Pred. No. 2e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15  
: : : : :  
Db 3492 QREVMINTNTWATTR 3506

RESULT 6  
US-10-131-826A-538

; Sequence 538, Application US/10131826A  
; Publication No. US20050245730A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: DeGoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gettleisen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumanabe, Daniel

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C128

CURRENT FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US/10/131.826A

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 538

LENGTH: 310

TYPE: prt

ORGANISM: Homo Sapien

US-10-131-826A-538

Query Match 45.9%; Score 34; DB 6; Length 310;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15  
: : : : :  
Db 175 RNDVPLPTDSRANPR 189

Db 175 RNDVPLPTDSRANPR 189

RESULT 7  
US-11-025-834A-13

; Sequence 13, Application US/11025834A  
; Publication No. US20050266426A1

GENERAL INFORMATION:

APPLICANT: IMHOFF, BEAT ALBERT

APPLICANT: AURRAND-LIONS, MICHEL

TITLE OF INVENTION: CONFLUENCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASC

TITLE OF INVENTION: PERMEABILITY

FILE REFERENCE: 011422-0314432

CURRENT APPLICATION NUMBER: US/11/025.834A

CURRENT FILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: 09/524,531

PRIOR FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: EP 99.200746.8

PRIOR FILING DATE: 1999-03-11

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 310

TYPE: prt

ORGANISM: Mus musculus

US-11-025-834A-13

Query Match 45.9%; Score 34; DB 7; Length 310;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15  
: : : : :  
Db 175 RNDVPLPTDSRANPR 189

RESULT 8  
US-11-025-834A-15

; Sequence 15, Application US/11025834A

; Publication No. US20050266426A1

GENERAL INFORMATION:

APPLICANT: IMHOFF, BEAT ALBERT

APPLICANT: AURRAND-LIONS, MICHEL

TITLE OF INVENTION: CONFLUENCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASC

TITLE OF INVENTION: PERMEABILITY

FILE REFERENCE: 011422-0314432

CURRENT APPLICATION NUMBER: US/11/025.834A

CURRENT FILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: 09/524,531

PRIOR FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: EP 99.200746.8

PRIOR FILING DATE: 1999-03-11

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 310

TYPE: prt

ORGANISM: Homo sapiens

US-11-025-834A-15

Query Match 45.9%; Score 34; DB 7; Length 310;  
Best Local Similarity 46.7%; Pred. No. 11;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15  
: : : : :  
Db 175 RNDVPLPTDSRANPR 189

RESULT 9  
US-10-821-234-1148

; Sequence 1148, Application US/10821234  
; Publication No. US20050255114A1

```
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1148
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1148
```

```
Query Match 45.9%; Score 34; DB 6; Length 362;
Best Local Similarity 46.7%; Pred. No. 14;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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```
QY 1 RNNVLIQTDOQATR 15
Db 227 RNDVPLPTDSRANR 241
```

```
RESULT 10
US-10-793-626-2926
; Sequence 2926, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2926
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2926
```

```
Query Match 45.9%; Score 34; DB 6; Length 377;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 RNNVLIQTDOQ 11
Db 118 RNVIVFSDQ 127
```

```
RESULT 11
US-10-793-626-456
; Sequence 456, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
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```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 456
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-456
```

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Query Match 45.3%; Score 33.5; DB 6; Length 522;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
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```
QY 1 RNNVLIQTDO-QATT 14
Db 394 RRGALISMDQQAITS 408
```

```
RESULT 12
US-10-793-626-2042
; Sequence 2042, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2042
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2042
```

```
Query Match 45.3%; Score 33.5; DB 6; Length 522;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
```

```
QY 1 RNNVLIQTDO-QATT 14
Db 394 RRGALISMDQQAITS 408
```

```
RESULT 13
US-10-793-626-2252
; Sequence 2252, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2252
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2252
```

Query Match 44.6%; Score 33; DB 6; Length 114;  
Best Local Similarity 38.5%; Pred. No. 5.4;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 NNVLQTDQATR 15  
DB 52 NILVTDKTRK 64

RESULT 14  
US-10-793-626-3154  
; Sequence 3154, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PUJ480US  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3154  
; LENGTH: 1095  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-3154

Query Match 44.6%; Score 33; DB 6; Length 1095;  
Best Local Similarity 60.0%; Pred. No. 80;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLQTDQ 11  
DB 318 NNALVQAKQ 327

RESULT 15  
US-11-113-424-52  
; Sequence 52, Application US/11113424  
; Publication No. US20050260713A1  
; GENERAL INFORMATION:  
; APPLICANT: Gangoli et al.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-225  
; CURRENT APPLICATION NUMBER: US/11/113,424  
; CURRENT FILING DATE: 2005-04-21  
; PRIOR APPLICATION NUMBER: 60/256,704  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/311,590  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/257,314  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/311,613  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/315,617  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/307,506  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/322,358  
; PRIOR FILING DATE: 2001-09-14  
; PRIOR APPLICATION NUMBER: 60/294,075  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 60/288,153  
; PRIOR FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52

; LENGTH: 2725  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-113-424-52

Query Match 44.6%; Score 33; DB 7; Length 2725;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLQTDQAT 14  
DB 1691 RNNVLQTDQAT 1704

Search completed: December 12, 2005, 20:19:48  
Job time : 2.4569 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 12.6724 Seconds  
(without alignments)  
113.889 Million cell updates/sec

Title: US-10-758-165A-3

Perfect score: 74

Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	60.8	917	2 P95884	probable sensory h
2	43.5	58.8	285	2 H84219	hypothetical prote
3	43	58.1	580	2 T45064	arginine deiminase
4	41	55.4	312	2 T32446	hypothetical prote
5	41	55.4	312	2 A89460	protein H42K12.1 l
6	41	55.4	2145	2 S61041	glutamate synthase
7	39	52.7	263	2 B85042	hypothetical prote
8	39	52.7	716	2 H84421	probable receptor-
9	38	51.4	138	2 G97191	probable membrane
10	38	51.4	829	2 A12531	hypothetical prote
11	38	51.4	1827	1 A23945	sucrose alpha-gluc
12	37	50.0	128	1 H64842	probable translati
13	37	50.0	128	2 H80785	hypothetical prote
14	37	50.0	128	2 H85645	hypothetical prote
15	36.5	49.3	1017	2 S67804	Lrg1 protein - yea
16	36	48.6	140	2 S72252	hemoglobin, extrac
17	36	48.6	205	2 B88095	protein F3959.5 (l
18	36	48.6	407	2 AG2150	serine proteinase
19	36	48.6	412	2 T24441	GTP-binding protei
20	36	48.6	433	2 C70163	histidine protein
21	36	48.6	441	2 G98126	probable sensor h
22	36	48.6	441	2 B95261	protein-tyrosine-p
23	36	48.6	468	2 A53889	targeted effector
24	36	48.6	468	2 T43622	violence protein
25	36	48.6	487	2 S01054	glutamate receptor
26	36	48.6	487	1 S07062	kinase-binding pr
27	36	48.6	962	2 C81060	translational initia
28	36	48.6	962	2 C81060	probable mmp14 pro
29	36	48.6	967	2 C70831	

30	36	48.6	1157	2 AD1728	ATP-dependent deox
31	36	48.6	1418	2 T15232	hypothetical prote
32	36	48.6	1449	2 T20181	hypothetical prote
33	36	48.6	1464	2 JCS144	murinoglobulin pre
34	36	48.6	1584	2 T20180	hypothetical prote
35	36	48.6	1586	2 T20179	hypothetical prote
36	36	48.6	2021	2 AD2267	serine/threonine k
37	36	47.3	185	2 T14523	hypothetical prote
38	35	47.3	225	2 AC0587	KDP operon transcr
39	35	47.3	225	2 B90719	transcription regu
40	35	47.3	225	2 C85569	hypothetical prote
41	35	47.3	225	2 B64804	transcription regu
42	35	47.3	252	2 T20321	hypothetical prote
43	35	47.3	276	2 B84597	probable disease r
44	35	47.3	345	2 S73498	MG456 homolog K05
45	35	47.3	386	2 T09019	phosphoprotein pho

#### ALIGNMENTS

RESULT 1  
P95884  
Probable sensory histidine kinase protein [imported] - Sinorhizobium meliloti (strain 1021)  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: P95884  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan-  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,583-Kb pSymb megaplasmid from the N2-fixing endo-  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: P95884  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-917 <KIR>  
A:Cross-references: UNIPROT:Q92WJ7, UNIPARC:UP100000CB4C5; GB:AL591985; PIN:CA648742.1;  
A:Experimental source: strain 1021, megaplasmid pSymb  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebalit, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: SMD20356  
A:Genome: plasmid

Query Match 60.8%; Score 45; DB 2; Length 917;  
Best Local Similarity 57.1%; Pred. No. 3.6;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQAT 14  
DB 188 RNEVVQTEKRTAT 201

RESULT 2  
H84219  
Hypothetical protein Vng0617h [imported] - Halobacterium sp. NRC-1  
C:Species: Halobacterium sp. NRC-1  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: H84219  
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Iasky, S.  
; Leitbauer, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon-  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li  
A:Title: Genome sequence of Halobacterium species NRC-1.  
A:Reference number: A84160; MUID:20504483; PMID:11016950  
A:Accession: H84219

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-285 <STO>  
A;Cross-references: UNIPROT:Q9HRM4; UNIPARC:UPI00000636A7; GB:AE004437; NID:G10580210; F  
C;Genetics:  
A;Gene: VNG0617H

Query Match 58.8%; Score 43.5; DB 2; Length 285;  
Best Local Similarity 58.8%; Pred. No. 1.8;  
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;  
QY 2 NNVLIOFDOQ---ATTR 15  
Db 212 NNVLIOFDSSTELTTTR 228

RESULT 3  
T45064  
arginine deiminase (EC 3.5.3.6) [validated] - Giardia intestinalis  
C;Species: Giardia intestinalis  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T45064  
R;Knodler, L.A.; Sekyere, E.O.; Stewart, T.S.; Schofield, P.J.; Edwards, M.R.  
J. Biol. Chem. 273, 4470-4477, 1998  
A;Title: Cloning and expression of a prokaryotic enzyme, arginine deiminase, from a pr  
A;Reference number: Z22902; MUID:98136144; PMID:9468500  
A;Accession: T45064  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-580 <KNO>  
A;Cross-references: UNIPROT:Q27657; UNIPARC:UPI000004CCBB; EMBL:U49236; PIDN:AAC06116.1  
A;Experimental source: strain Portland 1  
C;Function:  
A;Description: EC 3.5.3.6 [validated, MUID:98136144]  
C;Superfamily: Giardia intestinalis arginine deiminase  
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 580;  
Best Local Similarity 57.1%; Pred. No. 5.2;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 NNVLIOFDOQATTR 15  
Db 168 NNWVFMRDQOITTR 161

RESULT 4  
T32446  
hypothetical protein H42K12.1 - Caenorhabditis elegans (fragment)  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 05-Oct-2004  
C;Accession: T32446  
R;Meggi, L.; Harper, M.  
submitted to the EMBL Data Library, September 1997  
A;Description: The sequence of C. elegans cosmid H42K12.  
A;Reference number: Z21169  
A;Accession: T32446  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-312 <MAG>  
A;Cross-references: UNIPARC:UPI000017A469; EMBL:AF026207; PIDN:AAB71265.1; GSPDB:GN00028  
C;Experimental source: strain Bristol N2; clone H42K12  
C;Genetics:  
A;Gene: CESP:H42K12.1  
A;Map position: X  
A;Intons: 4/2; 40/3; 106/1; 167/1; 196/2; 251/3

Query Match 55.4%; Score 41; DB 2; Length 312;  
Best Local Similarity 57.1%; Pred. No. 6.1;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NNVLIOFDOQATTR 15  
:|||||:|:|

Db 159 DNVLIOKDEENTAR 172

RESULT 5  
A89460  
protein H42K12.1 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 31-Dec-2004  
C;Accession: A89460  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 283, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: A89460  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-312 <STO>  
A;Cross-references: UNIPARC:UPI000017A469; GB:chr\_X; PIDN:AAB71265.1; PID:G2435556; GSPDB  
A;Note: Similar to protein kinase  
C;Genetics:  
A;Gene: H42K12.1  
A;Map position: X

Query Match 55.4%; Score 41; DB 2; Length 312;  
Best Local Similarity 57.1%; Pred. No. 6.1;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLIOFDOQATTR 15  
Db 159 DNVLIOKDEENTAR 172

RESULT 6  
S61041  
glutamate synthase (NADH2) (EC 1.4.1.14) glt1 precursor [similarity] - yeast (Saccharomy  
N;Alternate names: protein D1448; protein YDL171c  
C;Species: Saccharomyces cerevisiae  
C;Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 12-Jul-2004  
C;Accession: S61041; S67723  
R;Pohl, T.M.  
submitted to the EMBL Data Library, November 1995  
A;Reference number: S61041  
A;Accession: S61041  
A;Molecule type: DNA  
A;Residues: 1-2145 <POH>  
A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z67750; NID:G1061256; PIDN:CAA91574.1; P  
R;Pohl, T.M.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67708  
A;Accession: S67723  
A;Molecule type: DNA  
A;Residues: 1-2145 <POH>  
A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z74219; NID:G1431273; PIDN:CAA98745.1; P  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:GLT1  
A;Cross-references: SGD:S0002330; MIPS:YDL171C  
A;Map position: 4L  
C;Superfamily: glutamate synthase (NADH/NADPH), eukaryotic type  
C;Keywords: 3fe-4S; metalloprotein; oxidoreductase; transmembrane protein  
F;1-53/Domain: propeptide #status predicted <PRO>  
F;54-2145/Product: glutamate synthase #status predicted <MAT>  
F;1077-1093/Domain: transmembrane #status predicted <TM1>  
F;1172-1188/Domain: transmembrane #status predicted <TM2>  
F;54/Active site: Cys #status predicted  
F;1185,1191,1196/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 55.4%; Score 41; DB 2; Length 2145;  
Best Local Similarity 57.1%; Pred. No. 55;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;



QY 1 RNNVLIQTDOQATT 14  
|||:|||||  
Db 1145 RNNVVTQTDGQLRT 1158

## RESULT 7

E85042  
hypothetical protein AT4G03350 (imported) - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: E85042  
R/Anonymous: The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A/Reference number: A85001; MUID:20083488; PMID:10617198  
A/Accession: E85042  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-263 <STO>  
A/Cross-references: UNIPROT:Q9ZQZ6; UNIPARC:UPI00000A63C9; GB:NC\_001268; NID:G7270205; F  
C/Genetics:  
A/Gene: AT4G03350  
A/Map position: 4

Query Match 52.7%; Score 39; DB 2; Length 263;  
Best Local Similarity 50.0%; Pred. No. 12;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 14  
|||:|||||  
Db 145 RNNVVTQTDGQLRT 158

## RESULT 8

H84421  
probable receptor-like protein kinase (imported) - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004  
C/Accession: H84421  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
W.; Koo, H.; Wolf, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umeyam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: H84421  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-716 <STO>  
A/Cross-references: UNIPROT:Q9ZU46; UNIPARC:UPI00000A1C90; GB:AE002093; NID:G4262228; PI  
C/Genetics:  
A/Gene: At2G01210  
A/Map position: 2  
C/Superfamily: Receptor-like protein kinase

Query Match 52.7%; Score 39; DB 2; Length 716;  
Best Local Similarity 53.3%; Pred. No. 38;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 15  
|||:|||||  
Db 568 QSNRIQTDDQQR 582

## RESULT 9

G97191  
probable membrane protein (imported) - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: G97191  
R/Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; Lee,  
J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: G97191  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-138 <KOR>  
A/Cross-references: UNIPROT:Q97GK0; UNIPARC:UPI00000CA4D0; GB:AE001437; PIDN:AAK80322.1;  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Gene: CAC2366

Query Match 51.4%; Score 38; DB 2; Length 138;  
Best Local Similarity 53.8%; Pred. No. 9;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLITDQDQATT 14  
|||:|||||  
Db 42 NNVLITDQDQAST 54

## RESULT 10

AT2531  
hypothetical protein alr7540 (imported) - Nostoc sp. (strain PCC 7120) plasmid pCC7120b  
C/Species: Nostoc sp. PCC 7120  
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AT2531  
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matsumbe, A.; Iriyuchi,  
N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab

A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: AT2531  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-829 <KOR>  
A/Cross-references: UNIPROT:Q8ZSH0; UNIPARC:UPI00000CCD69; GB:AP003602; PIDN:BAW7183.1;  
A/Experimental source: strain PCC 7120  
C/Genetics:  
A/Gene: alr7540  
A/Genome: plasmid

Query Match 51.4%; Score 38; DB 2; Length 829;  
Best Local Similarity 70.0%; Pred. No. 69;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNVLITDQDQ 11  
|||:|||||  
Db 591 NNVLITDQDKE 600

## RESULT 11

A23945  
sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) - rabbit  
N/Alternate names: small intestinal sucrase/isomaltase (SI)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 24-May-1996  
C/Accession: A23945; B25987; A29163  
R/Hunziker, W.; Spiess, W.; Semenza, G.; Lodish, H.F.  
Cell 46, 227-234, 1986  
A/Title: The sucrase-isomaltase complex: primary structure, membrane-orientation, and ev  
A/Reference number: A23945; MUID:86245068; PMID:3755079  
A/Accession: A23945  
A/Molecule type: mRNA  
A/Residues: 1-1827 <HUN>  
A/Cross-references: UNIPARC:UPI00001729E8  
R/Sjoestrom, H.; Noren, O.; Christensen, L.A.; Wacker, H.; Splies, M.; Bigler-Meier, B.  
FEBS Lett. 148, 321-325, 1982  
A/Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-isoma  
A/Reference number: A25987; MUID:83105704; PMID:7152027  
A/Accession: B25987  
A/Molecule type: protein  
A/Residues: 2-32, 'XXX', 36-38, 1008, 'N', 1010-1014, 'E' <SU2>

A;Cross-references: UNIPARC:UPI00001729B9; UNIPARC:UPI00001729EA  
R;Frank, G.; Brunner, U.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H.  
FEBS Lett. 96, 183-188, 1978  
A;Title: The hydrophobic anchor of small-intestinal sucrase-isomaltase. N-terminal sequ  
A;Reference number: A29163; MUID:79086207; PMID:729784  
A;Accession: A29163  
A;Molecule type: protein  
A;Residues: 2,'VNA',6-32,'XXX',36-38 <FRA>  
A;Cross-references: UNIPARC:UPI00001729EB  
C;Comment: Carbohydrate analysis of the mature enzyme complex indicates both N- and O-11  
C;Function: <TSM>  
A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic  
A;Pathway: carbohydrate digestion  
C;Function: <SUC>  
A;Description: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-gluc  
A;Pathway: carbohydrate digestion  
C;Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology  
C;Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m  
F;2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <ISO>  
F;13-33/Domain: membrane associated #status predicted <TMM>  
F;43-65/Region: serine/threonine-rich  
F;63-109/Domain: trefoil homology <TRF1>  
F;189-840/Domain: sucrase/isomaltase homology <SIM>  
F;931-977/Domain: trefoil homology <TRF2>  
F;1008-1827/Product: sucrase alpha-glucosidase (sucrase chain) #status experimental <SUC  
F;1062-1734/Domain: sucrase/isomaltase homology <STM2>  
F;12/Binding site: oligo-1,6-glucosidase (Thr) (covalent) #status experimental  
F;99,455,559,896,904,1235,1303,1355,1368,1403,1535,1572,1748,1763,1799/Binding  
F;1007-1008/Cleavage site: Arg-Ile (trypsin) #status predicted  
  
Query Match 51.4%; Score 38; DB 1; Length 1827;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
OY 2 NNVLIO7DQOATTR 15  
DB 144 NNVLTTESQTAHR 157  
  
RESULT 12  
H64842  
probable translation initiation regulator b1010 - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2004  
C;Accession: H64842  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: H64842  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-128 <BLAT>  
A;Cross-references: UNIPROT:P75896; UNIPARC:UPI000013A5E1; GB:AE000202; GB:U00096; NID:G  
A;Experimental source: strain K-12, substrain MG1655  
C;Superfamily: translation initiation inhibitor, TdcF type  
  
Query Match 50.0%; Score 37; DB 1; Length 128;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
OY 2 NNVLIO7DQOATTR 15  
DB 40 NNVLFPADDPKQTR 53  
  
RESULT 13  
H90785  
hypothetical protein Eca1256 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 31-Dec-2004

C;Accession: H90785  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom  
A;Reference number: A9629; MUID:21156231; PMID:11258796  
A;Accession: H90785  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-128 <HAY>  
A;Cross-references: UNIPROT:O8XAU5; UNIPARC:UPI00000D067E; GB:BA000007; PIDN:BA834679.1;  
A;Experimental source: strain O157:H7, substrain R1MD 0509952  
C;Genetics:  
A;Gene: Eca1256  
C;Superfamily: translation initiation inhibitor, TdcF type  
  
Query Match 50.0%; Score 37; DB 2; Length 128;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
OY 2 NNVLIO7DQOATTR 15  
DB 40 NNVLFPADDPKQTR 53  
  
RESULT 14  
F85645  
hypothetical protein Z1509 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Dec-2004  
C;Accession: F85645  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
Miller, L.; Grobeck, E.C.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: F85645  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-128 <STO>  
A;Cross-references: UNIPROT:O8XAU5; UNIPARC:UPI00000D067E; GB:AE005174; NID:G12514367; PJ  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z1509  
C;Superfamily: translation initiation inhibitor, TdcF type  
  
Query Match 50.0%; Score 37; DB 2; Length 128;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
OY 2 NNVLIO7DQOATTR 15  
DB 40 NNVLFPADDPKQTR 53  
  
RESULT 15  
S67804  
Lrg1 protein - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein D0764; protein YDL240w  
C;Species: Saccharomyces cerevisiae  
C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: S67804; S43158; S47956  
R;Alt-Moerke, J.; Schneider, C.; Moro, M.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67798  
A;Accession: S67804  
A;Molecule type: DNA  
A;Residues: 1-1017 <ALT>  
A;Cross-references: UNIPROT:P35688; UNIPARC:UPI000012E93A; EMBL:Z74288; NID:G1431407; PIR  
A;Experimental source: strain S288C  
R;Muller, A.; Xu, G.; Wells, R.; Hollenberg, C.P.; Piepersberg, W.  
submitted to the EMBL Data Library, March 1994  
A;Description: Lrg1 is expressed during sporulation in Saccharomyces cerevisiae and cont

A:Reference number: S43158  
A:Accession: S43158  
A:Molecule type: DNA  
A:Residues: 1-530, 'O', 532-765, 'S', 767-790, 'T', 792-820, 'O', 822-837, 'S', 839-848, 'L', 850-859  
A:Cross-references: UNIPARC:UPI0000168CBB, EMBL:X78453, NID:G468734, PID:G468735  
R:Mueller, L.; Xu, G.; Wells, R.; Hollenberg, C.P.; Piletsky, W.  
Nucleic Acids Res. 22, 3151-3154, 1994  
A>Title: LRGI is expressed during sporulation in *Saccharomyces cerevisiae* and contains  
A:Reference number: S47956; MUID:94344779; PMID:8065929  
A:Accession: S47956  
A:Molecule type: DNA  
A:Residues: 28-69;99-136, 'MF', 139-148;157-184;419-474;755-765, 'S', 767-790, 'T', 792-820, 'Q'  
A:Cross-references: UNIPARC:UPI000017B2C8; UNIPARC:UPI000017B2C9; UNIPARC:UPI000017B2CA  
A:Genetics:  
A:Gene: SGD:LRG1  
A:Cross-references: SGD:S0002339; MIPS:YDL240w  
A:Map position: 4L  
A:Keywords: transmembrane protein  
A:28-89/Domain: LIM metal-binding repeat homology <LIM1>  
A:98-148/Domain: LIM metal-binding repeat homology <LIM2>  
A:157-184/Domain: LIM metal-binding repeat homology <LIM3>  
A:348-364/Domain: transmembrane #status predicted <TM1>  
A:419-474/Domain: LIM metal-binding repeat homology <LIM4>  
A:487-503/Domain: transmembrane #status predicted <TM2>

Query Match	49.3%	Score 36.5	DB 2	Length 1017
Best Local	Similarity	0.0%	Pred No. 1.7e+02	
Matches	9	Conservative	3	Mismatches 1
				Indels 5
				Gaps 1

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QY      3 NVLIQTD-----QQATTR 15
          |::||| | | | | |
Db      583 NLVIQTDDPSSSQQVSTR 600
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Job time : 13.6724 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 81.4655 Seconds  
(without alignments)  
129.907 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
Sequence: 1 RNNVLIQTDQOATTR 15

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	63.5	2081	Q9LH98_ARATH	Q9LH98 arabidopsis
2	45	60.8	917	Q92WJ7_RHIME	Q92WJ7 rhizobium m
3	44	59.5	649	Q54AY3_DICDI	Q54AY3 dictyosteli
4	44	59.5	649	Q55B16_DICDI	Q55B16 dictyosteli
5	43.5	58.8	285	Q9HRN4_HALSA	Q9HRN4 halobacteri
6	43	58.1	416	Q5WV87_LRGPL	Q5WV87 legionelell
7	43	58.1	417	Q5XJ05_LRGPL	Q5XJ05 legionelell
8	43	58.1	463	Q5XU51_LRGPH	Q5XU51 legionelell
9	43	58.1	505	Q2R036_GIALA	Q2R036 giardia lam
10	43	58.1	580	Q27657_GIALA	Q27657 giardia lam
11	41.5	56.1	854	Q7ZX14_XENLA	Q7ZX14 xenopus lae
12	41	55.4	106	Q8H475_ORYSA	Q8H475 oryza sativ
13	41	55.4	247	Q6FP28_CANGA	Q6FP28 candida gla
14	41	55.4	260	Q48VPS_TENNG	Q48VPS tetraodon n
15	41	55.4	540	Q4RX65_TENNG	Q4RX65 tetraodon n
16	41	55.4	550	Q7XUQ6_ORYSA	Q7XUQ6 oryza sativ
17	41	55.4	2141	Q6CMK0_KULUA	Q6CMK0 kluyveromyc
18	41	55.4	2144	GLT1_YEAST	Q12680 saccharomyc
19	41	55.4	2152	Q6FLS3_CANGA	Q6FLS3 candida gla
20	41	55.4	2195	Q75917_ASHGO	Q75917 ashiya goos
21	41	55.4	4936	Q6D5C2_ERWCT	Q6D5C2 erwinia car
22	40	54.1	135	Q5GV0D_IDILO	Q5GV0D idiomatina
23	40	54.1	136	Q9XRP4_AMBME	Q9XRP4 ambystoma m
24	40	54.1	136	Q9XRP5_AMBME	Q9XRP5 ambystoma m
25	40	54.1	828	Q6MA42_PARUM	Q6MA42 paracanthamyd
26	39	52.7	166	Q74K19_LACUO	Q74K19 lactobacill
27	39	52.7	263	Q9ZQZ6_ARATH	Q9ZQZ6 arabidopsis
28	39	52.7	359	Q5LNB7_SILPO	Q5LNB7 silicibacte
29	39	52.7	346	Q5VLKO_NPVSF	Q5VLKO spodiopora
30	39	52.7	676	Q9C2A6_NEUCR	Q9C2A6 neurospora
31	39	52.7	716	Q9ZU46_ARATH	Q9ZU46 arabidopsis

32	39	52.7	946	2	Q6JPV5_ACTSU	Q6JPV5 actinobacil
33	39	52.7	946	2	Q6JPV7_ACTSU	Q6JPV7 actinobacil
34	39	52.7	948	2	Q84I43_ACTPL	Q84I43 actinobacil
35	39	52.7	1401	2	Q54J46_DICDI	Q54J46 dictyosteli
36	39	52.7	1460	2	Q6CVK3_KULUA	Q6CVK3 kluyveromyc
37	38	51.4	138	2	Q97GK0_CLOAB	Q97GK0 clostridium
38	38	51.4	271	2	Q467L7_TENNG	Q467L7 tetraodon n
39	38	51.4	370	2	Q4MOR3_BACCE	Q4MOR3 bacillus ce
40	38	51.4	407	2	Q4FUE6_PGAMM	Q4FUE6 psychrobact
41	38	51.4	442	2	Q73DS1_BACCI	Q73DS1 bacillus ce
42	38	51.4	448	2	Q6HNN4_BACCK	Q6HNN4 bacillus th
43	38	51.4	448	2	Q81I41_BACCR	Q81I41 bacillus ce
44	38	51.4	448	2	Q63G64_BACCC	Q63G64 bacillus ce
45	38	51.4	448	2	Q81VB9_BACAN	Q81VB9 bacillus an

## ALIGNMENTS

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RESULT 1
Q9LH98_ARATH PRELIMINARY; PRT; 2081 AA.
AC Q9LH98;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 3, II.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 pl, TAC
RT and BAC clones."
RL DNA Res. 7:217-221(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002057; BAB03174.1; -, Genomic_DNA.
DR HSRP; P01096; IHR9.
DR InterPro; IPR009605; DUF1216.
DR Pfam; PF06746; DUF1216; 2.
SQ SEQUENCE 2081 AA; 232852 MW; D3603E1F85EFPF29 CRC64;

Query Match 63.5%; Score 47; DB 2; Length 2081;
Best Local Similarity 53.3%; Pred. No. 27;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 RNNVLIQTDQOATTR 15
Db 1302 KNEILMQADSQATTG 1316

RESULT 2
Q92WJ7_RHIME PRELIMINARY; PRT; 917 AA.
AC Q92WJ7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative sensory histidine kinase protein.
GN Ordered locus names=RB0342; ORF names=SMB20356;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxId=382;

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Query Match	60.8%	Score 45	DB 2	Length 917
Best Local Similarity	57.1%	Pred. NO. 25		
Matches 8, Conservative		4, Mismatches	2, Indels	0, Gaps 0

RA Plichter K., Chen G., Saunders D., Sodergren E., Davis P.,  
RA Kerkhoun A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,  
RA Fathbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,  
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,  
RA Murny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,  
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,  
RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,  
RA Loulgesed H., Mangal K., Oliver K., Price C., Quail M.A.,  
RA Urushihara H., Hernandez J., Rabinowitch E., Steffen D., Sanders M.,  
RA Ma Y., Kohara Y., Sharp S., Szymonds M., Spiegler S., Tivey A.,  
RA Shualey S., White B., Walker D., Woodard J., Winkler T., Tanaka Y.,  
RA Shualey G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,  
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,  
RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuspa A.,  
RA "The genome of the social amoeba Dictyostelium discoideum.",  
RL Nature 0:0-0(2005).  
CC -I- CAUTION: The sequence shown here is derived from an  
CC EMBL/Genbank/DBD whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAF01000301; EAL60430.1; -; Genomic DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 649 AA; 77580 MW; B366A94429ECD53 CRC64;

Query March 59.5%; Score 44; DB 2; Length 649;  
Best Local Similarity 61.5%; Pred. No. 26;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0

QY 2 NNVLIOFDOQATT 14  
Db 611 NNIIIOFQQQKPT 623

RESULT 4  
O55B16.DICDI PRELIMINARY; PRT; 649 AA.

ID O55B16.DICDI  
AC O55B16  
DT 13-SEP-2005 (TRENBLREL 31, Created)  
DT 13-SEP-2005 (TRENBLREL 31, Last sequence update)  
DT 13-SEP-2005 (TRENBLREL 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=DD80216848;  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AX4;  
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,  
RA Sugang R., Berriman M., Song J., Olsen R., Szafianski K., Xu Q.,  
RA Tunkgal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,  
RA Bunkler A.T., Lehman R., Hamlin R., Davies R., Gaudet P., Fey P.,  
RA Plichter K., Chen G., Saunders D., Sodergren E., Davis P.,  
RA Kerkhoun A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,  
RA Fathbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,  
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,  
RA Murny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,  
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,  
RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,  
RA Loulgesed H., Mangal K., Oliver K., Price C., Quail M.A.,  
RA Urushihara H., Hernandez J., Rabinowitch E., Steffen D., Sanders M.,  
RA Ma Y., Kohara Y., Sharp S., Szymonds M., Spiegler S., Tivey A.,  
RA Shualey S., White B., Walker D., Woodard J., Winkler T., Tanaka Y.,  
RA Shualey G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,  
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,  
RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuspa A.,  
RA "The genome of the social amoeba Dictyostelium discoideum.",  
RL Nature 0:0-0(2005).  
CC -I- CAUTION: The sequence shown here is derived from an  
CC EMBL/Genbank/DBD whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAF0100013; EAL71869.1; -; Genomic DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 649 AA; 77580 MW; B366AD152ACDA23 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 649;  
 Best Local Similarity 61.5%; Pred. No. 26;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLQTDQOATT 14  
 Db 611 NNVLQTDQOQKPT 623

## RESULT 5

Q5HRN4\_HALSA PRELIMINARY; PRT; 285 AA.  
 AC Q5HRN4;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Vng0617h.  
 GN OrderedLocustNames=VNG0617H;  
 OS Halobacterium salinarum (Halobacterium halobium).  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
 OC Halobacteriaceae; Halobacterium.  
 NCBI\_TaxID=2242;

## NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=NR-1 / ATCC 700922 / JCM 11081;  
 MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;  
 NG W.V., Kennedy S.P., Mahaira G.G., Bergquist B., Pan M.,  
 Shukla H.D., Lahey S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
 Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,  
 Lettshauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
 Maddocks D.G., Jablonksi P.E., Krebs M.P., Angwine C.M., Dale H.,  
 Isebnarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,  
 Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
 Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;  
 RT "Genome sequence of Halobacterium species NRC-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
 DR EMBL; AE005010; AAG19124.1; -; Genomic\_DNA.  
 DR PIR; H84219; H84219.  
 KW Complete proteome.  
 SQ SEQUENCE 285 AA; 29163 MW; 31223D1A949BC1B3 CRC64;

Query Match 58.8%; Score 43.5; DB 2; Length 285;  
 Best Local Similarity 58.8%; Pred. No. 12;  
 Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 2 NNVLQTDQO--ATTR 15  
 Db 212 NNVLQTDSETELTTR 228

## RESULT 6

Q5WV87\_LEGPL PRELIMINARY; PRT; 416 AA.  
 AC Q5WV87;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=lp11930;  
 OS Legionella pneumophila (strain Lens).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.  
 NCBI\_TaxID=297245;

## NUCLEOTIDE SEQUENCE.

PubMed=15467720; DOI=10.1038/ng1447;  
 RA Casalez C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,  
 Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,  
 Etienne J., Glaeser P., Buchrieser C.;  
 RT "Evidence in the Legionella pneumophila genome for exploitation of  
 host cell functions and high genome plasticity.";  
 RL Nat. Genet. 36:1165-1173(2004).

DR EMBL; CR628337; CAH16170.1; -; Genomic\_DNA.  
 DR Legiolist; lp11930; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 416 AA; 48861 MW; 0E153EDD3778559E CRC64;

Query Match 58.1%; Score 43; DB 2; Length 416;  
 Best Local Similarity 69.2%; Pred. No. 24;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLQTDQOATT 14  
 Db 63 NNVLPLEQOQPT 75

## RESULT 7

Q5X3U5\_LEGPA PRELIMINARY; PRT; 417 AA.  
 AC Q5X3U5;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=lp11939;  
 OS Legionella pneumophila (strain Paris).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.  
 NCBI\_TaxID=297246;

## NUCLEOTIDE SEQUENCE.

PubMed=15467720; DOI=10.1038/ng1447;  
 RA Casalez C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,  
 Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,  
 Etienne J., Glaeser P., Buchrieser C.;  
 RT "Evidence in the Legionella pneumophila genome for exploitation of  
 host cell functions and high genome plasticity.";  
 RL Nat. Genet. 36:1165-1173(2004).  
 DR EMBL; CR628336; CAH13091.1; -; Genomic\_DNA.  
 DR Legiolist; lp11939; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 417 AA; 49131 MW; 01F6B5A430C7E2 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 417;  
 Best Local Similarity 69.2%; Pred. No. 24;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLQTDQOATT 14  
 Db 63 NNVLPLEQOQPT 75

## RESULT 8

Q5ZU51\_LEGPH PRELIMINARY; PRT; 463 AA.  
 AC Q5ZU51;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Ebha protein.  
 GN OrderedLocustNames=lp1957;  
 OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /  
 OS ATCC 33152).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Legionellaceae; Legionella.  
 NCBI\_TaxID=272624;

## NUCLEOTIDE SEQUENCE.

PubMed=15448271; DOI=10.1126/science.1099776;  
 RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,  
 Assemani G., Hill K., Nwara J., Feder M., Rineer J., Greenberg J.J.,  
 Stehenko V., Park S.H., Zhao B., Teplickaya E., Edwards J.R.,  
 Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.B.,  
 Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,  
 Segal G., Qu X., Rzhetsky A., Zhang P., Cavanis E., De Jong P.J.,

RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.,  
RT "The genomic sequence of the accidental pathogen *Legionella*  
RL *pneumophila*."  
RW Science 305:1966-1968(2004).  
DR EMBL: AEO17354; AAU28026.1; -: Genomic\_DNA.  
KW Complete proteome.  
SQ SEQUENCE 463 AA; 54449 MW; BE76CBED5D81D264 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 463;  
Best Local Similarity 69.2%; Pred. No. 27;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOQTQOQATT 14  
Db 87 NNVLIPLEQOQPT 99

RESULT 9  
Q7R036\_GIALA PRELIMINARY; PRT; 505 AA.

AC Q7R036;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DE GIP\_456\_18539\_20056.  
OS *Giardia lamblia* ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; *Giardia*.  
NCBI\_TaxID=184922;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=WB CG;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
RA Olsen G.J., Sogin M.L.;  
RT "Draft sequence of the *Giardia lamblia* genome."  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: AACB0100038; EAA40651.1; -: Genomic DNA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR InterPro: IPR003198; Amidino trans.  
DR Pfam: PF02274; Amidino transf.;  
SQ SEQUENCE 505 AA; 55735 MW; 99E2CBF5B56824B0 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 505;  
Best Local Similarity 57.1%; Pred. No. 30;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNVLIOQTQOQATT 15  
Db 93 NNWVFMRDQOITTR 106

RESULT 10  
Q27657\_GIALA PRELIMINARY; PRT; 580 AA.  
AC Q27657;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Arginine deiminase (EC 3.5.3.6).  
OS *Giardia lamblia* (Giardia intestinalis).  
OC Eukaryota; Diplomonadida; Hexamitidae; *Giardia*.  
NCBI\_TaxID=5741;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Portland 1;  
RA MEDLINE=98136144; PubMed=9468500; DOI=10.1074/jbc.273.8.4470;  
RA Knodler L.A., Sekyere E.O., Stewart T.S., Schofield P.J.,  
RA Edwards M.R.;  
RT "Cloning and expression of a prokaryotic enzyme, arginine deiminase,  
RT from a primitive eukaryote *Giardia intestinalis*."  
RL J. Biol. Chem. 273:4470-4477(1998).

DR EMBL: U49236; AAC06116.1; -: Genomic\_DNA.  
DR PIR: T45064; T45064.  
DR GO: GO:0016990; F:arginine deiminase activity; IEA.  
DR GO: GO:0016787; F:hydrolase activity; IEA.  
DR InterPro: IPR003198; Amidino trans.  
DR Pfam: PF02274; Amidino transf.;  
KW Hydrolase.  
SQ SEQUENCE 580 AA; 64131 MW; 4812F389D0F5357A CRC64;

Query Match 58.1%; Score 43; DB 2; Length 580;  
Best Local Similarity 57.1%; Pred. No. 35;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNVLIOQTQOQATT 15  
Db 168 NNWVFMRDQOITTR 181

RESULT 11  
Q7ZX14\_XENLA PRELIMINARY; PRT; 854 AA.

AC Q7ZX14;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE MGCS2979 protein.  
OS *Xenopus laevis* (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; *Xenopus*; *Xenopus*.  
NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Sleptchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gurnatne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Rahy J., Heaton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Snevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S., Strausberg R.,  
RA Klein S., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*  
RT initiative".  
RT Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.,  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the AAA ATPase family.  
DR EMBL: BC044980; AAH44980.1; -: mRNA.  
DR HSP: Q01853; IR7R.  
DR GO: GO:0016021; C:integral to membrane; IEA.



DR GO:0005739; C:mitochondrion; IEA.  
 DR GO:0005524; F:ATP binding; IEA.  
 DR GO:0017111; F:nucleoside-triphosphatase activity; IEA.  
 DR GO:0000166; F:nucleotide binding; IEA.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003559; AAA\_ATPase\_centre.  
 DR InterPro: IPR003960; AAA\_sub.  
 DR Pfam: PF00004; AAA; 2.  
 DR SMART: SM00382; AAA; 2.  
 DR PROSITE: PS00674; AAA; 2.  
 DR ATP-binding; Nucleotide-binding; Transmembrane.  
 SQ SEQUENCE 854 AA; 93597 MW; F91339502C41BB3 CRC64;

Query Match 56.1%; Score 41.5; DB 2; Length 854;  
 Best Local Similarity 78.6%; Pred. No. 1.1e+02;  
 Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 2 NNVLITQ-TDQQT 14  
 DB 483 NRVLIQIKDQQT 496

RESULT 12  
 O8H475\_ORYSA PRELIMINARY; PRT; 106 AA.

AC O8H475;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein P0470D12.115.  
 GN Name=P0470D12.115;  
 OS Oryza sativa (Japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 CX NCBI\_TaxID=39947;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsunoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
 clone: P0470D12."  
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP004300; BAC15985.1; -; Genomic\_DNA.  
 DR Gramene; O8H475; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 106 AA; 12281 MW; 8016731B1945298F CRC64;

Query Match 55.4%; Score 41; DB 2; Length 106;  
 Best Local Similarity 46.7%; Pred. No. 12;  
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNNVLITQDQQT 15  
 DB 10 RNNGVMELEQATSR 24

RESULT 13  
 O6FP28\_CANGA PRELIMINARY; PRT; 247 AA.  
 AC O6FP28;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Similar to sp|P39721|Saccharomyces cerevisiae YAL049c.  
 GN OrderedLocustNames=CAGL00071289;  
 OS Candida glabrata (Yeast) (Torulopsis glabrata).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 CX NCBI\_TaxID=5478;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 2001 / CBS 138;  
 RX PubMed=15229592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Nevegilise C., Talla E.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barre S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boirame A., Boyer J., Catrolicco L., Confanioli F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicoud J.-M., Nikolski M., Ozas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierri A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004)  
 DR EMBL; CR380956; CAG60967.1; -; Genomic\_DNA.  
 DR GO:0016787; F:hydrolase activity; IEA.  
 DR InterPro: IPR02925; Dienelectro\_hydro.  
 DR Pfam: PF01738; DLH; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 247 AA; 27274 MW; ABE540BB8B628D35 CRC64;

Query Match 55.4%; Score 41; DB 2; Length 247;  
 Best Local Similarity 66.7%; Pred. No. 32;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NNVLITQDQQT 13  
 DB 57 NNVLITADQQT 68

RESULT 14  
 O4SVFS\_TETNG PRELIMINARY; PRT; 260 AA.

AC O4SVFS;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Chromosome 7 SCAR13760, whole genome shotgun sequence.  
 GN ORFNames=GSTENG00012005001;  
 OS Tetradon nigriviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neocleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 CX NCBI\_TaxID=99883;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costez C., Bernot A.,  
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Daesliwa C., Salanoubat M., Levy M., Boudet N., Castellan S.,  
 RA Anthouard V., Jubin C., Caestele V., Katin M., Vacherie B.,  
 RA Biemont C., Skalli Z., Catrolicco L., Poulain J., De Bernardis V.,  
 RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Boeck S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli H.,  
 RA Wincker P., Lander E.S., Weissbach J., Roest Croallius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigriviridis reveals  
 the early vertebrate proto-karyotype."  
 RL Nature 431:946-957(2004).

RA NUCLEOTIDE SEQUENCE.  
 RG Genoscope, Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAE01013760; CAP95377.1; -; Genomic\_DNA.  
 SQ SEQUENCE 260 AA; 28404 MW; 7E3DC627AF6D1A2 CRC64;

```

Query Match          55.4%; Score 41; DB 2; Length 260;
Best Local Similarity 70.0%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY      2  NNVLITQTDQ 11
      |||:|||||
Db      69  NNILAQTDQ 78

```

## RESULT 15

## OARX65\_TESTNG

```

ID  OARX65_TESTNG PRELIMINARY; PRT; 540 AA.
AC  OARX65;
DT  13-SEP-2005 (TREMBlrel. 31, Created)
DT  13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT  13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE  Chromosome 11 SCAP14979, whole genome shotgun sequence.
GN  ORFNames=GSTENG0027545001;
OS  Tetradodon nigroviridis (Green puffer).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC  Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes;
OC  Tetradontidae; Tetradontidae; Tetradon.
OX  NCBI_TaxID=99883;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA  Mucelli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA  Niclaud S., Jaffe D., Fisher S., Lutfalla G., Dossest C., Segurens B.,
RA  Desilva C., Salenoudat M., Levy M., Boudet N., Castellano S.,
RA  Authouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA  Biemont C., Skalli Z., Cattoiico L., Poullain J., De Berardinis V.,
RA  Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA  Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA  Kellie W., Volf J.N., Guigo R., Zody M.C., Mesirov J.,
RA  Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA  Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA  Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT  "Genome duplication in the teleost fish Tetradon nigroviridis reveals
RT  the early vertebrate proto-karyotype."
RL  Nature 431:946-957(2004).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RG  Genoscope; Whitehead Institute Centre for Genome Research;
RL  Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; CAHE01014979; CAG07017.1; -; Genomic DNA.
SQ  SEQUENCE 540 AA; 61012 MW; BFDPE580B06E83DE CRC64;

```

```

Query Match          55.4%; Score 41; DB 2; Length 540;
Best Local Similarity 60.0%; Pred. No. 79;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY      1  RNNVLITQTDQATTR 15
      |||||:|||||
Db      54  RNNVRAQLKORANTR 68

```

Search completed: December 12, 2005, 20:41:07  
 Job time : 83.4655 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:50 ; Search time 109.333 Seconds  
(without alignments)  
72.337 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGKATNIPPTAPGTR 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 827869

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  $\lambda$ \_Geneseq\_21:\*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*
9:	Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0609	Adri0609 Dog IGE e
2	87	89.7	18	ADRI0610	Adri0610 Cat IGE e
3	55	56.7	18	ADRI0612	Adri0612 Sheep IGE
4	37	38.1	15	ADCS6890	Adcs6890 Peptide f
5	34	35.1	15	ADCS6859	Adcs6859 Horse Imm
6	34	35.1	18	ADRI0611	Adri0611 Horse IGE
7	32.5	33.5	15	ADW78189	Adw78189 Human met
8	32	33.0	9	AAU76520	Aau76520 Anti-Inte
9	32	33.0	9	AAE15818	Aae15818 Human mAb
10	32	33.0	11	ADT40399	Adt40399 hSARS vlr
11	32	33.0	11	ADG79816	Adg79816 SARS vlr
12	32	33.0	11	ADT37929	Adt37929 hSARS vlr
13	32	33.0	12	AAW52787	Aaw52787 CCR5-bind
14	32	33.0	12	ADV13048	Adv13048 Human pho
15	32	33.0	15	AAV65747	Aav65747 Breast ca
16	32	33.0	15	ADN64911	Adn64911 HLA bindi
17	31	32.0	13	ADG37003	Adg37003 Strainless
18	31	32.0	14	AAV31329	Aav31329 B. subcil
19	31	32.0	15	ADN64927	Adn64927 HLA bindi
20	31	32.0	18	ADG84934	Adg84934 Beta-site
21	30	30.9	9	ABJ19961	Abj19961 MHC bindi
22	30	30.9	9	ADD94584	Add94584 Human STM
23	30	30.9	10	ADD94544	Add94544 Human STM
24	30	30.9	14	AAH39162	Aah39162 Human sec

25	30	30.9	14	3	AAH39163	Aah39163 Human sec
26	30	30.9	16	2	AAH53562	Aah53562 Birch pol
27	30	30.9	16	8	ADQ90450	Adq90450 RANPES re
28	30	30.9	17	2	AAH95159	Aah95159 bcl-x(L)/
29	29	29.9	9	2	AAW24775	Aaw24775 Human Imm
30	29	29.9	9	2	AAW80144	Aaw80144 Light cha
31	29	29.9	9	2	AAW80142	Aaw80142 Light cha
32	29	29.9	9	2	AAV40427	Aav40427 Amino aci
33	29	29.9	9	5	ABP62411	Abp62411 Human Imm
34	29	29.9	9	6	ABJ26739	Abj26739 VEGF bind
35	29	29.9	9	6	ABR06299	Abro6299 Human can
36	29	29.9	9	8	ADK18234	Adk18234 Mouse VEG
37	29	29.9	9	8	ADV26692	Adv26692 Human 109
38	29	29.9	9	8	ADV29257	Adv29257 Human 109
39	29	29.9	10	6	ABR06391	Abro6391 Human can
40	29	29.9	10	6	ABR06436	Abro6436 Human can
41	29	29.9	10	8	ADQ73723	Adq73723 Cancer re
42	29	29.9	10	8	ADQ72657	Adq72657 Cancer re
43	29	29.9	10	8	ADQ68445	Adq68445 Cancer re
44	29	29.9	10	8	ADQ70207	Adq70207 Cancer re
45	29	29.9	10	8	ADQ69505	Adq69505 Cancer re

## ALIGNMENTS

RESULT 1  
ADRI0609  
ID ADRI0609 standard; peptide: 18 AA.  
XX  
AC ADRI0609;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.  
XX  
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
OS Canis familiaris.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PP 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
PY (UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
DR WPI, 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian IGE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.  
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAGTK 18  
 |||||  
 1 VDGQKATNIFPYTAGTK 18

RESULT 2

ADRI0610  
 ID ADRI0610 standard; peptide; 18 AA.

AC ADRI0610;

DT 21-OCT-2004 (first entry)

XX Cat IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.

KW Antiaesthetic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 cat.

XX Felis catus.

PN WO2004065936-A2.

PD 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful  
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IgE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC cat IgE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAGP 16  
 |||||  
 1 VDGQKATNIFPYTAGP 16

DB

RESULT 3  
 ADRI0612  
 ID ADRI0612 standard; peptide; 18 AA.

AC ADRI0612;

DT 21-OCT-2004 (first entry)

XX Sheep IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

KW Antiaesthetic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 sheep.

XX Ovis aries.

PN WO2004065936-A2.

PD 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful  
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IgE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC sheep IgE 3.76 recognition site.

SQ Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.067;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAGP 15  
 |||||  
 1 VDGQEDRNLFSTYTAGP 15

DB

RESULT 4

ADCS6890  
 ID ADCS6890 standard; peptide; 15 AA.

```

XX AC ADC66890;
XX DT 18-DEC-2003 (first entry)
XX DE Peptide fragment Seq ID7 related to human protein 36-41.
XX KW human; protein 36-41; arrhythmia; asthma; dementia.
XX OS Homo sapiens.
XX PN CN382718-A.
XX PD 04-DEC-2002.
XX PF 26-APR-2001; 2001CN-00112751.
XX PR 26-APR-2001; 2001CN-00112751.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2003-269480/27.
XX PT New human macroprotein-36-41, encoding polynucleotide, antagonist and
XX PT recombinant production, useful for treating dementia, arrhythmia, asthma
XX PT and digestive ulcers.
XX PS Example 6; SEQ ID NO 7; 33pp; Chinese.
XX CC This invention relates to a novel protein, human protein 36-41, and the
XX CC DNA sequence encoding it. The protein of the invention may be useful for
XX CC the treatment of diseases such as arrhythmia, asthma and dementia. The
XX CC present sequence is the amino acid sequence of a peptide fragment of
XX CC human protein 36-41 which was used in the exemplification of the
XX CC invention.
XX SQ Sequence 15 AA;

Query Match 38.1%; Score 37; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 58;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGGKATNIPPTAP 15
   :||: |||: ||
Db 1 MDGKMQPNSPFMQSP 15

RESULT 5
ADC64569
ID ADC64569 standard; peptide; 15 AA.
XX AC ADC64569;
XX DT 18-DEC-2003 (first entry)
XX DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P5.
XX KW Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX OS Equus caballus.
XX PN US2003087314-A1.
XX PD 08-MAY-2003.
XX PF 08-NOV-2001; 2001US-00052788.
XX PR 08-NOV-2001; 2001US-00052788.
XX PA (REGC ) UNIV CALIFORNIA.
XX

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PI Gershwin LJ, Pettigrew HD, Kalina WV;
XX DR WPI; 2003-765437/72.
XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
XX PT polypeptide that induces production of antibodies which specifically bind
XX PT to equine immunoglobulin E.
XX PS Example 1; Page 8; 14pp; English.
XX CC The invention relates to an immunogenic composition comprising an
XX CC isolated polypeptide having an amino acid sequence that is at least 80%
XX CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
XX CC equine immunoglobulin E (the composition induces production of an
XX CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six
XX CC polypeptides are not explicitly identified in the specification. Also
XX CC included are a composition comprising an antibody that specifically binds
XX CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
XX CC specifically binds to equine IGE made by the process of immunising an
XX CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
XX CC antibody that specifically binds to equine IGE (involving immunising the
XX CC animal with a composition further comprising an isolated polypeptide (the
XX CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-
XX CC (S6)), and collecting antiserum from the animal) and a kit for detection
XX CC of equine IGE in a biological sample comprising the antibody and means
XX CC for detecting specific binding of the antibody to equine IGE. The
XX CC antibody is useful for detecting equine IGE protein in a biological
XX CC sample (serum) which involves contacting the sample with the antibody,
XX CC thus forming an antigen/antibody complex, and detecting the presence or
XX CC absence of the antigen/antibody complex. The antibody and antigen are
XX CC immobilised on a solid surface. The antibody is labelled such that the
XX CC complex can be detected. The complex is detected using a second labelled
XX CC antibody. The peptides are useful for generating antibodies specific for
XX CC IGE which can serve as a diagnostic test for allergy. The present
XX CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
XX CC peptide from the middle portion of the C2 region.
XX SQ Sequence 15 AA;

Query Match 35.1%; Score 34; DB 7; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGGKATNIPPT 11
   :|||: ||
Db 2 IDGGKVDSEQFP 12

RESULT 6
ADR10611
ID ADR10611 standard; peptide; 18 AA.
XX AC ADR10611;
XX DT 21-OCT-2004 (first entry)
XX DE Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX KW horse.
XX OS Equus caballus.
XX PN WO2004065936-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX

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PI	Hammerberg B;
XX	
DR	WPI: 2004-593545/57.
XX	
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful
PT	for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT	or treating asthma or anaphylactic shock.
XX	
PS	Example 6; Page 9; 14pp; English.
XX	
CC	The present invention relates to a novel monoclonal antibody (I) that
CC	specifically binds to a mammalian IGE epitope, where the epitope is
CC	between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The
CC	allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC	and corn allergens. The sample is a biological sample collected from a
CC	dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC	treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC	antibodies recognise epitopes on canine IGE corresponding to amino acid
CC	residues 357-371 (ADK10601) and 146-162 (ADK10609) respectively of the
CC	canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC	cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC	3.76 were observed to have good cross-reactivity with the epsilon-chain
CC	of IGE from cat and horse, but did not exhibit cross-reactivity with
CC	either pig or human epsilon-chains of IGE. The present sequence is the
CC	horse IGE 3.76 recognition site.
XX	
SQ	Sequence 18 AA;
	Query Match 35.1%; Score 34; DB 8; Length 18;
	Best Local Similarity 54.5%; Pred. No. 2.2e+02;
	Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0.
OY	1 VDGKATNIFP 11
	:
	1 IDGKVDGFP 11
Dd	
RESULT 7	
ADW78189	
ID	ADW78189 standard; peptide; 15 AA.
XX	
AC	ADW78189;
XX	
DT	07-APR-2005 (first entry)
XX	
DE	Human metabolic therapy target peptide PACT.
XX	
KW	DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiant;
KW	vasotrophic; hypotensive; antiarteriosclerotic; antiinflammatory;
KW	antiallergic; immunosuppressive; antibacterial; antiasthmatic;
KW	dermatologic; antidiabetic; gastrointestinal-gen.; anticancer;
KW	thrombolytic; neuroprotective; ophthalmological; antihemetic;
KW	antipruritic; uropathic; antipsoriatic; hepatotropic; antianemic;
KW	muscular-gen.; thyromimetic; antihypoid; gynecological; nephrotropic;
KW	hepatocytic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
KW	endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
KW	antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;
KW	antifertility; cancer; cardiovascular disease; inflammation;
KW	metabolic disorder; neuropathy; sleep disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO2005007090-A2.
XX	
PD	27-JAN-2005.
XX	
PF	02-JUL-2004; 2004MO-US021514.
XX	
PR	03-JUL-2003; 2003US-0484761P.
XX	
PA	(HARD ) HARVARD COLLEGE.

PI	Blanis J, Murphy LO;
XX	
XX	WPI, 2005-112720/12.
DR	
PT	Identification of compound for treating e.g. cancer by culturing cells
PT	expressing target protein in the presence of growth factor, cytokine,
PT	tumor promoter or oncogene and assessing binding after contacting with
PT	the compound.
XX	
PS	Claim 14; Page 64; 104pp; English.
XX	
CC	The invention relates to a novel method for the identification of a
CC	therapeutic compound. The method involves providing test cells that
CC	express a target protein containing a DEF domain and MAP kinase,
CC	culturing the cells in the presence of growth factor, cytokine, tumor
CC	promoter or oncogene; contacting the cells with a candidate compound; and
CC	assessing the binding of the MAP kinase to the DEF domain relative to the
CC	binding in the absence of the candidate compound. The invention further
CC	comprises a method for the identification of a therapeutic compound: a
CC	method for treatment of cancer, which involves administering a compound
CC	that inhibits the binding of a MAP kinase to the DEF domain of a target
CC	protein; and an antibody that specifically binds to phospho-T-325 C-Fos
CC	(preferably polyclonal or monoclonal). The novel therapeutic compounds
CC	have the following activities: cytostatic, cardiovascular-gen., cardiant,
CC	vasotropic, hypotensive, antiteriosclerotic, antiinflammatory,
CC	antiallergic, immunosuppressive, antibacterial, antisthmatic,
CC	dermatological, antidiabetic, gastrointestinal-gen., antitumor,
CC	chemoprotective, neuroprotective, ophthalmological, antirheumatic,
CC	antiyeptic, uropathic, antiporiatic, hepatotropic, antianemic, muscular
CC	-gen., thyromimetic, antihypoid, gynecological, nephrotropic,
CC	hepatotropic, virucide, anti-HIV, anabolic, hypertensive, anorectic,
CC	endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,
CC	cardiopressant, antidiabetic, sedative, hypnotic, CNS-gen., and
CC	antifertility. The therapeutic compound may be used in the treatment
CC	of: cancer, cardiovascular disorders, inflammatory disorders, metabolic
CC	disorders, neuropathy or a behavioural disorder, and a sleep disorder.
CC	This sequence represents a metabolic therapy target peptide of the
CC	invention.
SQ	
	Sequence 15 AA;
OY	5 KATNIFFPYTAPG 16
DB	1 KAT---PYTPFG 9
RESULT 8	
ID	AAU76520 standard; peptide; 9 AA.
XX	
AC	AAU76520;
XX	
DT	05-JUN-2002 (first entry)
XX	
DE	Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.
XX	
KW	Human; antibody; anti-interleukin-12; CDR, light chain; circulatory;
KW	complementarity determining region; neuroprotective; antipsoriatic;
KW	immunostimulant; cytostatic; anti-microbial; psoriasis; infection;
KW	multiple sclerosis; immune disorder; cardiovascular; malignant disease;
KW	neurological disorder.
OS	Homo sapiens.
XX	
PN	WO2002122500-A2.
XX	
PD	14-FEB-2002.
XX	

PF 07-AUG-2001; 2001WO-US024720.  
 XX  
 PR 07-AUG-2000; 2000US-0223358P.  
 PR 29-SEP-2000; 2000US-0236827P.  
 PR 01-AUG-2001; 2001US-00920262.  
 XX  
 PA (CENZ ) CENTOCOR INC.  
 XX  
 PI Giles-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;  
 XX  
 DR WPI; 2002-257482/30.  
 XX  
 PT New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL  
 PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as  
 PT other for treating immune, infectious, malignant or neurological  
 PT disorders.  
 XX  
 PS Claim 41; Page 93; 96pp; English.  
 XX  
 CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL  
 CC -12) antibodies. The antibodies comprise at least one complementarity  
 CC determining region (CDR) of a heavy or light chain, a heavy chain or  
 CC light chain variable region, or a heavy chain or light chain constant  
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or  
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.  
 CC The antibodies are also useful for treating immune, cardiovascular,  
 CC infectious, malignant or neurological disorders or diseases. The present  
 CC sequence represents the amino acid sequence of human anti-Interleukin-12  
 CC (IL-12) antibody CDR3 light chain  
 XX  
 SQ Sequence 9 AA;

Query Match 33.0%; Score 32; DB 5; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0;

QY 8 NIPYPT 13  
 ||:||||  
 4 NIPYPT 9

RESULT 9  
 AAE15818  
 ID AAE15818 standard; peptide; 9 AA.  
 XX  
 AC AAE15818;

DT 26-MAR-2002 (first entry)

DE Human mAb 12B1 VK complementarity determining region (CDR) #3.

XX Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;  
 KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;  
 KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;  
 KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;  
 KW immunoglobulin; complementarity determining region; CDR; procoagulant;  
 KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;  
 KW fungicide; neuroprotective; light chain variable region; VK; mAb;  
 KW monoclonal antibody.

XX Homo sapiens.

OS WO200190193-A1.

PN 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US016864.

PR 24-MAY-2000; 2000US-00577930.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX

PI Abrahamson JA, Kikly KK;  
 XX  
 DR WPI; 2002-083094/11.  
 XX  
 PT Novel monoclonal antibody that binds to human sialoadhesin factor-3 for  
 PT treating or preventing cancer, inflammation, autoimmunity, allergy,  
 PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.  
 XX  
 PS Claim 13; Page 67; 69pp; English.

CC The invention relates to monoclonal antibodies that bind to human  
 CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or  
 CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central  
 CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple  
 CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections  
 CC for modulating an immune response in a mammal, where the immune response  
 CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and  
 CC therapeutic reagents, to subcharacterise cell populations during  
 CC haematopoietic development, to treat anaemia, as a diagnostic marker to  
 CC distinguish between different forms of cancer, to purge bone marrow ex  
 CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo  
 CC expansion (proliferation and/or differentiation) of haematopoietic  
 CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell  
 CC mobilisation into the periphery and as an vivo chemoprotective agent.  
 CC Protein comprising immunoglobulin complementarity determining region  
 CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and polypeptide in cells. The present sequence is  
 CC complementarity determining region of human monoclonal antibody (mAb)  
 CC 12B1 light chain variable region (VK), which binds to SAF-3  
 XX  
 SQ Sequence 9 AA;

Query Match 33.0%; Score 32; DB 5; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0;

QY 8 NIPYPT 13  
 ||:||||  
 4 NIPYPT 9

RESULT 10  
 ADT40399  
 ID ADT40399 standard; peptide; 11 AA.  
 XX  
 AC ADT40399;

DT 30-DEC-2004 (first entry)

DE hSARS virus peptide, SEQ ID 1387.

XX Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.

OS SARS coronavirus.

XX WO2004085650-A1.

PN 07-OCT-2004.

PD 24-MAR-2004; 2004WO-CN000246.

PF 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-0457730P.

PR 02-APR-2003; 2003US-0459931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-0464886P.

PR 25-APR-2003; 2003US-0465738P.

PR 14-MAY-2003; 2003US-0470935P.

XX (UYHK-) UNIV HONG KONG.

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XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
PI Leung FC;
XX WPI; 2004-737326/72.
XX
XX New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of
PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for
PT diagnosing and treating SARS.
XX
XX Example; SEQ ID NO 1387; 200pp; English.
XX
CC The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC hSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCTCC-V200303. The present invention also relates to novel
CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-
CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
CC methods for detecting the presence of a N- or S-gene of the hSARS virus
CC or of the protein in a biological sample and identifying a subject
CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein
CC sequences are useful as vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand.
CC ADT40120 is the full-length protein encoded by the first reading frame of
CC the complementary strand and ADT40121-ADT40601 are the peptides from the
CC first reading frame protein. ADT40602 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADT40603-
CC ADT40976 are the peptides from the second reading frame protein. ADT40977
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADT40978-ADT41482 are the peptides from the
CC third reading frame protein.
XX
XX Sequence 11 AA;
SQ
Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Oy 3 GOKATNIFPYT 13
Db 1 GQSQSNILPQT 11
RESULT 11
ID ADS79816 standard; protein; 11 AA.
XX ADS79816;
XX
XX 30-DEC-2004 (first entry)
XX
DE SARS virus complementary DNA strand reading frame 1 protein #279.
XX
XX virucide; vaccine; detection; severe acute respiratory syndrome;
XX real-time quantitative polymerase chain reaction; SARS.
XX
OS SARS coronavirus.
XX
XX WO2004085455-A1.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-CN000247.
XX
XX 24-MAR-2003; 2003US-0457031P.
XX 26-MAR-2003; 2003US-0457730P.
XX 02-APR-2003; 2003US-0459931P.
XX 03-APR-2003; 2003US-0460357P.
XX 08-APR-2003; 2003US-0461265P.
XX 14-APR-2003; 2003US-0462805P.
XX 23-APR-2003; 2003US-0464886P.
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PR 05-MAY-2003; 2003US-0468139P.
PR 16-MAY-2003; 2003US-0471200P.
XX
XX (UYHK-) UNIV HONG KONG.
XX
XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
PI WPI; 2004-737326/72.
XX
XX New isolated nucleic acid molecule useful for detecting, treating,
PT ameliorating, or preventing the virus causing severe acute respiratory
PT syndrome in humans using a real-time quantitative polymerase chain
PT reaction assay.
XX
XX Example; SEQ ID NO 1387; 183pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule consisting
CC essentially of, and/or hybridizes under stringent conditions to a fully
CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-
CC 2476, or its complement. The methods and compositions of the present
CC invention are useful for the detection of the virus causing Severe Acute
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
CC polymerase chain reaction (PCR) assay. They can also be used in treating,
CC ameliorating, managing or preventing SARS. This sequence corresponds to a
CC partial SARS protein sequence from the complementary reading frame 1.
XX
XX Sequence 11 AA;
SQ
Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Oy 3 GOKATNIFPYT 13
Db 1 GQSQSNILPQT 11
RESULT 12
ID ADT37929 standard; peptide; 11 AA.
XX ADT37929;
XX
XX 30-DEC-2004 (first entry)
XX
DE hSARS virus peptide, SEQ ID 1387.
XX
XX virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX
OS SARS coronavirus.
XX
XX WO2004085633-A1.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-CN000248.
XX
XX 24-MAR-2003; 2003US-0457031P.
XX 26-MAR-2003; 2003US-0457730P.
XX 02-APR-2003; 2003US-0459931P.
XX 03-APR-2003; 2003US-0460357P.
XX 08-APR-2003; 2003US-0461265P.
XX 14-APR-2003; 2003US-0462805P.
XX 23-APR-2003; 2003US-0464886P.
XX
XX (UYHK-) UNIV HONG KONG.
XX
XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
PI Leung FC;
XX WPI; 2004-728736/71.
XX
XX New isolated human severe acute respiratory syndrome (hSARS) virus,
```



PT useful as vaccine for diagnosing or treating SARS or in clinical and  
PT scientific research applications.  
XX  
PS Example; SEQ ID NO 1387; 176pp; English.  
XX  
CC The present invention relates to novel human Severe Acute Respiratory  
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a  
CC hSARS virus having China Center for Type Culture Collection Deposit  
CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein  
CC sequences are useful as vaccines for diagnosing or treating SARS. They  
CC are also useful in clinical and scientific research applications. The  
CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences  
CC of all three reading frames were deduced from the complementary strand.  
CC ADT37650 is the full-length protein encoded by the first reading frame of  
CC the complementary strand and ADT37651-ADT38131 are the peptides from the  
CC first reading frame protein. ADT38132 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT38133-  
CC ADT38506 are the peptides from the second reading frame protein. ADT38507  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT38508-ADT39012 are the peptides from the  
CC third reading frame protein.  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 2.9e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 3 GQKATNIPYT 13  
Db 1 GOSOSNIRPQT 11  
XX  
RESULT 13  
AAMS2787  
ID AAMS2787 standard; peptide; 12 AA.  
XX  
AC AAMS2787;  
XX  
XX 22-FEB-2002 (first entry)  
XX  
DE CCR5-binding phage display peptide #4.  
XX  
KM CCR5 binding peptide; CC chemokine receptor 5; human; HIV infection;  
KM human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
KM drug screening; identification; phage display library.  
XX  
XX Synthetic.  
XX  
XX WO200171346-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 21-MAR-2001; 2001WO-US009155.  
XX  
XX 21-MAR-2000; 2000US-0190946P.  
XX  
XX 21-MAR-2000; 2000US-019096P.  
XX  
XX 21-MAR-2000; 2000US-0191299P.  
XX  
XX 20-MAR-2001; 2001US-00813448.  
XX  
XX 20-MAR-2001; 2001US-00813651.  
XX  
XX 20-MAR-2001; 2001US-00813653.  
XX  
XX (CONS-) CONSENSUS PHARM INC.  
XX  
XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;  
XX  
XX WPI; 2002-010610/01.  
XX  
XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
XX  
XX computer binding a molecule from library to a molecule having binding  
XX  
XX property corresponding to CCR5 and identifying bound molecule.  
XX  
XX Claim 20; Page 33; 50pp; English.

XX  
XX The invention relates to a method for identifying a binding compound for  
CC CC chemokine receptor 5 (CCR5). The method involves screening a library  
CC of test molecules (particularly peptides) with immobilised CCR5, and then  
CC identifying those molecules which bind. The invention also relates to  
CC CCR5-binding molecules identified using the method of the invention,  
CC methods for identifying consensus motifs for CCR5-binding peptides, a  
CC transfer vector encoding tagged CCR5, a computer-aided methods for  
CC determining the relative binding affinity of a test molecule to CCR5 and  
CC a computer aided drug screening assay that utilises the three-dimensional  
CC structure of CCR5. Compounds identified using the methods of the  
CC invention are useful for treating or preventing HIV (human  
CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
CC syndrome) in a patient. The methods of the invention may also be used to  
CC identify agonists or antagonists of the interaction of CCR5 with its  
CC natural ligand, and to determine a binding motif for CCR5. Sequences  
CC AAMS2784-AAMS2805 and AAMS2814 represent specifically claimed CCR5-  
CC binding peptides identified using methods of the invention  
XX  
SQ Sequence 12 AA;  
XX  
Query Match 33.0%; Score 32; DB 5; Length 12;  
Best Local Similarity 62.5%; Pred. No. 3.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 10 PPYRAPGT 17  
Db 4 YPYSNPRT 11  
XX  
RESULT 14  
ADV13048  
ID ADV13048 standard; peptide; 12 AA.  
XX  
XX ADV13048;  
XX  
XX 10-MAR-2005 (first entry)  
XX  
XX Human phosphorylated peptide from phosphoprotein #986.  
XX  
XX Alzheimers disease; neuroprotective; nocotropic; degeneration; tumor;  
XX  
XX neoplasm; neurological disease; phosphorylation; protein sequencing;  
XX  
XX phosphoprotein.  
XX  
XX Homo sapiens.  
XX  
XX WO2004108948-A2.  
XX  
XX 16-DEC-2004.  
XX  
XX 04-JUN-2004; 2004WO-US017613.  
XX  
XX 04-JUN-2003; 2003US-0476010P.  
XX  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Gyl SP;  
XX  
XX WPI; 2005-031720/03.  
XX  
XX Characterizing phosphorylated polypeptides in a sample comprises  
XX  
XX digesting the polypeptides with a protease thus generating test peptides,  
XX  
XX and collecting a fraction of test peptides that enriched for positively  
XX  
XX charged peptides.  
XX  
XX Claim 16; Page 79; 123pp; English.  
XX  
XX The invention relates to characterizing phosphorylated polypeptides in a  
XX  
XX sample comprising digesting the polypeptides with a protease thus  
XX  
XX generating test peptides, and collecting a fraction of test peptides that  
XX  
XX enriched for positively charged peptides. Also included are a method  
XX  
XX (comprising determining the presence, absence or level of one or more  
XX  
XX phosphorylated peptides as identified above in cells having a cell state

CC and determining the degree of correlation between the presence, absence  
 CC or level of phosphorylated polypeptide with the cell state), an isolated  
 CC peptide of 5-50 amino acids comprising an amino acid sequence that is a  
 CC subsequence of any of the protein sequences given in the specification  
 CC (and which comprise a phosphorylation site within the subsequence), an  
 CC isolated polypeptide selected from any of the polypeptides listed in the  
 CC specification and is modified at a modification site, an isolated peptide  
 CC comprising a mass spectral peak signatures, a method for identifying a  
 CC treatment that modulates phosphorylation of an amino acid in a target  
 CC polypeptide, a method for generating a peptide standard, a pair of  
 CC peptide standards comprising the peptide obtained (where the peptide is  
 CC phosphorylated and a corresponding peptide comprising an identical amino  
 CC acid sequence but which is not phosphorylated), a system (comprising a  
 CC computer memory comprising data files storing information relating to the  
 CC identifying characteristics of positively charged peptides), and a data  
 CC analysis module capable of executing instructions for organizing and/or  
 CC searching the data files), a computer program product (comprising data  
 CC relating to the identifying characteristics of positively charged  
 CC peptides and comprising instructions for organizing and/or searching the  
 CC data), and a method for identifying N-terminal peptides in a sample. The  
 CC method is useful for characterizing phosphorylated polypeptides in a  
 CC sample. The present sequence is a peptide from a human phosphoprotein,  
 CC containing a phosphorylation site, identified by the method of the  
 CC invention.

CC Sequence 12 AA;

Query Match 33.0%; Score 32; DB 9; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPGT 17  
 | | | | |  
 Db 3 PATAPGT 9

RESULT 15

AY65747  
 ID AAY65747 standard; peptide; 15 AA.

AC AAY65747;

DT 10-FEB-2000 (first entry)

DE Breast cancer susceptibility (BRCA 2) mutant peptide 31.

XX Human; frameshift mutant; T cell response; tumour; treatment; cancer;  
 mutant.

OS Homo sapiens.

OS Synthetic.

PN WO958552-A2.

PD 18-NOV-1999.

PF 03-MAY-1999; 99WO-NO000143.

PR 08-MAY-1998; 98NO-00002097.

PA (NH2D ) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

DR WPI; 2000-039064/03.

PT New peptides derived from genes with frameshift mutations, used to  
 PT develop products for the treatment and prophylaxis of cancers.

PS Claim 13; Page 25; 166pp; English.

XX Peptides AAY65684-Y66142 are fragments of mutant proteins arising from a  
 CC frameshift mutation in a gene from a cancer cell. The peptides are

CC characterised in that they: (i) are at least 8 amino acids long and a  
 CC fragment of a mutant protein arising from a frameshift mutation in a gene  
 CC of a cancer cell; (ii) consist of at least one amino acid of the mutant  
 CC part of a protein sequence encoded by the gene; (iii) comprise 0-10 amino  
 CC acid from the carboxyl terminus of the normal part of the protein  
 CC sequence preceding the amino terminus of the mutant sequence and may  
 CC further extend to the carboxyl terminus of the mutant part of the protein  
 CC as determined by a new stop codon generated by the frameshift mutation;  
 CC and (iv) induce, either in their full lengths or after processing by an  
 CC antigen presenting cell (APC), T cell responses. The genes that the  
 CC peptides are derived from, are characterised as susceptible to frameshift  
 CC mutation by having a mono nucleoside base repeat sequence of at least 5  
 CC residues, or a di-nucleoside base repeat sequence of at least 4 di-  
 CC nucleoside base units. The peptides are created by the addition or  
 CC deletion of 1 or 2 nucleoside base residues from the repeat sequence. The  
 CC novel peptides can elicit T cell responses and toxicity against tumours  
 CC and cancer cells carrying genes with frameshift mutations. The novel  
 CC peptides and DNA sequences can be used for the preparation of a  
 CC composition for the treatment or prophylaxis of cancer

CC Sequence 15 AA;

Query Match 33.0%; Score 32; DB 3; Length 15;  
 Best Local Similarity 54.5%; Pred. No. 4e+02;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGQKATNIFP 11  
 | : | | : | |  
 Db 4 VEDQKTLVFP 14

Search completed: December 12, 2005, 21:52:02  
 Job time : 111.333 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:05:57 ; Search time 27 Seconds  
(without alignments)  
55.117 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDCGKATNIPPTAPGTR 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 208455

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	33.0	9	2	US-09-920-262A-6
2	32	33.0	15	2	US-09-674-973A-64
3	30	30.9	9	2	US-09-865-548A-126
4	30	30.9	17	1	US-08-333-555-22
5	30	30.9	17	1	US-08-661-479-22
6	29	29.9	9	2	US-09-042-353-366
7	29	29.9	9	2	US-08-758-417A-214
8	29	29.9	11	2	US-09-307-265A-14
9	29	29.9	15	2	US-08-278-774-20
10	29	29.9	15	2	US-09-526-195-9
11	29	29.9	16	2	US-08-957-130-19
12	29	29.9	16	2	US-08-856-920-1
13	28	28.9	10	2	US-09-641-803-18
14	28	28.9	10	2	US-09-641-802-18
15	28	28.9	10	2	US-09-641-801-18
16	28	28.9	10	2	US-10-281-652-18
17	28	28.9	15	1	US-08-080-073-26
18	27	27.8	8	2	US-08-981-392-83
19	27	27.8	8	2	US-09-908-322-83
20	27	27.8	9	1	US-08-346-333-41
21	27	27.8	9	4	PCT-US91-07506-41
22	27	27.8	11	1	US-07-958-903A-5
23	27	27.8	11	1	US-08-462-018-5
24	27	27.8	11	1	US-08-823-245-5
25	27	27.8	11	1	US-07-963-329A-69
26	27	27.8	11	2	US-09-318-001-5
27	27	27.8	11	2	US-09-064-159-5

28	27	27.8	11	2	US-09-809-517A-21	Sequence 21, Appl
29	27	27.8	11	4	PCT-US92-09443A-69	Sequence 69, Appl
30	27	27.8	13	1	US-07-958-903A-8	Sequence 8, Appl
31	27	27.8	13	1	US-08-462-018-8	Sequence 8, Appl
32	27	27.8	13	1	US-08-823-245-8	Sequence 8, Appl
33	27	27.8	13	2	US-07-963-329A-58	Sequence 58, Appl
34	27	27.8	13	2	US-09-318-001-8	Sequence 8, Appl
35	27	27.8	13	2	US-09-064-159-8	Sequence 8, Appl
36	27	27.8	13	4	PCT-US92-09443A-58	Sequence 8, Appl
37	27	27.8	17	1	US-08-325-553-9	Sequence 9, Appl
38	27	27.8	17	1	US-08-394-152A-9	Sequence 9, Appl
39	27	27.8	17	2	US-08-705-477E-9	Sequence 9, Appl
40	27	27.8	17	2	US-08-466-381C-9	Sequence 9, Appl
41	27	27.8	18	1	US-09-017-205-48	Sequence 48, Appl
42	27	27.8	18	1	US-09-017-205-49	Sequence 49, Appl
43	26	26.8	5	2	US-09-788-006-9	Sequence 9, Appl
44	26	26.8	9	2	US-09-197-854-59	Sequence 59, Appl
45	26	26.8	9	2	US-09-511-939-96	Sequence 96, Appl

## ALIGNMENTS

```
RESULT 1
US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Pettit, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: GEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6

Query Match      33.0% Score 32; DB 2; Length 9;
Beet Local Similarity 83.3% Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      8 NIPYPT 13
      |||||
Db      4 NIPYPT 9

RESULT 2
US-09-674-973A-64
; Sequence 64, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hydrø ASA
; TITLE OF INVENTION: Peptidases
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-09-674-973A-64

Query Match 33.0%; Score 32; DB 2; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDQKATNFP 11  
| | | | |  
| | | | |  
Db 4 VEDOKTLVFP 14

RESULT 3  
US-09-865-548A-126  
Sequence 126, Application US/09865548A

PATENT No. 6867283  
GENERAL INFORMATION:  
APPLICANT: Barnea, Eilon  
APPLICANT: Beer, Ilan  
APPLICANT: Ziv, Tamar  
APPLICANT: Admon, Arie  
TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE  
TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES  
FILE REFERENCE: 01/22080  
CURRENT APPLICATION NUMBER: US/09/865,548A  
CURRENT FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: US 60/290,958  
PRIOR FILING DATE: 2001-05-16  
NUMBER OF SEQ ID NOS: 204  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 126  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-09-865-548A-126

Query Match 30.9%; Score 30; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIFPY 12  
| | | | |  
| | | | |  
Db 1 NIFPY 5

RESULT 4  
US-08-333-565-22  
Sequence 22, Application US/08333565

PATENT No. 5622852  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-333-565-22

Query Match 30.9%; Score 30; DB 1; Length 17;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16  
| | | | |  
| | | | |  
Db 3 PYLAPG 8

RESULT 5  
US-08-661-479-22  
Sequence 22, Application US/08661479

PATENT No. 5834209  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,479  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,565  
FILING DATE: 31-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-661-479-22

Query Match 30.9%; Score 30; DB 1; Length 17;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16

Db 3 PYLAPG 8

RESULT 6  
US-09-042-353-366  
Sequence 366, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/16433  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/21803  
FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 366:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-042-353-366  
Query Match 29.9% Score 29; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 8 NIPFYT 13  
Db 4 NSFPYT 9  
RESULT 7  
US-08-758-417A-214  
Sequence 214, Application US/08758417A  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-DEC-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 10-OCT-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 214:  
US-08-758-417A-214

Query Match 29.9%; Score 29; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NTFPYT 13  
| | | | |  
Db 4 NSFPPY 9

RESULT 8  
US-09-307-265A-14  
Sequence 14, Application US/09307265A  
Patent No. 6225456  
GENERAL INFORMATION:  
APPLICANT: Gu, Trent  
APPLICANT: Orita, Satoshi  
APPLICANT: Han, Min  
TITLE OF INVENTION: RAS SUPPRESSOR SUR-5  
FILE REFERENCE: UTC-03732  
CURRENT APPLICATION NUMBER: US/09/307,265A  
CURRENT FILING DATE: 1999-05-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 14  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-307-265A-14

Query Match 29.9%; Score 29; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 PYTAPGK 18  
| | | | |  
Db 1 PYTSSGK 8

RESULT 9  
US-08-278-774-20  
Sequence 20, Application US/08278774  
Patent No. 6653450  
GENERAL INFORMATION:  
APPLICANT: Berg, Richard A  
APPLICANT: Toman, David P  
APPLICANT: Wallace, Donald  
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COLLAGEN CORPORATION  
STREET: 2500 Faber Place  
CITY: Palo Alto

STATE: California  
COUNTRY: USA  
ZIP: 94303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,774  
FILING DATE: 22-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ralayko, Kathi L  
REGISTRATION NUMBER: 36,644  
REFERENCE/DOCKET NUMBER: 94-018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 354-4642  
TELEFAX: (415) 354-4752  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-278-774-20

Query Match 29.9%; Score 29; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 3.2e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIPPY 12  
: | | | | |  
Db 2 ICGEKAGGFAPY 13

RESULT 10  
US-09-526-195-9  
Sequence 9, Application US/09526195  
Patent No. 6699478  
GENERAL INFORMATION:  
APPLICANT: Hancock, Gerald E.  
APPLICANT: Tebbey, Paul W.  
TITLE OF INVENTION: ENHANCED IMMUNE RESPONSE TO ATTACHMENT  
FILE REFERENCE: 1646.1030-004  
CURRENT APPLICATION NUMBER: US/09/526,195  
CURRENT FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: US 60/084,863  
PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: PCT/US98/19656  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: US 60/059,684  
PRIOR FILING DATE: 1997-09-19  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-09-526-195-9

Query Match 29.9%; Score 29; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 TNIFPYAPGK 18  
| | | | |  
Db 1 TTIATTPGK 12

```
RESULT 11
US-08-957-130-19
; Sequence 19, Application US/08957130
; Patent No. 6290959
; GENERAL INFORMATION:
; APPLICANT: WU, Xue-Ru
; APPLICANT: SUN, Tung-Tien
; TITLE OF INVENTION: METHOD FOR SCREENING COMPOUNDS FOR
; TITLE OF INVENTION: INHIBITING BACTERIAL ATTACHMENT TO HOST CELL RECEPTORS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,130
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SUN=8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 737-3528
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-957-130-19

Query Match 29.9%; Score 29; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 5 KAINIPYTPAGTK 18
: |||
: |||
Db 4 QVTNL---APGTK 13

RESULT 12
US-09-856-920-1
; Sequence 1, Application US/09856920
; Patent No. 6740325
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co.
; TITLE OF INVENTION: Peptide-based vaccine for influenza
; FILE REFERENCE: 9822 PCT
; CURRENT APPLICATION NUMBER: US/09/856,920
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Influenza virus
US-09-856-920-1

Query Match 29.9%; Score 29; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
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```
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 TNIPYTPAP 15
: |||
: |||
Db 5 SNCYPTDVP 13

RESULT 13
US-09-641-803-18
; Sequence 18, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,110
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-18

Query Match 28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 IFPYTPAP 15
: |||
: |||
Db 1 VYPFTGP 7

RESULT 14
US-09-641-802-18
; Sequence 18, Application US/09641802
; Patent No. 6852685
; GENERAL INFORMATION:
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOGS
; TITLE OF INVENTION: TO PROMOTE NEURAL CELL DIFFERENTIATION
; FILE REFERENCE: 265.00240101
; CURRENT APPLICATION NUMBER: US/09/641,802
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,633
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-802-18

Query Match 28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 IFPYTPAP 15
: |||
: |||
Db 1 VYPFTGP 7
```

```
RESULT 15
US-09-641-801-18
; Sequence 18: Application US/09641801
; Patent No. 6903068
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: GEORGIADIS, Jerry
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOG
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 265.00230101
; CURRENT APPLICATION NUMBER: US/09/641,801
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,311
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-801-18

Query Match      28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      9 IFPYTAP 15
       1 VYPPTGP 7
Db
```

Search completed: December 12, 2005, 21:20:08  
Job time : 28 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 12, 2005, 21:20:19 ; Search time 95 Seconds  
(without alignments)  
79.168 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97

Sequence: 1 VDGQKATNIPFYTAGTK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues 356231

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	US-10-758-165-9	Sequence 9, Appli
2	87	89.7	18	US-10-758-165-10	Sequence 10, Appl
3	55	56.7	18	US-10-758-165-12	Sequence 12, Appl
4	37	38.1	15	US-10-856-118-34	Sequence 34, Appl
5	34	35.1	15	US-10-052-788-5	Sequence 5, Appli
6	34	35.1	18	US-10-758-165-11	Sequence 11, Appl
7	32	33.0	9	US-09-920-262A-6	Sequence 6, Appli
8	32	33.0	9	US-10-912-994-6	Sequence 6, Appli
9	32	33.0	9	US-10-975-883-6	Sequence 6, Appli
10	32	33.0	9	US-10-975-740A-6	Sequence 6, Appli
11	32	33.0	9	US-10-975-708-6	Sequence 6, Appli
12	32	33.0	11	US-10-808-187-1387	Sequence 1387, Ap
13	32	33.0	11	US-10-807-807-1387	Sequence 1387, Ap
14	32	33.0	12	US-09-813-653-26	Sequence 26, Appl
15	32	33.0	12	US-10-862-195-1037	Sequence 1037, Ap
16	32	33.0	13	US-10-776-224-64	Sequence 64, Appl
17	31	32.0	13	US-10-300-694A-64	Sequence 64, Appl
18	31	32.0	14	US-09-229-751A-16	Sequence 16, Appl
19	31	32.0	18	US-10-685-896-81	Sequence 81, Appl
20	30	30.9	9	US-09-865-548A-126	Sequence 126, App
21	30	30.9	9	US-10-705-459-126	Sequence 126, App
22	30	30.9	18	US-10-195-730-360	Sequence 360, App
23	30	30.9	18	US-10-799-747-360	Sequence 360, App
24	30	30.9	18	US-10-979-183-360	Sequence 360, App
25	29	29.9	5	US-10-482-630-40	Sequence 40, Appl
26	29	29.9	12	US-10-894-672-39	Sequence 39, Appl
27	29	29.9	12	US-10-996-316-39	Sequence 39, Appl

28	29	29.9	15	US-10-783-455-9	Sequence 9, Appli
29	29	29.9	15	US-10-720-831-20	Sequence 20, Appl
30	29	29.9	17	US-09-992-896-51	Sequence 51, Appl
31	29	29.9	17	US-10-306-631-76	Sequence 76, Appl
32	29	29.9	18	US-10-846-548A-1	Sequence 1, Appli
33	28	28.9	9	US-10-160-506-34	Sequence 34, Appl
34	28	28.9	9	US-10-449-379-34	Sequence 34, Appl
35	28	28.9	9	US-10-688-015-34	Sequence 34, Appl
36	28	28.9	9	US-10-160-505-34	Sequence 34, Appl
37	28	28.9	9	US-10-482-284A-186	Sequence 186, App
38	28	28.9	10	US-10-281-652-18	Sequence 18, Appl
39	28	28.9	10	US-10-691-157-18	Sequence 18, Appl
40	28	28.9	10	US-10-691-330-18	Sequence 18, Appl
41	28	28.9	12	US-10-903-529-3	Sequence 3, Appli
42	28	28.9	12	US-10-903-529-25	Sequence 25, Appl
43	28	28.9	12	US-10-937-042-3	Sequence 3, Appli
44	28	28.9	14	US-09-880-748-2653	Sequence 2653, Ap
45	28	28.9	14	US-10-293-418-2653	Sequence 2653, Ap

## ALIGNMENTS

```
RESULT 1
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match      100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAGTK 18
      |||||
DB      1 VDGQKATNIPFYTAGTK 18

RESULT 2
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match      89.7%; Score 87; DB 5; Length 18;
```

Best Local Similarity 100.0%; Pred. NO. 4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	V	D	G	K	A	T	N	I	F	P	Y	A	P	C	16
Db	1	V	D	G	K	A	T	N	I	F	P	Y	A	P	C	16

RESULT 3  
US-10-75

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/ Sequence 12, Application US/10758165
/ Publication No. US20050196816A1
/ GENERAL INFORMATION:
/ APPLICANT: Hammerberg, Bruce
/ TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
/ FILE REFERENCE: 5051-661
/ CURRENT APPLICATION NUMBER: US/10/758,165
/ CURRENT FILING DATE: 2004-01-16
/ PRIOR APPLICATION NUMBER: US 60/440,472
/ PRIOR FILING DATE: 2003-01-16
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 12
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Sus scrofa
/ US-10-758-165-12

```

Query Match	Score	DB	Length
56.7%	55	5	18

Best Local Similarity 86.7%; P-Seq.No. 0.0/1;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
QY      1 VDGQKATNIEPYTAP 15
      |||:|:||||
Db      1 VDGQEDRNLFSTYAP 15
```

RESULT 4  
US-10-85

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1  Sequence 34, Application US/10856118
2  Publication No US20050025747A1
3  GENERAL INFORMATION:
4  APPLICANT: Latidaw, Stephan
5  APPLICANT: Skinner, Mike
6  APPLICANT: Hill, Adrian V.S.
7  APPLICANT: Gilbert, Sarah C.
8  APPLICANT: Anderson, Richard
9  TITLE OF INVENTION: Vaccine
10 FILE REFERENCE: 3742.1000-000
11 CURRENT APPLICATION NUMBER: US/10/856,118
12 CURRENT FILING DATE: 2004-05-27
13 PRIOR APPLICATION NUMBER: PCT/GB02/0054111
14 PRIOR FILING DATE: 2002-12-02
15 PRIOR APPLICATION NUMBER: GB0128733.3
16 PRIOR FILING DATE: 2001-11-30
17 PRIOR APPLICATION NUMBER: US 60/334,649
18 PRIOR FILING DATE: 2001-11-30
19 NUMBER OF SEQ ID NOS: 41
20 SOFTWARE: PastsEQ for Windows Version 4.0.0
21 SEQ ID NO 34
22 LENGTH: 15
23 TYPE: DRT
24 ORGANISM: Artificial Sequence
25 FEATURES:
26 OTHER INFORMATION: Flanking sequence
27 US-10-856-118-34

```

Query Match	38.1%	Score 37;	DB 5;	Length 15;
Best Local Similarity	55.6%	Pred. No. 52;		
Matches	5; Conservative	2; Mismatches	2; Indels	0; Gaps

QY 7 T N I F P Y T A P 1 5  
|| :: || |

Db 2 TINVYRYDVP 10

## RESULT 5

US-10-052-788-5  
; Sequence 5, Application US/10052788  
; Publication No. US20030087314A1  
GENERAL INFORMATION

```

; APPLICANT: G
; APPLICANT:

```

```

? APPLICANT: Kalina, Marlen V.
? APPLICANT: The Regents of the University of California
? TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
? TITLE OF INVENTION: Induction of Anti-19E Antibodies
? FILE REFERENCE: 023070-121000US
? CURRENT APPLICATION NUMBER: US/10/052,788
? CURRENT FILING DATE: 2001-11-08
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 5
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
? OTHER INFORMATION: P5, middle portion of C2 of equine 19E epsilon
? OTHER INFORMATION: heavy chain
? IS-10-052-788-5

```

Query Match	Score	DB	Length
35.1%	34	4	15

Best Local Similarity 54.5%; Pred. NO. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
QY      1 VDGQKATNIFP 11
        :|||         ||
Db      2 IDGQKVDEQFP 12
```

RESULT 6  
US-10-758-165-1

```

? Sequence 11, Application US/10758165
? Publication No. US20050196816m1
? GENERAL INFORMATION:
? APPLICANT: Hammerberg, Bruce
? TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
? FILE REFERENCE: 5051-661
? CURRENT APPLICATION NUMBER: US/10/758,165
? CURRENT FILING DATE: 2004-01-16
? PRIOR APPLICATION NUMBER: US 60/440,472
? PRIOR FILING DATE: 2003-01-16
? NUMBER OF SEQ ID NOS: 16
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 11
? LENGTH: 18
? TYPE: PRT
? ORGANISM: Equus caballus
? OS-10-758-165-11

```

Query Match	Score	DB	Length
35.1%	34	5	18

Best Local Similarity	54.5%;	Pred. NO. 2e+02;							
Matches	6;	Conservative	1;	Mismatches	4;	Indels	0;	Gaps	0;

```
Qy      1 VDQKATNIFP 11
          :|||      ||
Db      1 IDGQVDEQFP 11
```

RESULT 7  
US-09-920-262A-

;; Sequence 6, Application US/09920262A  
;; Publication No. US20030124123A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Shealy, David

```
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6
```

```
Query Match          33.0%; Score 32; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```
RESULT 8
US-10-912-994-6
; Sequence 6, Application US/10912994
; Publication No. US2005002937A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248DIV1
; CURRENT APPLICATION NUMBER: US/10/912,994
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-994-6
```

```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```
RESULT 9
US-10-975-883-6
; Sequence 6, Application US/10975883
; Publication No. US20050112127A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
```

```
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
; FILE REFERENCE: CEN0248DIV04
; CURRENT APPLICATION NUMBER: US/10/975,883
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-883-6
```

```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```
RESULT 10
US-10-975-740A-6
; Sequence 6, Application US/10975740A
; Publication No. US20050196638A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
; FILE REFERENCE: CEN0248DIV03
; CURRENT APPLICATION NUMBER: US/10/975,740A
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-740A-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```
RESULT 11
US-10-975-708-6
; Sequence 6, Application US/10975708
; Publication No. US20050214293A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
```

APPLICANT: Knight, David  
APPLICANT: Peritt, David  
APPLICANT: Scallion, Bernie  
APPLICANT: Shealy, David  
TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS  
FILE REFERENCE: GEN0248DIV02  
CURRENT APPLICATION NUMBER: US/10/975,708  
CURRENT FILING DATE: 2004-10-28  
PRIOR APPLICATION NUMBER: US 60/223,358  
PRIOR FILING DATE: 2000-08-07  
PRIOR APPLICATION NUMBER: US 60/236,827  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 09/920,262  
PRIOR FILING DATE: 2001-08-01  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn ver 3.1  
SEQ ID NO 6  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-975-708-6

Query Match 33.0%; Score 32; DB 5; Length 9;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0;

QY 8 NIPYPT 13  
Db 4 NIPYPT 9

RESULT 12  
US-10-808-187-1387  
Sequence 1387, Application US/10808187  
Publication No. US200500909A1  
GENERAL INFORMATION:  
APPLICANT: PEIRIS, JOSEPH S. M.  
APPLICANT: YUEN, KWOK YUNG  
APPLICANT: POON, LIT MAN  
APPLICANT: GUAN, YI  
APPLICANT: CHAN, KWOK HUNG  
APPLICANT: NICHOLLS, JOHN  
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE  
TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)  
FILE REFERENCE: V9661.0078  
CURRENT APPLICATION NUMBER: US/10/808,187  
CURRENT FILING DATE: 2004-03-24  
PRIOR APPLICATION NUMBER: 60/457,031  
PRIOR FILING DATE: 2003-03-24  
PRIOR APPLICATION NUMBER: 60/457,730  
PRIOR FILING DATE: 2003-03-26  
PRIOR APPLICATION NUMBER: 60/459,931  
PRIOR FILING DATE: 2003-04-02  
PRIOR APPLICATION NUMBER: 60/460,357  
PRIOR FILING DATE: 2003-04-03  
PRIOR APPLICATION NUMBER: 60/461,265  
PRIOR FILING DATE: 2003-04-08  
PRIOR APPLICATION NUMBER: 60/462,805  
PRIOR FILING DATE: 2003-04-14  
PRIOR APPLICATION NUMBER: 60/468,139  
PRIOR FILING DATE: 2003-05-05  
PRIOR APPLICATION NUMBER: 60/464,886  
PRIOR FILING DATE: 2003-04-23  
PRIOR APPLICATION NUMBER: 60/471,200  
PRIOR FILING DATE: 2003-05-16  
NUMBER OF SEQ ID NOS: 2476  
SOFTWARE: PatentIn ver. 3.2  
SEQ ID NO 1387  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Human severe acute respiratory system virus  
US-10-808-187-1387

Query Match 33.0%; Score 32; DB 5; Length 11;  
Best Local Similarity 54.5%; Pred. No. 2.5e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 4;

QY 3 GOKATNIFPYT 13  
Db 1 GQSQSNILPOT 11

RESULT 13  
US-10-807-807-1387  
Sequence 1387, Application US/10807807  
Publication No. US20050181357A1  
GENERAL INFORMATION:  
APPLICANT: LEUNG, FREDERICK C.  
APPLICANT: PEIRIS, JOSEPH S. M.  
APPLICANT: YUEN, KWOK YUNG  
APPLICANT: POON, LIT MAN  
APPLICANT: GUAN, YI  
APPLICANT: CHAN, KWOK HUNG  
APPLICANT: NICHOLLS, JOHN M.  
TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS  
TITLE OF INVENTION: CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)  
FILE REFERENCE: V9661.0077  
CURRENT APPLICATION NUMBER: US/10/807,807  
CURRENT FILING DATE: 2004-03-24  
PRIOR APPLICATION NUMBER: 60/457,031  
PRIOR FILING DATE: 2003-03-24  
PRIOR APPLICATION NUMBER: 60/457,730  
PRIOR FILING DATE: 2003-03-26  
PRIOR APPLICATION NUMBER: 60/459,931  
PRIOR FILING DATE: 2003-04-02  
PRIOR APPLICATION NUMBER: 60/460,357  
PRIOR FILING DATE: 2003-04-03  
PRIOR APPLICATION NUMBER: 60/461,265  
PRIOR FILING DATE: 2003-04-08  
PRIOR APPLICATION NUMBER: 60/462,805  
PRIOR FILING DATE: 2003-04-14  
PRIOR APPLICATION NUMBER: 60/464,886  
PRIOR FILING DATE: 2003-04-23  
PRIOR APPLICATION NUMBER: 60/465,738  
PRIOR FILING DATE: 2003-04-25  
PRIOR APPLICATION NUMBER: 60/470,935  
PRIOR FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 2487  
SOFTWARE: PatentIn ver. 3.2  
SEQ ID NO 1387  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Human severe acute respiratory system virus  
US-10-807-807-1387

Query Match 33.0%; Score 32; DB 5; Length 11;  
Best Local Similarity 54.5%; Pred. No. 2.5e+02; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 4;

QY 3 GOKATNIFPYT 13  
Db 1 GQSQSNILPOT 11

RESULT 14  
US-09-813-653-26  
Sequence 26, Application US/09813653  
Patent No. US20020064770A1  
GENERAL INFORMATION:  
APPLICANT: Nestor, John  
APPLICANT: Wilson, Carol  
APPLICANT: See, Raymond  
APPLICANT: Tan Hehir, Christina  
TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds  
FILE REFERENCE: CNS-005  
CURRENT APPLICATION NUMBER: US/09/813,653

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; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence identified through phage display for CCR5 binding
US-09-613-653-26

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```

Query Match          33.0%; Score 32; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      10 PPYAPGT 17
        :|||
Db       4 YPISAPRT 11

```

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RESULT 15
US-10-862-195-1037
; Sequence 1037, Application US/10862195
; Publication No. US20050164324A1
; GENERAL INFORMATION:
; APPLICANT: GYGI, STEVEN P.
; TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
; FILE REFERENCE: 58890(70207)
; CURRENT APPLICATION NUMBER: US/10/862,195
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/476,010
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 2245
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1037
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: See specification as filed for preferred embodiments
; OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1037

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Query Match          33.0%; Score 32; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      11 PYTAPGT 17
        :|||
Db       3 PATAAPT 9

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Search completed: December 12, 2005, 21:29:23  
Job time : 96 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:17:33 ; Search time 3 Seconds  
(without alignments)  
33.507 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97  
Sequence: 1 VDCGKATNIPFYTAFTK 18

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 9754

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:  
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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	28.9	14	7	US-11-054-515-2653
2	27	27.8	14	7	US-11-054-515-2682
3	25	25.8	9	7	US-11-009-939-10
4	25	25.8	9	7	US-11-009-939-40
5	25	25.8	18	6	US-10-828-033-36
6	24	24.7	8	6	US-10-999-866-57
7	24	24.7	16	6	US-10-507-275-17
8	23.5	24.2	14	7	US-11-054-515-2617
9	23	23.7	9	6	US-10-952-535A-28
10	23	23.7	9	6	US-10-952-535A-43
11	23	23.7	9	7	US-11-010-748A-334
12	23	23.7	9	7	US-11-010-748A-346
13	23	23.7	9	7	US-11-158-848-41
14	23	23.7	9	7	US-11-178-639-3
15	23	23.7	9	7	US-11-137-671-4
16	23	23.7	10	6	US-10-933-025-19
17	23	23.7	10	7	US-11-093-274-16
18	23	23.7	10	7	US-11-137-671-3
19	23	23.7	11	7	US-11-137-671-2
20	23	23.7	12	6	US-10-632-150-82
21	23	23.7	12	6	US-10-507-662-9
22	23	23.7	12	6	US-10-952-535A-33
23	23	23.7	12	6	US-11-069-858-1
24	23	23.7	12	7	US-11-073-457-82
25	23	23.7	12	7	US-11-137-671-1

26	23	23.7	13	6	US-10-511-559-719	Sequence 719, Appl
27	23	23.7	13	7	US-11-054-669-97	Sequence 97, Appl
28	23	23.7	13	7	US-11-089-551A-8	Sequence 8, Appl
29	23	23.7	14	7	US-11-054-515-2374	Sequence 2374, Ap
30	23	23.7	14	7	US-11-054-515-2474	Sequence 2474, Ap
31	23	23.7	14	7	US-11-054-515-2655	Sequence 2655, Ap
32	23	23.7	14	7	US-11-054-515-2656	Sequence 2656, Ap
33	23	23.7	14	7	US-11-054-515-2657	Sequence 2657, Ap
34	23	23.7	14	7	US-11-054-515-2658	Sequence 2658, Ap
35	23	23.7	14	7	US-11-054-515-2670	Sequence 2670, Ap
36	23	23.7	14	7	US-11-054-515-2673	Sequence 2673, Ap
37	23	23.7	14	7	US-11-054-515-2676	Sequence 2676, Ap
38	23	23.7	14	7	US-11-054-515-2679	Sequence 2679, Ap
39	23	23.7	14	7	US-11-054-515-2710	Sequence 2710, Ap
40	23	23.7	14	7	US-11-054-515-2719	Sequence 2719, Ap
41	23	23.7	15	6	US-10-952-535A-32	Sequence 32, Appl
42	23	23.7	15	7	US-11-058-735-1	Sequence 1, Appl
43	23	23.7	15	7	US-11-058-735-7	Sequence 28, Appl
44	23	23.7	17	7	US-11-058-735-28	Sequence 28, Appl
45	22.5	23.2	14	7	US-11-054-515-2361	Sequence 2361, Ap

## ALIGNMENTS

```
RESULT 1
US-11-054-515-2653
Sequence 2653, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23p3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2653
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2653
Query Match 28.9%; Score 28; DB 7; Length 14;
Beet Local Similarity 57.1%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 IFPYRAP 15
: ||| |
Db 6 LFPYMP 12
RESULT 2
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US-11-054-515-2682
; Sequence 2682, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2682
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2682

Query Match      27.8%; Score 27; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 IFPYT 13
Db      6 LFPT 10

RESULT 3
US-11-009-939-10
; Sequence 10, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-10

Query Match      25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 FPYT 13
Db      6 FPYT 9

RESULT 4
US-11-009-939-40
; Sequence 40, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-40

Query Match      25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 NIFPYT 13
Db      4 NTFPWT 9

RESULT 5
US-10-828-033-36
; Sequence 36, Application US/10828033
; Publication No. US20050250206A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher and Ruoguan Shen
; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND IMMUNOLOGICAL REAGENTS
; TITLE OF INVENTION: SPECIFIC FOR CELL
; TITLE OF INVENTION: SUPPRESSED MOLECULES AND TRANSFORMATION ASSOCIATED GENES
; FILE REFERENCE: 0667/37590-C-PCT-US
; CURRENT APPLICATION NUMBER: US/10/828,033
; CURRENT FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: US/08/875,553
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-10-828-033-36

Query Match      25.8%; Score 25; DB 6; Length 18;
Best Local Similarity 55.6%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 GOKATNIFP 11
Db      10 GQAVFYFP 18

RESULT 6
US-10-999-866-57
; Sequence 57, Application US/10999866
```



Publication No. US20050266004A1  
GENERAL INFORMATION:  
APPLICANT: GILES-KOMAR, Jill; SCALLION, Bernard J.; CAL, Ann  
TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND  
FILE REFERENCE: CEN5042NP  
CURRENT APPLICATION NUMBER: US/10/999,866  
CURRENT FILING DATE: 2004-11-30  
PRIOR APPLICATION NUMBER: 60/527,794  
PRIOR FILING DATE: 2003-12-08  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 57  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(8)  
OTHER INFORMATION: LC CDR3  
US-10-999-866-57

Query Match 24.7% Score 24; DB 6; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 NIPYPT 13  
Db 3 NTLPPT 8

RESULT 7  
US-10-507-275-17  
Sequence 17, Application US/10507275  
Publication No. US20050250166A1  
GENERAL INFORMATION:  
APPLICANT: Masai, Hisao  
APPLICANT: Tamai, Katsuyuki  
APPLICANT: Medical and Biological Laboratories Co., Ltd.  
APPLICANT: Japan Science and Technology Agency  
APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.  
TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,  
TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods  
TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK  
FILE REFERENCE: 082368-001100US  
CURRENT APPLICATION NUMBER: US/10/507,275  
CURRENT FILING DATE: 2004-09-09  
PRIOR APPLICATION NUMBER: JP 2002-067702  
PRIOR FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: WO PCT/JP03/02918  
PRIOR FILING DATE: 2003-03-12  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: an artificially  
US-10-507-275-17

Query Match 24.7% Score 24; DB 6; Length 16;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 9 IFPYTAP 15  
Db 1 MYPIYDP 7

RESULT 8  
US-11-054-515-2617

Sequence 2617, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523p3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2617  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-2617

Query Match 24.2% Score 23.5; DB 7; Length 14;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Oy 9 IFPYTAPGT 17  
Db 6 LFY-APLT 13

RESULT 9  
US-10-952-535A-28  
Sequence 28, Application US/10952535A  
Publication No. US20050255113A1  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Messer, Anne  
APPLICANT: Lecerf, Jean-Michel  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS  
FILE REFERENCE: INR-004CP  
CURRENT APPLICATION NUMBER: US/10/952,535A  
CURRENT FILING DATE: 2004-09-27  
PRIOR APPLICATION NUMBER: 60/146,047  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 28  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-952-535A-28

Query Match 23.7% Score 23; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 10 FPYTAP 15  
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Db 1 YPYDVP 6

RESULT 10  
US-10-952-535A-43  
; Sequence 43, Application US/10952535A  
; Publication No. US2005025511A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Messer, Anne  
; APPLICANT: Lecerc, Jean-Michel  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS  
; FILE REFERENCE: INR-004CP  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR FILING DATE: 2004-09-27  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: construct  
US-10-952-535A-43

Query Match 23.7%; Score 23; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 FPYTAP 15  
: || |  
Db 1 YPYDVP 6

RESULT 11  
US-11-010-748A-334  
; Sequence 334, Application US/11010748A  
; Publication No. US2005024421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: MOHL, Heidrun  
; APPLICANT: SCHARM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 334  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328  
US-11-010-748A-334

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 KATNIPFY 12  
: || ||  
Db 1 KIQEIFPF 8

RESULT 12  
US-11-010-748A-346  
; Sequence 346, Application US/11010748A  
; Publication No. US2005024421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: MOHL, Heidrun  
; APPLICANT: SCHARM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 346  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328  
US-11-010-748A-346

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 KATNIPFY 12  
: || ||  
Db 1 KIQEIFPF 8

RESULT 13  
US-11-158-848-41  
; Sequence 41, Application US/11158848  
; Publication No. US20050249703A1  
; GENERAL INFORMATION:  
; APPLICANT: Anne Dam Jensen  
; TITLE OF INVENTION: Interferon gamma polypeptide variants  
; FILE REFERENCE: 231u8410 - INFg variants  
; CURRENT APPLICATION NUMBER: US/11/158,848  
; CURRENT FILING DATE: 2005-06-22  
; PRIOR APPLICATION NUMBER: US/10/116,273  
; PRIOR FILING DATE: 2002-04-04  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Tag  
US-11-158-848-41

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 FPYTAP 15  
: || |  
Db 1 YPYDVP 6

RESULT 14

US-11-178-639-3  
; Sequence 3, Application US/11178639  
; Publication No. US20050250824A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A carboxylic acid derivative and a pharmaceutical  
; TITLE OF INVENTION: Composition containing the derivative as active  
; TITLE OF INVENTION: Ingredient  
; FILE REFERENCE: Q60772  
; CURRENT APPLICATION NUMBER: US/11/178,639  
; CURRENT FILING DATE: 2005-07-12  
; PRIOR APPLICATION NUMBER: US/09/623,913  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: JP 10-058444  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: JP 10-087560  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Influenza virus  
; FEATURE:  
; OTHER INFORMATION: hemagglutinin epitope  
US-11-178-639-3  
  
Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 10 PPYTPAP 15  
: || |  
Db 1 YPYDVP 6  
  
RESULT 15  
US-11-137-671-4  
; Sequence 4, Application US/11137671  
; Publication No. US20050268350A1  
; GENERAL INFORMATION:  
; APPLICANT: Kirschbaum, Bernd  
; Berglund, Erick  
; Melstereimst, Michael  
; Polites, Greg  
; TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION  
; COMPLEXES FROM TRANSGENIC  
; NON-HUMAN ANIMALS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HELLER, EHRMAN, WHITE & MCANULIFFE  
; STREET: 1666 K Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/137,671  
; FILING DATE: 25-May-2005  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/849,243  
; FILING DATE: 07-May-2001  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granados, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 38005-0148  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)912-2000

TELEFAX: (202)912-2020  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-11-137-671-4

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 10 PPYTPAP 15  
: || |  
Db 1 YPYDVP 6

Search completed: December 12, 2005, 21:20:42  
Job time : 3 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:18:48 ; Search time 10.6667 Seconds  
(without alignments)  
162.366 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97

Sequence: 1 VDGKATNIPFYTAGTK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	28.9	15	2	153284
2	27	27.8	15	2	PA0099
3	27	27.8	17	2	H49048
4	27	27.8	18	2	AS9137
5	26	26.8	18	2	A61577
6	25	25.8	15	2	D28587
7	25	25.8	15	2	F28587
8	25	25.8	16	2	B28587
9	25	25.8	16	2	F53284
10	24	24.7	15	2	B58502
11	24	24.7	17	2	PH1318
12	24	24.7	17	2	S18534
13	24	24.7	18	2	A25941
14	23	23.7	12	2	C20907
15	23	23.7	13	2	S22640
16	23	23.7	13	2	C53275
17	23	23.7	15	2	B45115
18	23	23.7	16	2	S03532
19	23	23.7	16	2	PS0383
20	23	23.7	16	2	S38292
21	23	23.7	18	2	P00072
22	23	23.7	18	2	S20322
23	23	23.7	12	2	C56046
24	22	22.7	18	2	P00786
25	22	22.7	13	2	S01904
26	22	22.7	14	2	PH1306
27	22	22.7	15	2	PA0056
28	22	22.7	15	2	PA0087
29	22	22.7	17	2	C64063

30	21	21.6	10	2	S71948	matrix metallopro
31	21	21.6	10	2	A39745	endo-glucosylceram
32	21	21.6	12	2	A53524	ubiquinol-cytochro
33	21	21.6	14	2	PL0142	carbon-monoxide de
34	21	21.6	14	2	S59495	formate dehydrogen
35	21	21.6	15	2	B61457	alpha-glucosidase
36	21	21.6	15	2	S36893	ribosomal protein
37	21	21.6	16	2	E53284	T-cell receptor be
38	21	21.6	17	2	S50901	chlorophyll a/b-bi
39	21	21.6	18	2	S57518	T cell receptor be
40	21	21.6	18	2	S70612	alpha-macroglobuli
41	20	20.6	9	2	D48186	ATPase, R1 subunit
42	20	20.6	9	2	S10784	enamelin 1 - bovin
43	20	20.6	13	2	B58533	CD61 homolog - cha
44	20	20.6	14	2	S22236	lipoxigenase (EC 1
45	20	20.6	14	2	G44957	photosystem II oxy

#### ALIGNMENTS

##### RESULT 1

T-cell receptor beta 2 chain J region, Ubeta2.7 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C:Accession: I53284

R:Harindranth, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity and J

A:Reference number: A53284; MUID:91342695; PMID:1678859

A:Accession: I53284

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <HAR>

A:Cross-references: UNIPARC:UPI0000115418; GB:S60737; NID:9233916; PIDN:AA819525.1; PID:

A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60747)

C:Keywords: T-cell receptor

Query Match 28.9%; Score 28; DB 2; Length 15;

Best Local Similarity 71.4%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 YTAGTK 18  
| | | | |  
Db 5 YFGPCTK 11

##### RESULT 2

phenotypic variation protein - fungus (Fusarium sporotrichioides) (fragment)

PA0099

C:Species: Fusarium sporotrichioides

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: PA0099

R:Chow, L.P.; Fukaura, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A:Reference number: PA0051

A:Accession: PA0099

A:Molecule type: protein

A:Residues: 1-15 <CHO>

A:Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI0000178405

Query Match 27.8%; Score 27; DB 2; Length 15;

Best Local Similarity 62.5%; Pred. No. 3.2e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 PFYTAGPT 17  
| | | | |  
Db 7 FKYSASGT 14

##### RESULT 3

H49048  
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C/Accession: H49048  
R/Stoud, M.; Kjelsgaard-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.  
Eur. J. Immunol. 22, 2413-2418, 1992  
A/Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile  
A/Reference number: A49048; MUID:92387250; PMID:1387614  
A/Accession: H49048  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-17 <STO>  
A/Cross-references: UNIPARC:UPI0000176DF0  
A/Experimental source: patient SS, IL-2R+ synovial T-cells  
A/Note: sequence extracted from NCBI backbone (NCBIP:113270)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 27.8%; Score 27; DB 2; Length 17;  
Best Local Similarity 62.5%; Pred. No. 3.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATNIFPYT 13  
DB 8 AWTFFPYT 15

RESULT 4  
A59137  
Protein Pil - golden needle mushroom (fragment)  
C/Species: Flammulina velutipes (golden needle mushroom)  
C/Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: A59137  
R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
Submitted to the Protein Sequence Database, November 1999  
A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A/Reference number: A59137  
A/Accession: A59137  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-18 <SAK>  
A/Cross-references: UNIPROT:Q7M4M6; UNIPARC:UPI000017CB27

Query Match 27.8%; Score 27; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15  
DB 2 PYTSP 6

RESULT 5  
A61577  
24K serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)  
C/Species: Streptomyces fradiae  
C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: A61577  
R/Sinha, U.; Wolz, S.A.; Lad, P.J.  
Int. J. Biochem. 23, 979-984, 1991  
A/Title: Two new extracellular serine proteases from Streptomyces fradiae.  
A/Reference number: A61577; MUID:9215439; PMID:1176859  
A/Accession: A61577  
A/Molecule type: protein  
A/Residues: 1-18 <STN>  
A/Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AE13  
C/Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 26.8%; Score 26; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 5.7e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIFPY 12  
DB 2 VGGTFAAQEPFW 13

RESULT 6  
D28587  
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: D28587  
R/Toyonaga, B.; Yoshikai, Y.; Vadász, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region genes  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: D28587  
A/Molecule type: DNA  
A/Residues: 1-15 <TOY>  
A/Cross-references: UNIPARC:UPI0000113CTC; GB:M14159; NID:g338852; PIDN:AAA60679.1; PID:5  
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAGTK 18  
DB 5 YFGGTR 11

RESULT 7  
F28587  
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: F28587  
R/Toyonaga, B.; Yoshikai, Y.; Vadász, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region genes  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: F28587  
A/Molecule type: DNA  
A/Residues: 1-15 <TOY>  
A/Cross-references: UNIPARC:UPI0000113CTE; GB:M14159; NID:g338852; PIDN:AAA60681.1; PID:5  
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAGTK 18  
DB 5 YFGGTR 11

RESULT 8  
B28587  
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: B28587  
R/Toyonaga, B.; Yoshikai, Y.; Vadász, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region genes  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: B28587  
A/Molecule type: DNA  
A/Residues: 1-16 <TOY>  
A/Cross-references: UNIPARC:UPI00002FDD6; GB:M14159; NID:g338852; PIDN:AAA60677.1; PID:5  
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 12 YTPGPK 18  
| | | |  
Db 6 YFGPKR 12

## RESULT 9

F53284  
T-cell receptor beta 2 chain J region, Jbeta2.3 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: F53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and J  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: F53284  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-16 <HAR>  
A:Cross-references: UNIPARC:UPI0000115415; GB:S60737; NID:9233916; PIDN:AA19522.1; PID:  
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:60744)  
C:Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 7.4e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPGPK 18  
| | | |  
Db 6 YFGPKR 12

## RESULT 10

B58502  
36K kidney stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C:Accession: B58502  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: B58502  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <BIN>  
A:Cross-references: UNIPARC:UPI000017A6D0  
A:Experimental source: human kidney stone containing Ca ox.monohydrate, 1% struvite, CaF  
A:Note: tentative identification of 8-Tyr and 9-Thr

Query Match 24.7%; Score 24; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 9.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIPPT 13  
| | | |  
Db 4 NIPGTT 9

## RESULT 11

PH1318  
Ig heavy chain DJ region (clone C527-121) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1318  
R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1318  
A:Molecule type: DNA

A:Residues: 1-15 <MAS>  
A:Cross-references: UNIPARC:UPI000017C244  
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 TNIPYTPAGT 17  
| | | | |  
Db 5 TGFPMYMGQT 15

## RESULT 12

S18534  
hypothetical protein 7 (eryg 3' region) - Saccharopolyspora erythraea (fragment)  
C:Species: Saccharopolyspora erythraea  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 07-Apr-1994  
C:Accession: S18534  
R:Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.  
Mol. Gen. Genet. 230, 120-128, 1991  
A:Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in  
methylintransferases.  
A:Reference number: S18530; MUID:92079886; PMID:1840640  
A:Accession: S18534  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-17 <HAY>  
A:Cross-references: UNIPARC:UPI000017AD81; EMBL:X60379  
A:Note: the authors translated the codon CTG for residue 12 as Gly

Query Match 24.7%; Score 24; DB 2; Length 17;  
Best Local Similarity 62.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 IFPYTPAG 16  
| | | | |  
Db 1 IFPAVASC 8

## RESULT 13

A25941  
Ig heavy chain J-HI region - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 05-Jun-1998 #sequence\_revision 05-Jun-1998 #text\_change 23-Jul-1999  
C:Accession: A25941; JH0666  
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986  
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody  
A:Reference number: A25941; MUID:86287397; PMID:3016742  
A:Accession: A25941  
A:Molecule type: DNA  
A:Residues: 1-18 <BRU>  
A:Cross-references: UNIPARC:UPI0000114C27; GB:M13798; NID:9204707; PIDN:AAA1371.1; PID:  
R:Lang, P.; Mochkat, R.  
Gene 102, 261-264, 1991  
A:Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and  
A:Reference number: JH0666; MUID:91340162; PMID:1908401  
A:Accession: JH0666  
A:Molecule type: DNA  
A:Residues: 1-18 <LAN>  
A:Cross-references: UNIPARC:UPI0000114C27; EMBL:X56791  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPTAPGT 17  
| | | | |  
Db 5 FDFWPGGT 12

## RESULT 14

C20907

Ig kappa-1 chain J3 region - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 16-Aug-1996

C/Accession: C20907

R/Emorine, L./ Max, E.E.

Nucleic Acids Res. 11, 8877-8890, 1983

A/Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple

A/Reference number: A20907; MUID:64169523; PMID:6324107

A/Accession: C20907

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-12 &lt;EMO&gt;

A/Cross-references: UNIPARC:UPI000017C5CF

C/Keywords: heterotetramer; immunoglobulin

## Query Match

23.7%; Score 23; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18

Db 5 PGTK 8

## RESULT 15

S23640

Ig kappa chain J segment (J-kappa-3) - human

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C/Accession: S23640

R/Huber, C./ Klobeck, H.G.; Zachau, H.G.

Eur. J. Immunol. 22, 1561-1565, 1992

A/Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa)

A/Reference number: S23637; MUID:92289816; PMID:1601042

A/Accession: S23640

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-13 &lt;HUB&gt;

A/Cross-references: UNIPARC:UPI0000116784; EMBL:X63370

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991

C/Keywords: heterotetramer; immunoglobulin

## Query Match

23.7%; Score 23; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18

Db 5 PGTK 8

Search completed: December 12, 2005, 21:24:31  
 Job time : 10.6667 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:17:48 ; Search time 61.6667 Seconds  
(without alignments)  
205.938 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGQKATNIPFYTAFTK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 11298

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.1	17	2	046473 FELCA
2	32	33.0	8	2	070Y88_9LAMI
3	28.5	29.4	18	2	09TWL4_LUCCU
4	27.5	28.4	15	2	08L1Y7_PLEBO
5	27	27.8	15	2	07M4Y7_FUSSE
6	27	27.8	15	2	07M4W6_FLAVE
7	26	26.8	18	2	07S007_NEUCR
8	26	26.8	18	2	07M198_STRFR
9	25	25.8	15	2	09UR63_EMENT
10	24	24.7	14	2	0714T5_9CRYP
11	24	24.7	15	2	069142_STRPY
12	24	24.7	17	2	065Y26_HORSE
13	23	23.7	8	2	05ZEY7_HUMAN
14	23	23.7	10	2	09Z1B1_CLODI
15	23	23.7	14	2	09Z1B1_CLODI
16	23	23.7	14	2	082435_TORAC
17	23	23.7	15	2	05D4R7_9CYAN
18	23	23.7	15	2	085HM7_9PASS
19	23	23.7	16	2	07M263_SECCS
20	23	23.7	16	2	08L1Y8_9CYAN
21	23	23.7	16	2	089560_HMYR
22	23	23.7	16	2	05R3U1_XENLA
23	23	23.7	17	2	09PRU8_CHICK
24	23	23.7	18	2	07M4Q7_HUMAN
25	23	23.7	18	2	07M1G0_WHEAT
26	22	22.7	8	2	059AB6_HUMAN
27	22	22.7	10	2	071VN2_MOUSE
28	22	22.7	12	2	07M2G3_VICFA
29	22	22.7	14	2	070Y94_9LAMI
30	22	22.7	15	2	07M4Z7_FUSSE
31	22	22.7	15	2	09TRES_BOVIN

32	22	22.7	15	2	09TRN8_PIG	09trn8 sus scrofa
33	22	22.7	16	2	070Y93_9LAMI	070y93 platostoma
34	22	22.7	17	2	09K7Q4_BACDH	09k7q4 bacillus ha
35	22	22.7	18	2	09TWL5_LUCCU	09twl5 lucilia cup
36	22	22.7	18	2	09TRB6_PIG	09trb6 sus scrofa
37	22	22.7	18	2	070Y99_9LAMI	070y99 basilicum p
38	21.5	22.2	17	1	COG2_CARNA	P81609 carcinus ma
39	21.5	22.2	17	2	079E46_COXBU	079e46 coxiella bu
40	21	21.6	9	2	030790_ERWAM	030790 erwina amy
41	21	21.6	9	2	065711_BEV	065711 beine virus
42	21	21.6	10	2	075SW3_ECOLI	075sw3 escherichia
43	21	21.6	10	2	07MOK7_RHOSO	07mok7 rhodococcus
44	21	21.6	10	2	09QVE9_9MURI	09qve9 mus sp. pro
45	21	21.6	11	2	08KTN1_CANTP	08ktn1 candidatus

## ALIGNMENTS

```

RESULT 1
046473 FELCA PRELIMINARY; PRT; 17 AA.
ID 046473 FELCA PRELIMINARY; PRT; 17 AA.
AC 046473;
DT 01-JUN-1998 (TRENBLREL. 06, Created)
DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Lactase dehydrogenase A (Fragment).
GN Name-LDHA;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=domesticus;
RX MEDLINE=97141918; PubMed=8988168;
RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,
RT O'Brien S.J.;
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of
RT mammalian genomes.";
RL Nat. Genet. 15:47-56(1997).
DR EMBL; AF012095; AAC00072.2; -; Genomic_DNA.
FT NON TER 1
FT NON TER 17
SQ SEQUENCE 17 AA; 2018 MM; E47943B2E187C1FC CRC64;
Query Match 35.1%; Score 34; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 3 GQKATNIPFYTAFTK 15
Db 3 GQKATNIPFYTAFTK 15
QY 3 GQKATNIPFYTAFTK 15
Db 3 GQKATNIPFYTAFTK 15
RESULT 2
070Y88_9LAMI PRELIMINARY; PRT; 8 AA.
ID 070Y88_9LAMI PRELIMINARY; PRT; 8 AA.
AC 070Y88;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rp816;
OS Platostoma fimbriatum.
OC Chlorofila.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platanostoma.
OX NCBI_TaxID=204168;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;  
 RA Paton A., Springate D.A., Suda S., Otleno D., Grayer R., Harley M.M.,  
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.,  
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)  
 based on three plastid DNA regions";  
 RL Mol. Phylogenet. Evol. 31:277-299(2004).  
 DR EMBL, AJ505368; CAD45489.1; -, Genomic DNA.  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 769 MW; 86786772D1BB4772 CRC64;

Query Match 33.0%; Score 32; DB 2; Length 8;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16  
 Db 2 PYTVP 7

## RESULT 3

Q9TWL4\_LUCCU  
 ID Q9TWL4\_LUCCU PRELIMINARY; PRT; 18 AA.  
 AC Q9TWL4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE 25 kDa chymotrypsin-like enzyme (Fragment)  
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Cecidoidea;  
 OC Calliphoridae; Lucilia.  
 OX NCBI\_Taxid=7375;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA MEDLINE=95219141; PubMed=7704304;  
 RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,  
 RA Telling R.L.;  
 RT "Excretory/secretory chymotrypsin from *Lucilia cuprina*: purification,  
 RT enzymatic specificity and amino acid sequence deduced from mRNA.";  
 RL Insect Mol. Biol. 3:201-211(1994).  
 SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126511 CRC64;

Query Match 29.4%; Score 28.5; DB 2; Length 18;  
 Best Local Similarity 58.3%; Pred. No. 1.9e+03;  
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 DQKAT-NIRPY 12  
 Db 3 NQGEATVGQFPY 14

## RESULT 4

Q8LIY7\_PLEBO  
 ID Q8LIY7\_PLEBO PRELIMINARY; PRT; 16 AA.  
 AC Q8LIY7;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Proteolysis-inducing tag (Fragment).  
 OS Plectonema boryanum.  
 OC Bacteria; Cyanobacteria; Oscillatoriales; Leptolyngbya.  
 OX NCBI\_Taxid=1184;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA STRAIN=UTEX 485;  
 RX MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;  
 RA Williams K.P.;  
 RT "Descent of a split RNA."  
 RL Nucleic Acids Res. 30:2025-2030(2002).  
 DR EMBL, AY082652; AAM03311.1; -, Genomic DNA.

FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1640 MW; 60FE5985B9B00982 CRC64;  
 Query Match 28.4%; Score 27.5; DB 2; Length 16;  
 Best Local Similarity 53.8%; Pred. No. 2.5e+03;  
 Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 6 ATNIPY--TAP 15  
 Db 1 ANNIVFPARKTAP 13

## RESULT 5

Q7M4Y7\_FUSSP  
 ID Q7M4Y7\_FUSSP PRELIMINARY; PRT; 15 AA.  
 AC Q7M4Y7;  
 DT 01-MAR-2004 (TREMBlrel. 26, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Phenotypic variation protein (Fragment).  
 OS Fusarium sporotrichioides.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
 OX NCBI\_Taxid=5514;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Chow I.P., Fukaya N., Sugiyura Y., Ueno Y., Tabuchi K., Tsugita A.;  
 RL Submitted (OCT-1994) to the PIR data bank.  
 DR PIR; PA0099; PA0099.  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1648 MW; 4CAFAF966995807 CRC64;

Query Match 27.8%; Score 27; DB 2; Length 15;  
 Best Local Similarity 62.5%; Pred. No. 2.8e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPTAPGT 17  
 Db 7 FKYSASGT 14

## RESULT 6

Q7M4W6\_FLAVE  
 ID Q7M4W6\_FLAVE PRELIMINARY; PRT; 18 AA.  
 AC Q7M4W6;  
 DT 01-MAR-2004 (TREMBlrel. 26, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Protein P11 (Fragment).  
 OS Flammulina velutipes.  
 OC Agaricales; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Agaricales; Tricholomataceae; Flammulina.  
 OX NCBI\_Taxid=38945;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Sakamoto Y., Ando A., Tamai Y., Miura K.;  
 RL Submitted (NOV-1999) to the PIR data bank.  
 DR PIR; A59137; A59137.  
 FT NON\_TER 1  
 FT NON\_TER 18  
 SQ SEQUENCE 18 AA; 1956 MW; FB0434B0AF005AEC CRC64;

Query Match 27.8%; Score 27; DB 2; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15  
 Db 2 PYTSP 6

## RESULT 7

```

Q7S007_NEUCR
ID Q7S007_NEUCR PRELIMINARY; PRT; 15 AA.
AC Q7S007;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU09752.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
ON NCU1_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Gajagan J.E., Galvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-Y., Smirnov S., Purcell S., Rehman B.,
RA Elvine T., Engels R., Wang S., Nielsen C.B., Butler J., Enditzzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seiltrennkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Steben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanwaseelis M., Maucelli E., Bielke C., Rudd S., Frisman D.,
RA Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Narvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nudbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RC Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABX01000580; EAA28619.1; -; Genomic_DNA.
DR EMBL; AABX01000580; EAA28619.1; -; Genomic_DNA.
SQ SEQUENCE 15 AA; 1832 MW; 012D0180A8C7089D CRC64;

Query Match 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIPPYT 13
|:|:|
Db 2 NVFEXT 7

RESULT 8
Q7M198_STRFR PRELIMINARY; PRT; 18 AA.
ID Q7M198_STRFR PRELIMINARY;
AC Q7M198;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
ON NCU1_TaxID=1906;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=92155439; PubMed=178659; DOI=10.1016/0020-711X(91)90133-8;
RA Silha U., Moitz S.A., Lad P.J.;
RT "Two new extracellular serine proteases from Streptomyces fradiae.";
RL Int. J. Biochem. 23:979-984(1991).
DR PIR; A61577; A61577.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 VDQKATNIPY 12
|:|:|
Db 2 VGTTRAAQEPFW 13

RESULT 9
Q9UR63_EMEMI PRELIMINARY; PRT; 15 AA.
ID Q9UR63_EMEMI PRELIMINARY;
AC Q9UR63;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
DE isoform (EC 3.2.1.26) (Fragment).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
ON NCU1_TaxID=162425;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;
RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;
RT "Purification and partial characterization of the high and low
RT molecular weight form (S- and F-form) of invertase secreted by
RT Aspergillus nidulans.";
RL Biochim. Biophys. Acta 1296:207-218(1996).
DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAP 15
|:|:|
Db 10 PYTSP 14

RESULT 10
Q714T5_9CRYP PRELIMINARY; PRT; 14 AA.
ID Q714T5_9CRYP PRELIMINARY;
AC Q714T5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE tRNA proceolysis tag (Fragment).
GN Name=sstrA;
OS Rhodomonas salina.
OC Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
ON NCU1_TaxID=52970;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCMP1319;
RX PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Guenau de Novoa P., Williams K.P.;
RT "The tRNA website: reductive evolution of tRNA in plastids and other
RT endosymbionts.";
RL Nucleic Acids Res. 32:D104-D108(2004).
DR EMBL; AF550355; AAQ12671.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATNIFPYT 13
|:|:|
Db 1 ANNVIFFS 8

RESULT 11

```

069142\_STRPY  
 ID 069142\_STRPY PRELIMINARY; PRT; 15 AA.  
 AC 069142;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Protein SIC (Fragment).  
 GN Name=SIC;  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=API;  
 RX MEDLINE=98298075; PubMed=9632622;  
 RA Berge A., Rasmussen M., Bjorck L.;  
 RT "Identification of an insertion sequence located in a region encoding  
 RT virulence factors of Streptococcus pyogenes.";  
 RL Infect. Immun. 66:3449-3453 (1998).  
 DR EMBL; AF064540; AAC38769.1; -; Genomic\_DNA.  
 FT NON TER 1  
 SQ SEQUENCE 15 AA; 1552 MW; 87655FEF847401FF CRC64;

Query Match 24.7%; Score 24; DB 2; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 8.9e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 NIFPYTAPGT 17  
 : : | | | |  
 Db 6 SVTPYTPSAT 15

RESULT 12  
 ID 065YZ6\_HORSE PRELIMINARY; PRT; 17 AA.  
 AC 065YZ6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Asparagine-linked glycosylation 8 homolog (Fragment).  
 GN Name=ALG8;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hasegawa T., Sato F., Tozaki T., Hirota K.;  
 RT "Fine mapping of equine chromosomes corresponding to HSA11.";  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB167785; BAD4704.1; -; Genomic\_DNA.  
 FT NON TER 1  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1907 MW; 24AB4757508FF8FC CRC64;

Query Match 24.7%; Score 24; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 1e+04;  
 Matches 5; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

QY 8 NIFP--YTAP 15  
 : : | | | |  
 Db 6 SLFPLFLTPAP 15

RESULT 13  
 ID 05ZEY7\_HUMAN PRELIMINARY; PRT; 8 AA.  
 AC 05ZEY7;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Taxol resistance associated gene 3 (Fragment).

GN Name=CSAG2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Dominguez O., Lombardía L.;  
 RT "DNA probes built and sequenced for microarray hybridisations.";  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ844639; CAH59758.2; -; mRNA.  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 742 MW; 9975B87321A86772 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18  
 : : | | | |  
 Db 2 PGTK 5

RESULT 14  
 ID 09ZIB1\_CLODI PRELIMINARY; PRT; 10 AA.  
 AC 09ZIB1;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE Toxin B (Fragment).  
 GN Name=ToxB;  
 OS Clostridium difficile.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1496;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=8864;  
 RA Dodson A.P., Borriello S.P.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF035716; AAD02038.1; -; Genomic\_DNA.  
 FT NON TER 1  
 SQ SEQUENCE 10 AA; 1120 MW; 913DA042C736DDC1 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTA 14  
 : : | | | |  
 Db 1 PYTA 4

RESULT 15  
 ID P78359\_HUMAN PRELIMINARY; PRT; 14 AA.  
 AC P78359;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NF-kappa-B transcription factor p65 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Unlabeled vein;  
 RA Remacle J.E., Byrs R., Pype S., Nelles L., Huybrecock D.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U88316; AAB48487.1; -; mRNA.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query March 23.7%; Score 23; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. NO. 1.2e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 IFPYTAP 15  
||| : |  
Db 8 IFPQSQP 14

Search completed: December 12, 2005, 21:23:54  
Job time : 63.6667 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using SW model

Run on: December 12, 2005, 19:37:19 ; Search time 97.6034 Seconds  
(without alignments)  
81.030 Million cell updates/sec

Title: US-10-758-165a-9  
Perfect score: 97  
Sequence: 1 VDGQKATNIPYPATGTK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003s:\*
- 7: geneseqp2003s:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0609	Adt10609 Dog IGE e
2	97	100.0	312	AAV79995	Aay79995 Dog immun
3	97	100.0	417	AAW23067	Aaw23067 Canine Ig
4	97	100.0	426	AAr97753	Aar97753 Canine Ig
5	97	100.0	426	ABP96583	Abp96583 Dog IGE h
6	87	89.7	18	ADRI0610	Adt10610 Cat IGE e
7	87	89.7	431	ADG73237	Adg73237 Cat immun
8	87	89.7	496	ABP96580	Abp96580 Cat IGE h
9	87	89.7	496	ABU09338	Abu09338 Feline Ig
10	87	89.7	496	ABU09336	Abu09336 Feline Ig
11	87	89.7	496	ADG73251	Adg73251 Cat parti
12	87	89.7	577	ADG73225	Adg73225 Cat parti
13	75.3	75.3	6	ABP96584	Abp96584 Duckbille
14	68	70.1	343	AA060204	Aa060204 Platyphus
15	58	59.8	337	ADP90022	Adp90022 Opossum-r
16	58	59.8	337	ADN00643	Adn00643 ORO prote
17	58	59.8	338	ADP90025	Adp90025 Opossum-h
18	58	59.8	341	ADN00646	Adn00646 OSO prote
19	58	59.8	341	AA060206	Aa060206 Opossum-h
20	58	59.8	341	AA031644	Aa031644 Opossum I
21	58	59.8	341	AA060208	Aa060208 Immunogen
22	58	59.8	342	AA060205	Aa060205 Immunogen
23	58	59.8	345	AA060207	Aa060207 Immunogen
24	58	59.8	347	ADP90033	Adp90033 Opossum-h

25	58	59.8	347	8	ADN00654	Adn00654 OSO-H pro
26	58	59.8	353	8	ADN00661	Adn00661 H-OCO-H p
27	58	59.8	427	6	ABP96591	Abp96591 Bruchta11
28	58	59.8	446	6	ABP96587	Abp96587 Opossum I
29	58	59.8	555	8	ADP90027	Adp90027 Opossum-r
30	58	59.8	555	8	ADN00648	Adn00648 ORO pro
31	58	59.8	557	8	ADP90031	Adp90031 Opossum-h
32	58	59.8	557	8	ADP90035	Adp90035 Opossum-h
33	58	59.8	557	8	ADN00656	Adn00656 OSO pro
34	58	59.8	557	8	ADN00652	Adn00652 modOSO
35	58	59.8	566	8	ADP90029	Adp90029 Opossum-h
36	58	59.8	566	8	ADP90037	Adp90037 Opossum-h
37	58	59.8	566	8	ADN00658	Adn00658 OSO-H p
38	58	59.8	566	8	ADN00650	Adn00650 modOSO-H
39	55	56.7	18	8	ADRI0612	Adt10612 Sheep IGE
40	55	56.7	567	6	ABP96588	Abp96588 Pig IGE h
41	53	54.6	341	3	AA060202	Aa060202 Immunogen
42	53	54.6	342	3	AA060201	Aa060201 Immunogen
43	46	47.4	135	2	AAV76530	Aay76530 Human ova
44	46	47.4	135	7	ABO81258	Ab081258 Pseudomon
45	46	47.4	386	8	ADU00341	Adu00341 Iron hydr

## ALIGNMENTS

RESULT 1  
ADRI0609  
ID ADRI0609 standard; peptide, 18 AA.  
XX  
AC ADRI0609;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.  
XX  
KM Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
OS Canis familiaris.  
XX  
FN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
PA (UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
XX WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
XX Example 6; Page 9; 14pp; English.  
XX  
XX The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine IGE corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IgB from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE.  
 XX

SO Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIFPYTAPGTK 18  
 1 VDGOKATNIFPYTAPGTK 18  
 Db

RESULT 2  
 AAY79995

ID AAY79995 standard; protein; 312 AA.

AC AAY79995;

DT 15-MAY-2000 (first entry)

XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Canis sp.

PN WO967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US013959.

PR 20-JUN-1998; 98US-00100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

PS Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

SO Sequence 312 AA;

Query Match

Best Local Similarity 100.0%; Score 97; DB 3; Length 312;  
 100.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIFPYTAPGTK 18  
 1 VDGOKATNIFPYTAPGTK 18  
 Db 48 VDGOKATNIFPYTAPGTK 65

RESULT 3  
 AAW23067  
 ID AAW23067 standard; protein; 417 AA.

AC AAW23067;

DT 30-JUN-2005 (revised)

DT 16-JUN-2005 (revised)

DT 19-FEB-1998 (first entry)

DE Canine IgE heavy chain constant region (exon 1-4 product).

XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;  
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

OS Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEXX LAB INC.

XX Mermer B, Harris RA, Siefing AB;

XX WPI; 1997-425031/39.

XX N-PSDB; AAT79278.

XX Isolated canine IgE heavy chain constant region DNA - useful to develop  
 PT products for treatment of canine allergies and for immunomodulation in  
 PT dogs.

PS Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE  
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,  
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant  
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or  
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are  
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to  
 CC treat type I immediate hypersensitivity, and for immunomodulation



CC Revised record issued on 30-JUN-2005 : Typo in comments  
XX  
SQ Sequence 417 AA;

Query Match 100.0%; Score 97; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VDGQKATNIPFYTAAGTK 18  
|||  
Db 141 VDGQKATNIPFYTAAGTK 158

RESULT 4  
AAR97753  
ID AAR97753 standard; protein; 426 AA.

XX AAR97753;

DT 28-AUG-1996 (first entry)

XX Canine IGE.

XX IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.

XX Canis familiaris.

XX WO9614867-A1.

XX 23-MAY-1996.

XX 03-NOV-1995; 95WO-US013795.

XX 09-NOV-1994; 94US-00336583.

XX 09-NOV-1994; 94US-00336891.

XX (MERI ) MERCK & CO INC.

XX HOLLIS GF, Patel MD;

XX WPI; 1996-277321/28.

XX N-PSDB; AAT29824.

XX New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense

XX therapy, assays, drug screening, etc.

XX Claim 11; Page 29-30; 49pp; English.

XX The canine IGB amino acid sequence (AAR97753) was deduced from an

XX isolated gene (AAT29824) obt'd. from a canine liver DNA library. The

XX cloning of the IGB gene allows prodn. of large quantities of recombinant

XX IGB using bacterial, yeast, mammalian, insect or viral systems. The IGB

XX development and anti-IGB antibody generation (e.g. small molecule screening, assay

XX can be used in drug development (e.g. small molecule screening, assay

XX used in vaccines or to prevent IGB-mediated hypersensitivity. The new

XX sequence information permits targeted modulation of IGB-mediated immune

XX response

XX Sequence 426 AA;

Query Match 100.0%; Score 97; DB 2; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VDGQKATNIPFYTAAGTK 18  
|||  
Db 146 VDGQKATNIPFYTAAGTK 163

RESULT 5  
ABP96583  
ID ABP96583 standard; protein; 426 AA.

AC ABP96583;  
XX  
XX 28-MAY-2003 (first entry)  
XX

Dog IGE heavy chain amino acid sequence SEQ ID NO:28.

XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
XX immune response; major histocompatibility complex; MHC; immunogenic;  
XX antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;  
XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;  
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
XX urticaria hives.

XX Canis familiaris.

XX WO2003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGBT-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
against IGE, by identifying peptide eliciting CTL response to IGE  
peptides naturally presented by major histocompatibility complex class I  
protein.

Example 7; Page 152-154; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides  
XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
XX E (IGE), comprising providing a test peptide (T) suspected of being able  
XX to bind to major histocompatibility complex (MHC) class I molecule, and  
XX evaluating (T) for ability to elicit in a mammal a CTL response to  
XX naturally processed and presented IGE peptides, where a peptide that  
XX induces such a response is identified. Also described are compositions:  
XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
XX (C2) comprising at least one isolated polynucleotide encoding (I); and  
XX (C3) comprising antigen-presenting cells that recognise at least one (I).  
XX Where C1-3 are able to bind to at least one MHC class I molecule and to  
XX elicit in a mammal a CTL response to naturally processed and presented  
XX IGE peptides, C1-3 have antiallergic, antiaesthetic, immunosuppressive,  
XX vasotropic, dermatological, antiinflammatory and cytostatic activities,  
XX and can be used as inducers of a CTL response against IGE, and in  
XX vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
XX mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
XX IGE-mediated atopic hypersensitivity condition. IGE-mediated non-atopic  
XX hypersensitivity condition. IGE myeloma in a mammal. Preferably, C1-3 are  
XX useful for treating atopic hypersensitivity conditions (such as allergic  
XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
XX hives). The present sequence represents an IGE heavy chain amino acid  
XX sequence, which is given in an example from the present invention

XX Sequence 426 AA;

Query Match 100.0%; Score 97; DB 6; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VDGQKATNIPFYTAAGTK 18  
|||  
Db 146 VDGQKATNIPFYTAAGTK 163

```

RESULT 6
ADRI0610
ID   ADRI0610 standard; peptide; 18 AA.
XX
AC   ADRI0610;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.
XX
KM   Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KM   anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KM   cat.
XX
OS   Felis catus.
XX
PN   WO2004065936-A2.
XX
PD   05-AUG-2004.
XX
PF   15-JAN-2004; 2004WO-US003566.
XX
PR   16-JAN-2003; 2003US-0440472P.
XX
PA   (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI   Hammerberg B;
XX
DR   WPI; 2004-593545/57.
XX
PT   Novel antibody that specifically binds to mammalian IGE epitope, useful
PT   for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT   or treating asthma or anaphylactic shock.
XX
PS   Example 6; Page 9; 14pp; English.
XX
CC   The present invention relates to a novel monoclonal antibody (I) that
CC   specifically binds to a mammalian IGE epitope, where the epitope is
CC   between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC   (I) is useful for testing an allergen reactivity of an IGE sample. The
CC   allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC   and corn allergens. The sample is a biological sample collected from a
CC   dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC   treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC   antibodies recognise epitopes on canine IGE corresponding to amino acid
CC   residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC   canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC   cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC   3.76 were observed to have good cross-reactivity with the epsilon-chain
CC   of IGE from cat and horse, but did not exhibit cross-reactivity with
CC   either pig or human epsilon-chains of IGE. The present sequence is the
CC   cat IGE 3.76 recognition site.
XX
SQ   Sequence 18 AA;
XX
Query Match      89.7%; Score 87; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 VDGOKATNIFPYTPAG 16
    1 VDGOKATNIFPYTPAG 16
DB   1 VDGOKATNIFPYTPAG 16

```

```

XX
KM   antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
KM   immune response; IGE-mediated response; allergy; cat; constant region.
XX
OS   Felis catus.
XX
PN   US2003216565-A1.
XX
PD   20-NOV-2003.
XX
PF   07-APR-2003; 2003US-00409772.
XX
PR   07-JAN-1999; 99US-0115033P.
XX
PR   07-JAN-2000; 2000US-00479614.
XX
PA   (MCCA/) MCCALL C.
XX
PA   (WEBE/) WEBER E.
XX
PI   Mccall C, Weber E;
XX
DR   WPI; 2004-010802/01.
XX
DR   N-PSDB; ADG73236.
XX
PT   New isolated nucleic acid molecule encoding a portion of a feline IGE
PT   heavy chain protein, useful for treating and/or eliciting feline immune
PT   responses for IGE-mediated responses, such as allergies.
XX
PS   Claim 12; SEQ ID NO 14; 44pp; English.
XX
CC   The invention describes an isolated nucleic acid molecule (I) encoding a
CC   portion of a feline IGE heavy chain protein. The methods and compositions
CC   of the present invention are useful for eliciting feline immune responses
CC   for and/or treating IGE-mediated responses, such as allergies. This is
CC   the amino acid sequence of a cat immunoglobulin E (IGE) constant region.
XX
SQ   Sequence 431 AA;
XX
Query Match      89.7%; Score 87; DB 8; Length 431;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 VDGOKATNIFPYTPAG 16
    1 VDGOKATNIFPYTPAG 16
DB   151 VDGOKATNIFPYTPAG 166

```

```

RESULT 8
ABP96580
ID   ABP96580 standard; protein; 496 AA.
XX
AC   ABP96580;
XX
DT   28-MAY-2003 (first entry)
XX
DE   Cat IGE heavy chain amino acid sequence SEQ ID NO:25.
XX
KM   Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KM   immune response; major histocompatibility complex; MHC; immunogenic;
KM   antiallergic; antiasthmatic; immunosuppressive; vasodilator; cytostatic;
KM   dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KM   atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KM   atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KM   urticaria hives.
XX
OS   Felis catus.
XX
PN   WO2003015716-A2.
XX
PD   27-FEB-2003.
XX
PF   08-AUG-2002; 2002WO-US026986.
XX
PR   13-AUG-2001; 2001US-0312120P.

```

(IGET-) IGE THERAPEUTICS INC.

Chen Sa, Yang Y, Barankiewicz T, Chen Z;  
WPI; 2003-268242/26.

Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I protein.

Example 7; Page 145-147; 187pp; English.

The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E (IgE), comprising providing a test peptide ('T') suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating ('V') for ability to elicit in a mammal a CTL response to naturally processed and presented IgE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I). Where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotrophic, dermatological, antiinflammatory and cyostatic activities, and can be used as inducers of a CTL response against IgE, and in vaccines. C1-3 can be used for modulating an IGE-mediated condition in a mammal. C1-3 are useful for modulating an IGE-mediated condition such as IGE-mediated atopie hypersensitivity condition, IGF-mediated non-atopic hypersensitively condition, Ige myeloma in a mammal. Preferably, C1-3 are useful for treating atopie hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopie dermatitis), non-atopie hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an IGE heavy chain amino acid sequence, which is given in an example from the present invention

Sequence 496 AA;

SQ  
XX  
Query March 89.7%; Score 87; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred.No. 9.6e+06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY           1 VDGKATNIFPYTAGG 16  
       |||||  
Db          216 VDGGKATNIFFYTARG 231  
            |||||||

RESULT 9  
ID ABUO9338 standard; protein; 496 AA.  
AC ABUO9338;  
XX  
DT 27-JUN-2003 (first entry)  
DE Feline IGE epsilon heavy chain #2.  
XX  
Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
KM antibody technology; antiallergic; antiparasitic; cystostatic.  
OS Felis catus.  
XS US2003013183-A1.  
PN  
PD 16-JAN-2003.  
XX  
PF 07-JAN-2000; 2000US-00479614.  
PR 07-JAN-1999; 99US-0115033P.

XX		
PA	(MCCA/) MCCALL C.	
XX	(WEBE/) WEBER E.	
PI	Mccall C, Weber E;	
DR	WPI; 2003-391997/37.	
N-P	PSDB; ABX95715.	
XX		
PT	New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or	
PR	light chain protein, useful for treating feline IgE-mediated responses	
XX	e.g. allergies, parasitic infections or neoplasia.	
PS	Claim 1; Page 37-39; 45pp; English.	
XX		
CC	The present invention relates to the isolation of feline immunoglobulin E	
CC	(IgE) kappa light chain and IgE epsilon heavy chain proteins, and the	
CC	polynucleotide sequences encoding them. The sequences of the invention	
CC	are useful for treating feline IgE-mediated immune responses (e.g.	
CC	allergies, parasitic infections or neoplasia), in vaccine technology,	
CC	small molecule/antibody technology, molecular biology, and various	
CC	immunological techniques related to feline IgE and its functions. The	
CC	present sequence represents feline IgE epsilon heavy chain #2	
XX		
SO	Sequence 496 AA:	
	Query Match	89.7%; Score 87; DB 6; Length 496;
	Best Local Similarity	100.0%; Pred. No. 9,6e-06;
Oy	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	1 VDSGKATNIPFYTAG 16	
Db	216 VDGGKATNIPFYTAG 231	
	RESULT 10	
ABU09336		
ID	ABU09336 standard; protein; 496 AA.	
XX		
AC	ABU09336;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Feline IgE epsilon heavy chain #1.	
XX		
KW	Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;	
KW	IgE-mediated immune response; allergy; neoplasia; vaccine technology;	
XX	antibody technology; antiallergic; antiparasitic; cytostatic.	
OS	Felis catus.	
XX		
PH	Key	Location/Qualifiers
FT	Region	66..496
FT	/note= "This sequence is given as SEQ ID No:14 and is	
FT	specifically claimed in Claim 12"	
FT	Region	284..309
FT	/note= "This sequence is given as SEQ ID No:11 and is	
FT	specifically claimed in Claim 9"	
FT	Region	288..305
FT	/note= "This sequence is given as SEQ ID No:8 and is	
FT	specifically claimed in Claim 10"	
FT	Region	291..302
FT	/note= "This sequence is given as SEQ ID No:5 and is	
FT	specifically claimed in Claim 11"	
PN	US2003013183-A1.	
XX		
PD	16-JAN-2003.	
XX		
PF	07-JAN-2000; 2000US-00479614.	
XX		
PR	07-JAN-1999; 99US-0115033P.	
XX		

PA (MCCA/) MCCA.L C.  
PA (WEBE/) WEBER E.  
XX  
XX Mccall C, Weber E;  
XX  
DR WPI: 2003-391997/37.  
DR N-PSDB; ABX95713.  
XX  
XX New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or  
PT light chain protein, useful for treating feline IGE-mediated responses  
PT e.g. allergies, parasitic infections or neoplasia.  
XX  
XX  
PS Claim 1; Page 24-25; 45pp; English.  
XX  
XX The present invention relates to the isolation of feline immunoglobulin E  
CC (1GE) kappa light chain and IGE epsilon heavy chain proteins, and the  
CC polynucleotide sequences encoding them. The sequences of the invention  
CC are useful for treating feline IGE-mediated immune responses (e.g.  
CC allergies, parasitic infections or neoplasia), in vaccine technology,  
CC small molecule/antibody technology, molecular biology, and various  
CC immunological techniques related to feline IGE and its functions. The  
CC present sequence represents feline IGE epsilon heavy chain #1  
XX  
SQ Sequence 496 AA;  
XX  
Query Match 89.7%; Score 87; DB 6; Length 496;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VDGQKATNIFPYTAPG 16  
Db 216 VDGQKATNIFPYTAPG 231  
XX  
RESULT 11  
ADG73251  
ID ADG73251 standard; protein; 496 AA.  
XX  
AC ADG73251;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Cat partial immunoglobulin E (IGE) heavy chain #2.  
XX  
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;  
KM immune response; IGE-mediated response; allergy; cat; heavy chain.  
XX  
XX Felis catus.  
XX  
XX US2003216565-A1.  
XX  
XX 20-NOV-2003.  
XX  
XX 07-APR-2003; 2003US-00409772.  
XX  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX (MCCA/) MCCA.L C.  
PA (WEBE/) WEBER E.  
XX  
XX Mccall C, Weber E;  
XX  
XX WPI: 2004-010802/01.  
DR N-PSDB; ADG73250.  
XX  
XX New isolated nucleic acid molecule encoding a portion of a feline IGE  
PT heavy chain protein, useful for treating and/or eliciting feline immune  
PT responses for IGE-mediated responses, such as allergies.  
XX  
XX Claim 8; SEQ ID NO 29; 44pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a

CC portion of a feline IGE heavy chain protein. The methods and compositions  
CC of the present invention are useful for eliciting feline immune responses  
CC for and/or treating IGE-mediated responses, such as allergies. This is  
CC the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy  
CC chain.  
XX  
XX  
SQ Sequence 496 AA;  
XX  
Query Match 89.7%; Score 87; DB 8; Length 496;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VDGQKATNIFPYTAPG 16  
Db 216 VDGQKATNIFPYTAPG 231  
XX  
RESULT 12  
ADG73225  
ID ADG73225 standard; protein; 496 AA.  
XX  
AC ADG73225;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
XX Cat partial immunoglobulin E (IGE) heavy chain #1.  
XX  
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;  
KM immune response; IGE-mediated response; allergy; cat; heavy chain.  
XX  
XX Felis catus.  
XX  
XX US2003216565-A1.  
XX  
XX 20-NOV-2003.  
XX  
XX 07-APR-2003; 2003US-00409772.  
XX  
XX 07-JAN-1999; 99US-0115033P.  
XX 07-JAN-2000; 2000US-00479614.  
XX  
XX (MCCA/) MCCA.L C.  
PA (WEBE/) WEBER E.  
XX  
XX Mccall C, Weber E;  
XX  
XX WPI: 2004-010802/01.  
DR N-PSDB; ADG73224.  
XX  
XX New isolated nucleic acid molecule encoding a portion of a feline IGE  
PT heavy chain protein, useful for treating and/or eliciting feline immune  
PT responses for IGE-mediated responses, such as allergies.  
XX  
XX  
XX Claim 8; SEQ ID NO 2; 44pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
CC portion of a feline IGE heavy chain protein. The methods and compositions  
CC of the present invention are useful for eliciting feline immune responses  
CC for and/or treating IGE-mediated responses, such as allergies. This is  
CC the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy  
CC chain.  
XX  
XX  
SQ Sequence 496 AA;  
XX  
Query Match 89.7%; Score 87; DB 8; Length 496;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VDGQKATNIFPYTAPG 16  
Db 216 VDGQKATNIFPYTAPG 231

RESULT 13  
ABP96584  
ID ABP96584 standard; protein; 577 AA.  
XX  
AC ABP96584;  
XX  
DT 28-MAY-2003 (first entry)  
XX  
DE Duckbilled platypus IGE heavy chain amino acid sequence SEQ ID NO:29.  
XX  
KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
KW immune response; major histocompatibility complex; MHC; immunogenic;  
KW anti-allergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;  
KW dermatological; antiinflammatory; IGE-mediated condition; food allergy;  
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
KW urticaria hives.  
XX  
OS Ornithorhynchus anatinus.  
XX  
PN MO2003015716-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 08-AUG-2002; 2002MO-US026986.  
XX  
PR 13-AUG-2001; 2001US-0312120P.  
XX  
PA (IGET-) IGE THERAPEUTICS INC.  
XX  
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
XX  
DR WPI; 2003-268242/26.  
XX  
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
PT against IGE, by identifying peptide eliciting CTL response to IGE  
PT peptides naturally presented by major histocompatibility complex class I  
PT protein.  
XX  
PS Example 7; Page 154-157; 187pp; English.  
XX  
CC The present invention describes a method (M1) for identifying peptides  
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
CC E (IGE), comprising providing a test peptide (T) suspected of being able  
CC to bind to major histocompatibility complex (MHC) class I molecule, and  
CC evaluating (T) for ability to elicit in a mammal a CTL response to  
CC naturally processed and presented IGE peptides, where a peptide that  
CC induces such a response is identified. Also described are compositions:  
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
CC elicit in a mammal a CTL response to naturally processed and presented  
CC IGE peptides. C1-3 have anti-allergic, antiaesthetic, immunosuppressive,  
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,  
CC and can be used as inducers of a CTL response against IGE, and in  
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
CC useful for treating atopic hypersensitivity conditions (such as allergic  
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
CC hives). The present sequence represents an IGE heavy chain amino acid  
CC sequence, which is given in an example from the present invention  
XX  
SQ Sequence 577 AA;  
XX  
Query Match 75.3%; Score 73; DB 6; Length 577;  
Best Local Similarity 86.7%; Pred. No. 0.0025;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 295 VDGQKATNIFPYTAP 309  
||| ||| : ||| |||  
RESULT 14  
AAB06204  
ID AAB06204 standard; protein; 343 AA.  
XX  
AC AAB06204;  
XX  
DT 22-NOV-2000 (first entry)  
XX  
DE Platypus IGE heavy chain constant regions 2, 3 and 4.  
XX  
KW Platypus; immunoglobulin E; IGE; vaccination; infection; allergy; asthma;  
KW eczema; immunogenic peptide.  
XX  
OS Ornithorhynchus anatinus.  
XX  
PN MO200025722-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 21-OCT-1999; 99WO-SE001896.  
XX  
PR 02-NOV-1998; 98US-0106652P.  
XX  
PR 22-SEP-1999; 99US-00401636.  
XX  
PA (RESI-) RESISTENTIA PHARM AB.  
XX  
PI Hellman LT;  
XX  
DR WPI; 2000-365342/31.  
XX  
PT Immunogenic polypeptides useful for preventing the harmful effects of  
PT Immunoglobulin E in mammals.  
XX  
PS Disclosure; Fig 2; 50pp; English.  
XX  
CC The present sequence is an immunogenic peptide consisting of the heavy  
CC chain constant regions 2, 3 and 4 of the platypus IGE. It was used to  
CC construct a number of immunogenic peptides which consisted of regions of  
CC IGE from different mammals, which appear to cause a stronger polyclonal  
CC anti-self IGE response than peptides consisting of the same regions from  
CC one mammal. Immunogenic peptides, particularly those consisting of  
CC different heavy chain constant regions, can be used for vaccination in  
CC humans, against bacterial and viral infections and allergies, such as  
CC asthma, fur, pollen and food allergies and eczema  
XX  
SQ Sequence 343 AA;  
XX  
Query Match 70.1%; Score 68; DB 3; Length 343;  
Best Local Similarity 80.0%; Pred. No. 0.0099;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 61 VDGQKATNIFPYTAP 75  
||| ||| : ||| |||  
RESULT 15  
ADF90022  
ID ADF90022 standard; protein; 337 AA.  
XX  
AC ADF90022;  
XX  
DT 26-FEB-2004 (first entry)  
XX

DE Opossum-rat chimeric IGE polypeptide.  
XX IGE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;  
KW antiasthmatic; dermatological.  
XX  
XX  
OS Chimeric.  
OS Didelphis virginiana.  
OS Ratus ep.  
XX WO2003096966-A2.  
XX  
XX  
PD 27-NOV-2003.  
XX  
PF 15-MAY-2003; 2003WO-IB002503.  
XX  
XX 21-MAY-2002; 2002US-0382552P.  
XX  
XX  
PA (RESI-) RESISTENTIA PHARM AB.  
PI Lundgren M, Fuentes A, Magnusson A;  
XX  
XX  
DR WPI; 2004-042496/04.  
DR N-PSDB; ADF90020, ADF90021.  
XX  
XX  
PT New host cell comprising a nucleic acid vector comprising a  
PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or  
PT SV40 late polyadenylation sequence, useful in producing a chimeric IGE  
PT polypeptide.  
XX  
XX  
PS Claim 3; SEQ ID NO 3; 23pp; English.  
XX  
XX  
CC The present sequence is the protein sequence of an opossum CH2-rat CH3-  
CC opossum CH4 (ORO) chimeric IGE polypeptide. A vector comprising a nucleic  
CC acid encoding ORO can be used for recombinant production of this chimeric  
CC IGE in host, e.g. CHO, cells. The invention provides methods and  
CC materials related to expressing chimeric IGE proteins. Nucleic acid  
CC vectors, host cells, and methods for producing chimeric IGE polypeptides  
CC are provided. When administered to a mammal, the chimeric polypeptides  
CC can reduce the IGE antibody effects of IGE-related diseases such as  
CC asthma, allergies and eczema.  
XX  
XX  
SQ Sequence 337 AA;

Query Match 59.8%; Score 58; DB 8; Length 337;  
Best Local Similarity 76.9%; Pred. No. 0.46;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VDGOKATNRPYT 13  
|||:|:|:|  
Db 56 VDGQEAENLPYT 68

Search completed: December 12, 2005, 20:30:29  
Job time : 97.6034 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 24.5172 Seconds  
(without alignments)  
60.699 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDCGKATNIPFYTAGTK 18

Scoring table: BLOSUM62  
Gap0 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:  
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2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	108	US-09-281-760E-35	Sequence 35, Appl
2	97	100.0	312	US-09-701-623C-2	Sequence 2, Appl
3	97	100.0	426	US-08-336-583-2	Sequence 2, Appl
4	97	100.0	426	PCT-US95-13795-2	Sequence 2, Appl
5	87	89.7	431	US-09-479-614-14	Sequence 14, Appl
6	87	89.7	496	US-09-479-614-2	Sequence 2, Appl
7	87	89.7	496	US-09-479-614-29	Sequence 29, Appl
8	73	75.3	343	US-09-401-636-7	Sequence 7, Appl
9	58	59.8	341	US-09-401-636-3	Sequence 3, Appl
10	58	59.8	341	US-09-401-636-4	Sequence 4, Appl
11	58	59.8	341	US-09-401-636-6	Sequence 6, Appl
12	58	59.8	341	US-09-401-636-9	Sequence 9, Appl
13	58	59.8	341	US-09-401-636-11	Sequence 11, Appl
14	58	59.8	342	US-09-401-636-5	Sequence 5, Appl
15	58	59.8	342	US-09-401-636-8	Sequence 8, Appl
16	58	59.8	345	US-09-401-636-10	Sequence 10, Appl
17	46	47.4	135	US-09-252-991A-10004	Sequence 10004, A
18	46	47.4	497	US-10-077-699C-5	Sequence 5, Appl
19	45	46.4	350	US-09-094-103-6	Sequence 6, Appl
20	45	46.4	350	US-09-080-963-2	Sequence 2, Appl
21	45	46.4	350	US-08-947-251-2	Sequence 2, Appl
22	45	46.4	350	US-09-769-787-89	Sequence 89, Appl
23	45	46.4	358	US-09-583-110-5009	Sequence 5009, Ap
24	45	46.4	358	US-09-107-433-2960	Sequence 2960, Ap
25	45	46.4	583	5256558-4	Patent No. 5256558
26	44	45.4	121	US-09-710-279-2524	Sequence 2524, Ap
27	44	45.4	132	US-09-134-001C-4212	Sequence 4212, Ap

28	43	44.3	475	US-08-840-767-10	Sequence 10, Appl
29	43	44.3	586	5256558-2	Patent No. 5256558
30	42	43.3	557	US-09-902-540-12884	Sequence 12884, A
31	42	43.3	985	US-09-993-777-6	Sequence 6, Appl
32	42	43.3	985	US-09-993-777-66	Sequence 66, Appl
33	42	43.3	985	PCT-US96-03916-6	Sequence 6, Appl
34	42	43.3	985	PCT-US96-03916-66	Sequence 66, Appl
35	41	42.3	232	US-09-489-039A-8106	Sequence 8106, Ap
36	41	42.3	570	US-08-967-364-1	Sequence 7, Appl
37	41	42.3	570	US-08-967-364-7	Sequence 7, Appl
38	41	42.3	570	US-09-368-408-1	Sequence 1, Appl
39	41	42.3	570	US-09-368-408-7	Sequence 7, Appl
40	41	42.3	1364	US-09-252-991A-26880	Sequence 26880, A
41	40.5	41.8	464	US-09-543-681A-4924	Sequence 4924, Ap
42	40.5	41.8	608	US-09-252-991A-27624	Sequence 27624, A
43	40	41.2	63	US-09-612-402B-29	Sequence 29, Appl
44	40	41.2	63	US-09-542-520-29	Sequence 29, Appl
45	40	41.2	284	US-09-248-796A-20559	Sequence 20559, A

## ALIGNMENTS

```
RESULT 1
US-09-281-760E-35
; Sequence 35, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Wermer, Brian
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81)..(81)
; OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,
; OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82)..(82)
; OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
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FEATURE:
NAME/KEY: misc feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-35
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Query Match 100.0%; Score 97; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.2e-08;

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Qy 1 VDGOKATNIFPYTAPGK 18
Db 47 VDGOKATNIFPYTAPGK 64
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## RESULT 2

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US-09-701-623C-2
Sequence 2, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION:
APPLICANT: Wang Ph.D., Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: Dog
FEATURE:
OTHER INFORMATION: CH2CH3n of dog IgE
PUBLICATION INFORMATION:
AUTHORS: Patel,
JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
DATE: 1995
US-09-701-623C-2
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Query Match 100.0%; Score 97; DB 2; Length 312;

Best Local Similarity 100.0%; Pred. No. 1e-07;

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Qy 1 VDGOKATNIFPYTAPGK 18
Db 48 VDGOKATNIFPYTAPGK 65
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RESULT 3
US-08-336-583-2
Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,583

FILING DATE: 09-NOV-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: CARTY, CHRISTINE E.

REGISTRATION NUMBER: 36,099

REFERENCE/DOCKET NUMBER: 19211

TELEPHONE: (908) 594-6734

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 426 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-336-583-2

Query Match 100.0%; Score 97; DB 1; Length 426;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

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Qy 1 VDGOKATNIFPYTAPGK 18
Db 146 VDGOKATNIFPYTAPGK 163
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## RESULT 4

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PCT-US95-13795-2
Sequence 2, Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:



```

; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match          100.0%; Score 97; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 18
Db      146 VDGQKATNIPFYTAG 163

RESULT 5
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-479-614-14

Query Match          89.7%; Score 87; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 16
Db      151 VDGQKATNIPFYTAG 166

RESULT 6
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-479-614-2

Query Match          89.7%; Score 87; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 16
Db      216 VDGQKATNIPFYTAG 231

RESULT 7
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-479-614-29

Query Match          89.7%; Score 87; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 16
Db      216 VDGQKATNIPFYTAG 231

RESULT 8
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-7

Query Match          75.3%; Score 73; DB 2; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.00079;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 15

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Db          61 VDGQKAEHLFPYTP 75

RESULT 9
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match          59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 VDGQKATNIFPYT 13
          |||||:|:||||
Db          62 VDGQEAENLFPYTP 74

RESULT 10
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match          59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 VDGQKATNIFPYT 13
          |||||:|:||||
Db          62 VDGQEAENLFPYTP 74

RESULT 11
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

Query Match          59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 VDGQKATNIFPYT 13
          |||||:|:||||
Db          62 VDGQEAENLFPYTP 74

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match          59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY          1 VDGQKATNIFPYT 13
          |||||:|:||||
Db          62 VDGQEAENLFPYTP 74

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match          59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-11

Query Match 59.8%; Score 58; DB 2; Length 341;  
Best Local Similarity 76.9%; Pred. No. 0.2;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYT 13  
|||:|:|:|  
Db 62 VDGQEAENLFPHYT 74

## RESULT 14

US-09-401-636-5  
; Sequence 5, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401,636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-5

Query Match 59.8%; Score 58; DB 2; Length 342;  
Best Local Similarity 76.9%; Pred. No. 0.2;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYT 13  
|||:|:|:|  
Db 62 VDGQEAENLFPHYT 74

## RESULT 15

US-09-401-636-8  
; Sequence 8, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401,636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-8

Query Match 59.8%; Score 58; DB 2; Length 342;  
Best Local Similarity 76.9%; Pred. No. 0.2;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYT 13  
|||:|:|:|  
Db 62 VDGQEAENLFPHYT 74

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 80.3793 Seconds  
(without alignments)  
93.568 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGQKATNIFPYTAPGTK 18

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-9
2	97	100.0	426	4	US-10-214-524-28
3	87	89.7	18	5	US-10-758-165-10
4	87	89.7	431	3	US-09-479-614-14
5	87	89.7	431	4	US-10-409-772-14
6	87	89.7	496	3	US-09-479-614-2
7	87	89.7	496	3	US-09-479-614-29
8	87	89.7	496	4	US-10-214-524-25
9	87	89.7	496	4	US-10-409-772-2
10	87	89.7	496	4	US-10-409-772-29
11	73	75.3	343	3	US-09-401-636-7
12	73	75.3	343	4	US-10-176-664-7
13	73	75.3	343	4	US-10-673-594-7
14	73	75.3	577	4	US-10-214-524-29
15	58	59.8	337	4	US-10-438-794-3
16	58	59.8	337	4	US-10-453-915-3
17	58	59.8	338	4	US-10-438-794-6
18	58	59.8	338	4	US-10-453-915-6
19	58	59.8	341	3	US-09-401-636-3
20	58	59.8	341	3	US-09-401-636-4
21	58	59.8	341	3	US-09-401-636-6
22	58	59.8	341	3	US-09-401-636-9
23	58	59.8	341	3	US-09-401-636-11
24	58	59.8	341	4	US-10-176-664-3
25	58	59.8	341	4	US-10-176-664-4
26	58	59.8	341	4	US-10-176-664-6
27	58	59.8	341	4	US-10-176-664-9

28	58	59.8	341	4	US-10-176-664-11	Sequence 11, Appli
29	58	59.8	341	4	US-10-673-594-3	Sequence 3, Appli
30	58	59.8	341	4	US-10-673-594-4	Sequence 4, Appli
31	58	59.8	341	4	US-10-673-594-6	Sequence 6, Appli
32	58	59.8	341	4	US-10-673-594-9	Sequence 9, Appli
33	58	59.8	341	4	US-10-673-594-11	Sequence 11, Appli
34	58	59.8	342	3	US-09-401-636-5	Sequence 5, Appli
35	58	59.8	342	3	US-09-401-636-8	Sequence 8, Appli
36	58	59.8	342	4	US-10-176-664-5	Sequence 5, Appli
37	58	59.8	342	4	US-10-176-664-8	Sequence 8, Appli
38	58	59.8	342	4	US-10-673-594-5	Sequence 5, Appli
39	58	59.8	342	4	US-10-673-594-8	Sequence 8, Appli
40	58	59.8	345	3	US-09-401-636-10	Sequence 10, Appli
41	58	59.8	345	4	US-10-176-664-10	Sequence 10, Appli
42	58	59.8	345	4	US-10-673-594-10	Sequence 10, Appli
43	58	59.8	347	4	US-10-438-794-14	Sequence 14, Appli
44	58	59.8	347	4	US-10-453-915-14	Sequence 14, Appli
45	58	59.8	353	4	US-10-453-915-21	Sequence 21, Appli

ALIGNMENTS

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RESULT 1
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN B DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match      100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 9; ie-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VDGQKATNIFPYTAPGTK 18
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Db      1 VDGQKATNIFPYTAPGTK 18

RESULT 2
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN B VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICB-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
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US-10-214-524-28

Query Match 100.0%; Score 97; DB 4; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAGTK 18  
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DB 146 VDGOKATNIPYTPAGTK 163

RESULT 3

US-10-758-165-10  
; Sequence 10, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammetberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-10

Query Match 89.7%; Score 87; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAG 16  
|||||  
DB 1 VDGOKATNIPYTPAG 16

RESULT 4

US-09-479-614-14  
; Sequence 14, Application US/09479614  
; Publication No. US2003003183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-14

Query Match 89.7%; Score 87; DB 3; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAG 16  
|||||  
DB 151 VDGOKATNIPYTPAG 166

RESULT 5

US-10-409-772-14  
; Sequence 14, Application US/10409772

; Publication No. US20030216565A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/10/409,772  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/479,614  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-409-772-14

Query Match 89.7%; Score 87; DB 4; Length 431;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAG 16  
|||||  
DB 151 VDGOKATNIPYTPAG 166

RESULT 6

US-09-479-614-2  
; Sequence 2, Application US/09479614  
; Publication No. US2003003183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-2

Query Match 89.7%; Score 87; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAG 16  
|||||  
DB 216 VDGOKATNIPYTPAG 231

RESULT 7

US-09-479-614-29  
; Sequence 29, Application US/09479614  
; Publication No. US2003003183A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 29

LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-09-479-614-29

Query Match 89.7%; Score 87; DB 3; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16  
|||  
Db 216 VDGQKATNIPFYTAG 231

RESULT 8  
US-10-214-524-25  
Sequence 25, Application US/10214524  
Publication No. US20030073142A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Swei-Shen Alex  
APPLICANT: Yang, Yong-Min  
APPLICANT: Barankiewicz, Theresa J.  
APPLICANT: Chen, Zhong  
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF  
FILE REFERENCE: IGE-00101.P.1.1  
CURRENT APPLICATION NUMBER: US/10/214,524  
CURRENT FILING DATE: 2002-08-08  
PRIOR APPLICATION NUMBER: 60/312,120  
PRIOR FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 25  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Cat (Felis catus)  
US-10-214-524-25

Query Match 89.7%; Score 87; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16  
|||  
Db 216 VDGQKATNIPFYTAG 231

RESULT 9  
US-10-409-772-2  
Sequence 2, Application US/10409772  
Publication No. US20030216565A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/10/409,772  
CURRENT FILING DATE: 2003-04-07  
PRIOR APPLICATION NUMBER: US/09/479,614  
PRIOR FILING DATE: 2000-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-2

Query Match 89.7%; Score 87; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16  
|||

Db 216 VDGQKATNIPFYTAG 231

RESULT 10  
US-10-409-772-29  
Sequence 29, Application US/10409772  
Publication No. US20030216565A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine  
APPLICANT: Weber, Eric  
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
FILE REFERENCE: P-1047  
CURRENT APPLICATION NUMBER: US/10/409,772  
CURRENT FILING DATE: 2003-04-07  
PRIOR APPLICATION NUMBER: US/09/479,614  
PRIOR FILING DATE: 2000-01-07  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 496  
TYPE: PRT  
ORGANISM: Felis catus  
US-10-409-772-29

Query Match 89.7%; Score 87; DB 4; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16  
|||  
Db 216 VDGQKATNIPFYTAG 231

RESULT 11  
US-09-401-636-7  
Sequence 7, Application US/09401636  
Patent No. US2001003843A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/006001  
CURRENT APPLICATION NUMBER: US/09/401,636  
CURRENT FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 343  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-7

Query Match 75.3%; Score 73; DB 3; Length 343;  
Best Local Similarity 86.7%; Pred. No. 0.0019;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 15  
|||  
Db 61 VDGQKATNIPFYTAG 75

RESULT 12  
US-10-176-664-7  
Sequence 7, Application US/10176664  
Publication No. US20030031663A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/006001  
CURRENT APPLICATION NUMBER: US/10/176,664

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; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAP 15
        ||||| :|||
Db      61 VDGQKAKENLPYTP 75

RESULT 13
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAP 15
        ||||| :|||
Db      61 VDGQKAKENLPYTP 75

RESULT 14
US-10-214-524-29
; Sequence 29, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Duckbilled platypus (Ornithorhynchus anatinus)
US-10-214-524-29

Query Match      75.3%; Score 73; DB 4; Length 577;
Best Local Similarity 86.7%; Pred. No. 0.0034;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAP 15
        ||||| :|||
Db      295 VDGQKAKENLPYTP 309

RESULT 15
US-10-438-794-3
; Sequence 3, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric IGE Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated ORO
US-10-438-794-3

Query Match      59.8%; Score 58; DB 4; Length 337;
Best Local Similarity 76.9%; Pred. No. 0.055;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYT 13
        ||||| :|||
Db      56 VDGQKAKENLPYTP 68

Search completed: December 12, 2005, 20:19:25
Job time : 81.3793 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.94828 Seconds  
(without alignments)  
34.094 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97

Sequence: 1 VDGQKATNIPFYTAFTK 18

Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published\_Applications\_AA\_New:

1: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/PC1\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	312	6	US-10-723-207-2
2	46	47.4	497	6	US-10-763-712A-24
3	46	47.4	497	6	US-10-763-712A-91
4	44	45.4	121	6	US-10-793-626-2524
5	43	44.3	102	6	US-10-821-234-1457
6	43	44.3	254	6	US-10-485-517-168
7	40	41.2	430	6	US-10-467-657-2346
8	38	39.2	241	6	US-10-485-517-189
9	38	39.2	530	6	US-10-131-826A-130
10	37	38.1	32	6	US-10-467-657-8080
11	37	38.1	345	6	US-10-793-626-3168
12	37	38.1	468	6	US-10-957-569-28
13	36	37.1	375	6	US-10-793-626-2172
14	36	37.1	532	7	US-11-184-380-6
15	36	37.1	588	7	US-11-184-380-5
16	36	37.1	724	7	US-11-184-380-4
17	35.5	36.6	811	7	US-11-055-822-1142
18	35.5	36.6	811	7	US-11-055-822-1144
19	35.5	36.6	811	7	US-11-124-291-4
20	35.5	36.6	1045	7	US-11-113-424-54
21	35.5	36.6	1094	6	US-10-821-234-1097
22	35.5	36.6	2376	7	US-11-096-051-4
23	35.5	36.6	2715	7	US-11-096-051-2
24	35.5	36.6	2715	7	US-11-113-424-51
25	35.5	36.6	2721	7	US-11-096-051-10

26	35.5	36.6	2725	7	US-11-096-051-8	Sequence 8, Appli
27	35	36.1	288	6	US-10-467-657-1682	Sequence 1682, Ap
28	35	36.1	433	6	US-10-131-826A-6	Sequence 6, Appli
29	35	36.1	517	6	US-10-485-517-310	Sequence 310, App
30	35	36.1	605	6	US-10-821-234-1207	Sequence 1207, Ap
31	35	36.1	805	6	US-10-518-559-4	Sequence 4, Appli
32	35	36.1	805	6	US-10-518-559-24	Sequence 24, Appli
33	35	36.1	826	6	US-10-793-626-1066	Sequence 1066, Ap
34	35	36.1	853	6	US-10-821-234-1110	Sequence 1110, Ap
35	35	36.1	901	6	US-10-793-626-342	Sequence 342, App
36	35	36.1	1006	6	US-10-467-657-8400	Sequence 8400, Ap
37	35	36.1	2335	6	US-10-821-234-1610	Sequence 1610, Ap
38	34.5	35.6	2011	7	US-11-080-991-56	Sequence 56, Appli
39	34	35.1	119	6	US-10-763-712A-63	Sequence 63, Appli
40	34	35.1	124	6	US-10-467-657-2914	Sequence 2914, Ap
41	34	35.1	146	7	US-11-000-463-881	Sequence 881, App
42	34	35.1	232	6	US-10-510-386-116	Sequence 116, App
43	34	35.1	240	7	US-11-054-515-1989	Sequence 1989, Ap
44	34	35.1	409	6	US-10-793-626-1002	Sequence 2002, Ap
45	34	35.1	409	6	US-10-793-626-2306	Sequence 2306, Ap

## ALIGNMENTS

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RESULT 1
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; PRIOR APPLICATION NUMBER: 2003-11-24
; PRIOR FILING DATE: 2000-12-01
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IGE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-10-723-207-2

Query Match 100.0%; Score 97; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 9.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAFTK 18
Db 48 VDGQKATNIPFYTAFTK 65

RESULT 2
US-10-763-712A-24
; Sequence 24, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
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; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-763-712a-24
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Query Match 47.4%; Score 46; DB 6; Length 497;
Best Local Similarity 55.6%; Pred. No. 0.81;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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QY 1 VDQKATNIFPYTAPGK 18
Db 324 MDGKKTNTMTWPAFGSK 341
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RESULT 3
US-10-763-712a-91
; Sequence 91, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 497
; TYPE: PRT
; ORGANISM: C. reinhardtii
US-10-763-712a-91
```

```
Query Match 47.4%; Score 46; DB 6; Length 497;
Best Local Similarity 55.6%; Pred. No. 0.81;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 VDQKATNIFPYTAPGK 18
Db 324 MDGKKTNTMTWPAFGSK 341
```

```
RESULT 4
US-10-793-626-2524
; Sequence 2524, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
```

```
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2524
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2524
```

```
Query Match 45.4%; Score 44; DB 6; Length 121;
Best Local Similarity 60.0%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 3 GQKATNIFPYTAPGT 17
Db 44 GKTATNIEKYSQGT 58
```

```
RESULT 5
US-10-821-234-1457
; Sequence 1457, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc seq_genes Version 1.0
; SEQ ID NO 1457
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1457
```

```
Query Match 44.3%; Score 43; DB 6; Length 102;
Best Local Similarity 46.7%; Pred. No. 0.47;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 DQKATNIFPYTAPG 16
Db 14 DQKAPDPVAVFAPG 28
```

```
RESULT 6
US-10-485-517-188
; Sequence 188, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P10629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; PRIOR FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
```

NUMBER OF SEQ ID NOS: 424  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 188  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-10-485-517-188

Query Match 44.3%; Score 43; DB 6; Length 254;  
Best Local Similarity 88.9%; Pred. No. 1.3;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KATNIFPYT 13  
DB 58 KDTNIFPYT 66

RESULT 7  
US-10-467-657-2346  
Sequence 2346, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 2346  
LENGTH: 430  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2346

Query Match 41.2%; Score 40; DB 6; Length 430;  
Best Local Similarity 46.7%; Pred. No. 7.4;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 VDSOKATNIFPYTAP 15  
DB 127 LDGQDITKLAPYDRP 141

RESULT 8  
US-10-485-517-189  
Sequence 189, Application US/10485517  
Publication No. US20050256299A1  
GENERAL INFORMATION:  
APPLICANT: University of Sheffield  
APPLICANT: Biomex Incorporated  
APPLICANT: Foster, Simon  
APPLICANT: Mond, James  
TITLE OF INVENTION: Antigenic Polypeptides  
FILE REFERENCE: P100629WO  
CURRENT APPLICATION NUMBER: US/10/485,517  
CURRENT FILING DATE: 2004-02-02  
PRIOR APPLICATION NUMBER: GB 0118825.9  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: GB 0200349.9  
PRIOR FILING DATE: 2002-01-09  
NUMBER OF SEQ ID NOS: 424  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 189  
LENGTH: 241  
TYPE: PRT  
ORGANISM: Staphylococcus aureus

US-10-485-517-189

Query Match 39.2%; Score 38; DB 6; Length 241;  
Best Local Similarity 87.5%; Pred. No. 8.6;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KATNIFPY 12  
DB 46 KDTNIFPY 53

RESULT 9  
US-10-131-826A-130  
Sequence 130, Application US/10131826A  
Publication No. US20050245730A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C128  
CURRENT APPLICATION NUMBER: US/10/131,826A  
CURRENT FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-131-826A-130  
SEQ ID NO 130  
LENGTH: 530  
TYPE: PRT  
ORGANISM: Homo Sapien

Query Match 39.2%; Score 38; DB 6; Length 530;  
Best Local Similarity 50.0%; Pred. No. 20;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATNIFPYTAPGT 17  
DB 242 STNIYHSPGCT 253

RESULT 10  
US-10-467-657-8080  
; Sequence 8080, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASNANI Vega  
; APPLICANT: MONACI Elisabeth  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8080  
; LENGTH: 32  
; TYPE: PR1  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8080

Query Match 38.1%; Score 37; DB 6; Length 32;  
Best Local Similarity 56.2%; Pred. No. 1.4;  
Matches 9; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 3 GQKATNFFPYTAPGK 18  
Db 8 GRRFTNI--ATVPGTK 21

RESULT 11  
US-10-793-626-3168  
; Sequence 3168, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3168  
; LENGTH: 345  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-3168

Query Match 38.1%; Score 37; DB 6; Length 345;  
Best Local Similarity 63.6%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGQKATNFFP 11  
Db 223 LDGSKANITP 233

RESULT 12  
US-10-957-569-28  
; Sequence 28, Application US/10957569  
; Publication No. US20050246785A1  
; GENERAL INFORMATION:  
; APPLICANT: COOK, Zhifong et al.

; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES  
; FILE REFERENCE: THEREOF  
; CURRENT APPLICATION NUMBER: US/10/957,569  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: US 10/950,321  
; PRIOR FILING DATE: 2004-09-23  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 28  
; LENGTH: 468  
; TYPE: PR1  
; ORGANISM: Arabidopsis thaliana  
US-10-957-569-28

Query Match 38.1%; Score 37; DB 6; Length 468;  
Best Local Similarity 53.8%; Pred. No. 26;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 KATNFFPYTAPGT 17  
Db 203 KGYSFPMSPGT 215

RESULT 13  
US-10-793-626-2172  
; Sequence 2172, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2172  
; LENGTH: 375  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
US-10-793-626-2172

Query Match 37.1%; Score 36; DB 6; Length 375;  
Best Local Similarity 50.0%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 VDGQKATNFFPYTAPGK 18  
Db 114 VDTTKTENIEQYIKPEIK 131

RESULT 14  
US-11-184-380-6  
; Sequence 6, Application US/11184380  
; Publication No. US20050255089A1  
; GENERAL INFORMATION:  
; APPLICANT: Chioirini, John  
; APPLICANT: Kotin, Robert M.  
; TITLE OF INVENTION: AAVS NUCLEIC ACIDS  
; FILE REFERENCE: 14014.032303  
; CURRENT APPLICATION NUMBER: US/11/184,380  
; CURRENT FILING DATE: 2005-07-19  
; PRIOR APPLICATION NUMBER: PCT/US99/11958  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,029  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 6
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: Synthetic construct
US-11-184-380-6

```

```

Query Match      37.1%; Score 36; DB 7; Length 532;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      1 VDGQKATNIPPYTAP 15
        ||| | | | | |
Db      63 VDGSNANAYFGYSTP 77

```

```

RESULT 15
US-11-184-380-5
; Sequence 5, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chiorini, John
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.0323U3
; CURRENT APPLICATION NUMBER: US/11/184,380
; PRIOR FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: Synthetic construct
US-11-184-380-5

```

```

Query Match      37.1%; Score 36; DB 7; Length 588;
Best Local Similarity 46.7%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      1 VDGQKATNIPPYTAP 15
        ||| | | | | |
Db      119 VDGSNANAYFGYSTP 133

```

Search completed: December 12, 2005, 20:19:49  
Job time : 3.94828 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 15.2069 Seconds  
(without alignments)  
113.889 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGOKATNIFPYTPAGTK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_80:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2	T16880
2	46	47.4	579	2	JW0071
3	46	47.4	586	2	SG9183
4	45	46.4	658	2	AH0110
5	45	46.4	350	2	G95009
6	45	46.4	350	2	E97881
7	45	46.4	583	1	ATPMN2
8	44	45.4	511	2	T16279
9	43	44.3	322	2	AD3488
10	43	44.3	586	1	ADPMN1
11	42	43.3	258	2	AF0306
12	42	43.3	381	2	AD2436
13	42	43.3	476	2	AC2465
14	42	43.3	623	2	T22177
15	42	43.3	683	2	B71325
16	42	43.3	1686	2	A87692
17	41	42.3	241	2	T17798
18	41	42.3	272	2	H87075
19	41	42.3	359	2	G83039
20	41	42.3	570	2	JC5722
21	41	42.3	619	2	H64416
22	41	42.3	643	1	S15623
23	41	42.3	713	2	JF0230
24	41	42.3	859	2	AE2217
25	41	42.3	909	2	T06246
26	41	42.3	916	2	T06242
27	41	42.3	1032	2	S74487
28	41	42.3	1055	2	C82600
29	40.5	41.8	795	2	B83608

30	40	41.2	101	2	G69203	conserved hypothet
31	40	41.2	109	2	F89886	hypothetical prote
32	40	41.2	137	2	A83751	hypothetical prote
33	40	41.2	179	2	D90167	conserved hypothet
34	40	41.2	189	2	S49846	asparagine synthas
35	40	41.2	217	1	GMBPT4	gene 59 protein -
36	40	41.2	227	2	C7582	conserved hypothet
37	40	41.2	240	2	C89967	serine proteinase
38	40	41.2	302	2	T03109	probable membrane
39	40	41.2	327	2	S40753	hypothetical prote
40	40	41.2	357	1	A48511	protein-glutamate
41	40	41.2	374	2	G81926	probable polyamine
42	40	41.2	419	2	C81179	spermidine/putresc
43	40	41.2	454	2	AH2821	conserved hypothet
44	40	41.2	470	2	H97599	BH0982 hypothetical
45	40	41.2	584	2	T12989	asparagine synthas

#### ALIGNMENTS

##### RESULT 1

T16880  
hypothetical protein T14G12.4 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 05-Oct-2004  
C:Accession: T16880  
R:WILCOX, L.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid T14G12.  
A:Reference number: Z18596  
A:Accession: T16880  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-270 <WIL>  
A:Cross-references: UNIPROT:Q22510; UNIPARC:UPI0000075025; EMBL:U41268; NID:G1086843; PI  
A:Gene: CESP:T14G12.4  
A:Introns: 37/1; 72/3; 164/1  
F:93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;  
Best Local Similarity 57.1%; Pred. No. 2;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Cy 3 GOKATNIFPYTPAG 16  
Db 205 GAAANLFPYFPG 218

##### RESULT 2

JW0071  
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - soybean  
C:Species: *Glycine max* (soybean)  
C:Date: 13-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: JW0071  
R:Yamagata, H.; Nakajima, A.; Bowler, C.; Iwasaki, T.  
BioSci. Biotechnol. Biochem. 62, 148-150, 1998  
A>Title: Molecular cloning and characterization of a cDNA encoding asparagine synthetase  
A:Reference number: JW0071; MUID:98162148; PMID:9501527  
A:Accession: JW0071  
A:Molecule type: mRNA  
A:Residues: 1-579 <YAM>  
A:Cross-references: UNIPROT:Q42792; UNIPARC:UPI00000A95EC; GB:U55874; NID:G1305548; PIDN  
C:Superfamily: asparagine synthase (glutamine-hydrolysing)  
C:Keywords: asparagine biosynthesis; ligase  
F:2-579/Product: asparagine synthase (glutamine-hydrolysing) #status predicted <DUM>  
F:2/Active site: Cys #status predicted

Query Match 47.4%; Score 46; DB 2; Length 579;  
Best Local Similarity 34.4%; Pred. No. 10;  
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDGOK-----ATNIPYPYAPGK 18  
: ||| :  
DB 462 IDGKKAHAKVYDMMANANIPFPTTK 493

RESULT 3  
S69183  
asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Lotus japonicus  
C:Species: Lotus japonicus  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S69183; S57932  
R:Waterhouse, R.N.; Smyth, A.J.; Massemeau, A.; Proseer, I.M.; Clarkson, D.T.  
Plant Mol. Biol. 30, 883-897, 1996  
A:Title: Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus  
A:Reference number: S69182; MUID:96270369; PMID:8639748  
A:Accession: S69183  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-586 <WAT>  
A:Cross-references: UNIPROT:P49093; UNIPARC:UPI000016DE2B; EMBL:X89410; NID:G897772; PID  
A:Experimental source: strain B-129  
C:Genetics:  
A:Gene: AS2  
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)  
C:Keywords: asparagine biosynthesis; ligase  
F:2-586/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <DUM>  
F:2/Active site: Cys #status predicted

Query Match 47.4%; Score 46; DB 2; Length 586;  
Best Local Similarity 31.2%; Pred. No. 10;  
Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

QY 1 VDGOK-----ATNIPYPYAPGK 18  
: ||| :  
DB 462 IDGKKAHAKVYDMMANANIPFPTTK 493

RESULT 4  
AH0110  
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0110  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: UNIPROT:Q8ZHJ0; UNIPARC:UPI000000CD765; GB:AL590842; PIDN:CAC89747.1;  
C:Genetics:  
A:Gene: YPO0902

Query Match 47.4%; Score 46; DB 2; Length 658;  
Best Local Similarity 52.9%; Pred. No. 12;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYPYAPGK 17  
: ||| :  
DB 99 LINGOKATNLAPATISST 115

RESULT 5  
G95009  
sensor histidine kinase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: G95009  
R:Tettelein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I.  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: G95009  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-350 <KUR>  
A:Cross-references: UNIPROT:Q9SLJ1; UNIPROT:Q8DRK0; UNIPARC:UPI0000051BF0; GB:AE005672; I  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP0084

Query Match 46.4%; Score 45; DB 2; Length 350;  
Best Local Similarity 72.7%; Pred. No. 8.6;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 NIPYPYAPGK 18  
: ||| :  
DB 248 NAFKYSAPGK 258

RESULT 6  
E97881  
histidine kinase (EC 2.7.3.-) [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: E97881  
R:Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: E97881  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-350 <KUR>  
A:Cross-references: UNIPROT:Q9SLJ1; UNIPROT:Q8DRK0; UNIPARC:UPI0000051BF0; GB:AE007317; I  
C:Genetics:  
A:Gene: hk08  
C:Keywords: phosphotransferase

Query Match 46.4%; Score 45; DB 2; Length 350;  
Best Local Similarity 72.7%; Pred. No. 8.6;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 NIPYPYAPGK 18  
: ||| :  
DB 248 NAFKYSAPGK 258

RESULT 7  
AJPMN2  
asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [similarity] - garden pea  
N:Alternate names: asparagine synthetase (glutamine-hydrolyzing)  
C:Species: Pisum sativum (garden pea)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C:Accession: S11443  
R:Teal, F.Y.; Coruzzi, G.M.  
EMBO J. 9, 323-332, 1990  
A:Title: Dark-induced and organ-specific expression of two asparagine synthetase genes in  
A:Reference number: S11443; MUID:90151604; PMID:1968003  
A:Accession: S11443  
A:Molecule type: DNA  
A:Residues: 1-583 <TSA>  
A:Cross-references: UNIPROT:P19252; UNIPARC:UPI000016DFOB; EMBL:X52180; NID:G20651; PIDN  
C:Genetics:  
A:Gene: AS2  
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)



## RESULT 10

R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurutz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, T.; Nakazaki, N.; Shingo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: AD2436  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-381 <KUR>  
A/Cross-references: UNIPROT:Q8YMG2; UNIPARC:UPI00000CED3F; GB:BA000019; P1DN:BA876743.1;  
A/Experimental source: strain PCC 7120  
C/Genetics:  
A/Gene: all504

Query Match 43.3%; Score 42; DB 2; Length 381;  
Best Local Similarity 53.3%; Pred. No. 31;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VDGOKATNIPFYAP 15  
DB 80 IQGQPMNTNIPYRPP 94

RESULT 13  
AC2465  
6-phosphogluconate dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)  
C/Species: Nostoc sp. PCC 7120  
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C/Accession: AC2465  
R/Kaneke T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: AC2465  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-476 <KUR>  
A/Cross-references: UNIPROT:Q8YLM3; UNIPARC:UPI00000CEB0D; GB:BA000019; P1DN:BA876974.1;  
A/Experimental source: strain PCC 7120  
C/Genetics:  
A/Gene: all5275  
C/Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate de

Query Match 43.3%; Score 42; DB 2; Length 476;  
Best Local Similarity 72.7%; Pred. No. 39;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 NIPPYTAPGK 18  
DB 238 NIPPYIDPETK 248

RESULT 14  
T22177  
hypothetical protein F44F1.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T22177  
R/Dobson, R.  
submitted to the EMBL Data Library, October 1996  
A/Reference number: Z19527  
A/Accession: T22177  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-623 <WTL>  
A/Cross-references: UNIPROT:O02260; UNIPARC:UPI000017B9C4; EMBL:Z81083; P1DN:CAB03101.1;  
A/Experimental source: clone F44F1  
C/Genetics:  
A/Gene: CESP:F44F1.3  
A/Map position: 1  
A/Intons: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3

Query Match 43.3%; Score 42; DB 2; Length 623;

Best Local Similarity 50.0%; Pred. No. 53;  
Matches 11; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
QY 1 VDGOKATNI----FPYTAPGK 18  
DB 152 VDGQWKTIIDDFPTTDOIR 173

RESULT 15  
B71325  
conserved hypothetical protein TP0421 - syphilis spirochete  
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C/Accession: B71325  
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dobson, R.; Gwin  
rson, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McDor  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A/Reference number: A71250; MUID:98332770; PMID:9665876  
A/Accession: B71325  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-683 <COL>  
A/Cross-references: UNIPROT:Q83436; UNIPARC:UPI00000C0A71; GB:AE001220; GB:AE000520; NID:  
A/Experimental source: strain Nichols  
C/Genetics:  
A/Gene: TP0421

Query Match 43.3%; Score 42; DB 2; Length 683;  
Best Local Similarity 50.0%; Pred. No. 59;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 3 GOKATNIPYTAPG 16  
DB 278 GOKSARFFGSAFG 291

Search completed: December 12, 2005, 20:42:50  
Job time : 17.2069 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 97.7586 Seconds  
(without alignments)  
129.907 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGGKATNIPYATPGRK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	52.6	382	2	Q7PSV1_FUSNV
2	51	52.6	382	2	Q8R6B3_FUSNM
3	48	49.5	168	2	Q9S0A8_CAEEL
4	48	49.5	270	2	Q22510_CAEEL
5	47	48.5	1054	2	Q608X6_METCA
6	47	48.5	1538	2	Q94H26_ORYSA
7	46	47.4	497	2	Q9FYU1_CHLRE
8	46	47.4	579	2	P93168_SOYBN
9	46	47.4	579	2	Q42792_SOYBN
10	46	47.4	579	2	Q9SM55_PHAUV
11	46	47.4	585	1	ASNS2_LOTJA
12	46	47.4	641	2	Q8CKM1_YERPE
13	46	47.4	658	2	Q8ZHJ0_YERPE
14	45	46.4	190	2	Q68E47_ABRPU
15	45	46.4	279	2	Q619H6_CABBR
16	45	46.4	350	2	Q8DRK0_STRRP
17	45	46.4	350	2	Q9S1U1_STRRP
18	45	46.4	445	1	ALN_SPRCO
19	45	46.4	582	1	ASNS2_PEA
20	45	46.4	583	2	Q8RVU0_PFAVA
21	44	45.4	131	1	SSB_STAPB
22	44	45.4	131	2	Q8HMC5_STAEQ
23	44	45.4	340	2	Q9AYAO_ORYSA
24	44	45.4	395	2	Q9ZHQ4_STRFR
25	44	45.4	511	1	U171_CAEEL
26	44	45.4	525	2	Q6AL11_DESPP
27	44	45.4	584	2	Q9WB61_ASTSI
28	44	45.4	586	2	Q84X69_PFAVA
29	44	45.4	589	2	Q53Q04_ORYSA
30	44	45.4	760	2	Q6UDM4_ORYSA
31	44	45.4	875	2	Q7FAL9_ORYSA

32	44	45.4	884	2	Q53YX1_ORYSA	Q53YX1 oryza sativ
33	44	45.4	1436	2	Q7FAL2_ORYSA	Q7FAL2 oryza sativ
34	44	45.4	1685	2	Q7XSP1_ORYSA	Q7XSP1 oryza sativ
35	44	45.4	1829	2	Q70XV6_AMBTC	Q70XV6 amborella t
36	43.5	44.8	1335	2	Q91A54_9CAUD	Q91A54 bacterioph
37	43.5	44.8	1335	2	Q91A58_9CAUD	Q91A58 prophage p-
38	43	44.3	52	2	Q7WYM4_BACSH	Q7WYM4 bacillus sp
39	43	44.3	102	1	GAGC1_HUMAN	Q60829 homo sapien
40	43	44.3	102	2	Q61B11_HUMAN	Q61B11 homo sapien
41	43	44.3	120	2	Q52EG8_MAGGR	Q52EG8 magnaporthe
42	43	44.3	127	1	CRGB_NITPU	Q82U09 nitrosomona
43	43	44.3	166	2	Q6GCH5_STPAS	Q6GCH5 staphylococ
44	43	44.3	166	2	Q8NYE3_STPAW	Q8NYE3 staphylococ
45	43	44.3	240	2	Q9KH50_STPAW	Q9KH50 staphylococ

ALIGNMENTS

RESULT 1  
Q7PSV1\_FUSNV PRELIMINARY; PRT; 382 AA.  
ID Q7PSV1\_FUSNV  
AC Q7PSV1  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).  
GN Name=FV1343;  
OS Fusbacterium nucleatum subsp. vincentii ATCC 49256.  
OC Bacteria; Fusbacteriales; Fusbacteriaceae;  
OC Fusbacterium.  
OX NCBI\_TaxID=209882;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 49256;  
RA Kapratral V., Ivanova N., Anderson I., Reznik G., Bhattacharya A.,  
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,  
RA Haselkorn R., Overbeek R., Kyriides N.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC DR EMBL; AABF0100055; EAA24105.1; -; Genomic\_DNA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR InterPro; IPR010327; HGD-D.  
DR Pfam; PF06050; HGD-D; 1.  
KW Lyase.  
SQ SEQUENCE 382 AA; 43893 MW; 441C73816E1C761E CRC64;  
  
Query Match 52.6%; Score 51; DB 2; Length 382;  
Best Local Similarity 64.3%; Pred. No. 7.8;  
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 DGOKATNIPYATP 15  
Db 28 EGKAVGIFPYAP 41  
  
RESULT 2  
Q8R6B3\_FUSNM PRELIMINARY; PRT; 382 AA.  
ID Q8R6B3\_FUSNM  
AC Q8R6B3  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).  
GN Orderedlocusnames=FN0208;  
OS Fusbacterium nucleatum (subsp. nucleatum).  
OC Bacteria; Fusbacteriales; Fusbacteriaceae;  
OC Fusbacterium.  
OX NCBI\_TaxID=76856;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 25586;  
 RX MEDLINE=21866394; PubMed=11869109;  
 RA DOI=10.1128/JB.184.7.2005-2018.2002;  
 RA Kapatalay V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,  
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,  
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldstein E., Bernal A.,  
 RA Larsen N., D'Souza M., Malinas T., Pusch G., Haselkorn R.,  
 RA Fornslein M., Kyriplides N.C., Overbeek R.;  
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium  
 RT nucleatum strain ATCC 25586.";  
 RL J. Bacteriol. 184:2005-2018(2002).  
 DR EMBL: AE009951.1: AAL94414.1: -; Genomic\_DNA.  
 DR InterPro: IPR010327; HGD-D.  
 DR Pfam: PF06050; HGD-D; 1.  
 KW Complete proteome; Lyase.  
 SQ SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;  
 Best Local Similarity 64.3%; Pred. NO. 7.8;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGKATNIPPTAP 15  
 Db 28 EGKAVGIFPYAP 41

RESULT 3  
 ID Q950A9 CAEBL PRELIMINARY; PRT; 168 AA.  
 AC Q950A9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Forkhead transcription factor family protein 2, isoform b.  
 GN Name=fkh-2; ORFNames=TI4G12.4;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RG The C. elegans sequencing consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018(1998).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC EMBL: U41268; AAL02521.1; -; Genomic\_DNA.  
 DR HSSP: Q99958; 1D5V.  
 DR SMR: Q950A9; 2-68.  
 DR Ensemble: T14G12.4; Caenorhabditis elegans.  
 DR WormBase: WBGene0001434; fkh-2.  
 DR WormPep: T14G12.4b; CE29342.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription; DNA-dependent; IEA.  
 DR GO: GO:0006350; P:transcription; IEA.  
 DR InterPro: IPR001766; TF\_Fork\_head.  
 DR InterPro: IPR011991; Wing\_hlx\_DNA\_bd.  
 DR Pfam: PF00250; Fork\_head; 1.  
 DR PRINTS: PR00053; FORKHEAD.  
 DR PRODOM: PD000425; TF\_Fork\_head; 1.  
 DR SMART: SM00339; FH; 1.  
 DR PROSITE: PS00658; FORK\_HEAD\_2; 1.  
 DR PROSITE: PS50039; FORK\_HEAD\_3; 1.  
 KW Complete proteome; DNA-binding; Nuclear protein; Transcription;  
 KW Transcription regulation.  
 SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4B6968572 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 168;  
 Best Local Similarity 57.1%; Pred. NO. 11;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPPTAPG 16  
 Db 103 GAAANLFPYFSPG 116

RESULT 4  
 ID Q22510 CAEBL PRELIMINARY; PRT; 270 AA.  
 AC Q22510;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Forkhead transcription factor family protein 2, isoform a.  
 GN Name=fkh-2; ORFNames=TI4G12.4;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RG The C. elegans sequencing consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018(1998).  
 CC -1- INTERACTION:  
 CC Q21648:R02F2.5; NBExp=1; IntAct=EBI-327741, EBI-314179;  
 CC Q9XM88.Y75B8A.1; NBExp=1; IntAct=EBI-327741, EBI-316766;  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL: U41268; AAL82436.1; -; Genomic\_DNA.  
 DR PIR: T16880; T16880.  
 DR HSSP: Q99958; 1D5V.  
 DR SMR: Q22510; 93-170.  
 DR InterPro: IPR011991; Wing\_hlx\_DNA\_bd.  
 DR Pfam: PF00250; Fork\_head; 1.  
 DR PRINTS: PR00053; FORKHEAD.  
 DR PRODOM: PD000425; TF\_Fork\_head; 1.  
 DR SMART: SM00339; FH; 1.  
 DR PROSITE: PS00657; FORK\_HEAD\_1; 1.  
 DR PROSITE: PS00658; FORK\_HEAD\_2; 1.  
 DR PROSITE: PS50039; FORK\_HEAD\_3; 1.  
 KW Complete proteome; DNA-binding; Nuclear protein; Transcription;  
 KW Transcription regulation.  
 SQ SEQUENCE 270 AA; 30491 MW; 7C4911655EC76175 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 270;  
 Best Local Similarity 57.1%; Pred. NO. 17;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPPTAPG 16  
 Db 205 GAAANLFPYFSPG 218

RESULT 5  
 ID Q608X6 METCA PRELIMINARY; PRT; 1054 AA.  
 AC Q608X6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hydrophobe/ampiphile Efflux-1 (HAE1) family protein.



```

DR InterPro: IPR003149; Fe_hyd_SSU.
DR Pfam: PF02906; Fe_hyd_19_C; 1.
DR Pfam: PF02256; Fe_hyd_SSU; 1.
DR Oxidoreductase; Signal; Transic peptide.
FM TRANSIT 1 56 Potential.
FT CHAIN 57 497 Fe-hydrogenase.
SQ SEQUENCE 497 AA; 5311 MW; 2B618A259E6572F4 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 497;
Best Local Similarity 55.6%; Pred. No. 72;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAGTK 18
Db 324 MDGKETNTMVPAGSK 341
: ||| ||| |||
: ||| ||| |||

RESULT 8
P93168_SOYBN PRELIMINARY; PRT; 579 AA.
ID P93168
AC P93168
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Asparagine synthetase 1 (EC 6.3.5.4).
GN Name=AsI;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Century;
RX MEDLINE=9718563; PubMed=9037148; DOI=10.1023/A:1005784202450;
RA Hughes C.A., Beard H.S., Matthews B.F.;
RT "Molecular cloning and expression of two cDNAs encoding asparagine
synthetase in soybean.";
RL Plant Mol. Biol. 33:301-311(1997).
DR EMBL: U77679; AAC49614.1; -; mRNA.
DR HSP: P22106; ICT9.
DR GO: GO:0004066; F:asparagine synthase (glutamine-hydrolyzing). . .; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008652; P:amino acid biosynthesis; IEA.
DR GO: GO:0006529; P:asparagine biosynthesis; IEA.
DR GO: GO:0006541; P:glutamine metabolism; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR001962; Asn_synthase.
DR InterPro: IPR006426; Asn_synth_AEB.
DR InterPro: IPR000583; GATase_2.
DR Pfam: PF00733; Asn_synthase; 1.
DR Pfam: PF00310; GATase_2; 1.
DR TIGRFAMs: TIGR01536; asn_synth_AEB; 1.
DR PROSITE: PS00443; GATASE_Type_I; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 579 AA; 65366 MW; F7E80DA2019E0FCS CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 85;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDGOK-----ATNIPYTPAGTK 18
Db 462 IDGLKAHAEKVTDRMMLNANIFPNTPTTK 493
: ||| ||| |||
: ||| ||| |||

RESULT 9
Q42792_SOYBN PRELIMINARY; PRT; 579 AA.
ID Q42792
AC Q42792
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Asparagine synthetase (EC 6.3.5.4).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Corsoy;
RX MEDLINE=98162148; PubMed=9501527;
RA Yamagata H., Nakajima A., Bowler C., Iwasaki T.;
RT "Molecular cloning and characterization of a cDNA encoding asparagine
synthetase from soybean (Glycine max L.) cell cultures.";
RL Blosil, Biotechnol. Biochem. 62:148-150(1998).
DR EMBL: U55874; AAC09952.1; -; mRNA.
DR PIR: J00071; J00071.
DR HSP: P22106; ICT9.
DR GO: GO:0004066; F:asparagine synthase (glutamine-hydrolyzing). . .; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008652; P:amino acid biosynthesis; IEA.
DR GO: GO:0006529; P:asparagine biosynthesis; IEA.
DR GO: GO:0006541; P:glutamine metabolism; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR001962; Asn_synthase.
DR InterPro: IPR006426; Asn_synth_AEB.
DR InterPro: IPR000583; GATase_2.
DR Pfam: PF00733; Asn_synthase; 1.
DR Pfam: PF00310; GATase_2; 1.
DR TIGRFAMs: TIGR01536; asn_synth_AEB; 1.
DR PROSITE: PS00443; GATASE_Type_I; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 579 AA; 65231 MW; B6E7B7902DF2BC95 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 85;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDGOK-----ATNIPYTPAGTK 18
Db 462 IDGLKAHAEKVTDRMMLNANIFPNTPTTK 493
: ||| ||| |||
: ||| ||| |||

RESULT 10
Q9SM55_PHAVU PRELIMINARY; PRT; 579 AA.
ID Q9SM55
AC Q9SM55
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Asparagine synthetase (Type-I) (EC 6.3.5.4).
GN Name=asI;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseolus.
NCBI_TaxID=3885;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Great Northern, TISSUE=Root;
RA Galvez-Valdivieso G., Osuna D., Perez-Vicente R., Pineda M.,
RA Aguilar M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ13522; CAB57292.1; -; mRNA.
DR HSP: P22106; ICT9.
DR GO: GO:0004066; F:asparagine synthase (glutamine-hydrolyzing). . .; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008652; P:amino acid biosynthesis; IEA.
DR GO: GO:0006529; P:asparagine biosynthesis; IEA.
DR GO: GO:0006541; P:glutamine metabolism; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR001962; Asn_synthase.
DR InterPro: IPR006426; Asn_synth_AEB.
DR InterPro: IPR000583; GATase_2.

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DR Pfam; PF00733; Aen_synthase; 1.
DR Pfam; PF00310; GATase_2; 1.
DR TIGRFAMs; TIGR01536; aen_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
KW Ligase.
SQ SEQUENCE 579 AA; 65265 MW; 7A74FE5B852CE2B6 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 85;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

Oy 1 VDQOK-----ATNIPPYAPGK 18
Db 462 IDGLKHAKEKVTDRMLNANIPFENTPTK 493

RESULT 11
ASNS2_LOTUA STANDARD; PRT; 585 AA.
ID ASNS2_LOTUA
AC P49093;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Asparagine synthetase [glutamine-hydrolyzing] 2 (EC 6.3.5.4)
DE (Glutamine-dependent asparagine synthetase 2).
GN Name=AS2;
OS Lotus japonicus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; core eudicotyledons;
OC Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv Gifu / B-129;
RX MEDLINE=96270368; PubMed=8639748;
RA Waterhouse R.N., Smyth A.V., Massonau A., Proesser I.M.,
RA Clarkson D.T.;
RT "Molecular cloning and characterisation of asparagine synthetase from
RT Lotus japonicus: dynamics of asparagine synthesis in N-sufficient
RT conditions."
RL Plant Mol. Biol. 30:883-897 (1996).
CC -1- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP +
CC -1- diphosphate + L-asparagine + L-glutamate.
CC -1- PATHWAY: Asparagine biosynthesis.
CC -1- SIMILARITY: Contains 1 asparagine synthetase domain.
CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X89410; CAA61590.1; -; mRNA.
DR PIR; S69183; S69183.
DR HSSP; P22106; 1CT9.
DR InterPro; IPR006426; Aen_synth_AEB.
DR InterPro; IPR001962; Aen_synthase.
DR InterPro; IPR000583; GATase_2.
DR Pfam; PF00733; Aen_synthase; 1.
DR Pfam; PF00310; GATase_2; 1.
DR TIGRFAMs; TIGR01536; aen_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
KW Amino-acid biosynthesis; Asparagine biosynthesis;
KW Glutamine amidotransferase; Ligase; Multigene family.
FT INIT MET 0 By similarity.
FT DOMAIN 192 515 Asparagine synthetase.
FT REGION 1 107 Glutamine amidotransferase.
FT ACT_SITE 1 1 GATase (By similarity).
SQ SEQUENCE 585 AA; 65839 MW; F56DCA2015F73451 CRC64;

Query Match 47.4%; Score 46; DB 1; Length 585;
Best Local Similarity 31.2%; Pred. No. 86;
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Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

Oy 1 VDQOK-----ATNIPPYAPGK 18
Db 461 IDGLKHAKEKVTDRMLNANIPFENTPTK 492

RESULT 12
O8CKM1_YERPE PRELIMINARY; PRT; 641 AA.
ID O8CKM1_YERPE
AC O8CKM1_YERPE (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypoethetical.
GN OrderedLocustNames=y3288;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KIM5 / Biovar Mediavalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Niles W.L., Mason J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611 (2002).
DR EMBL; AE013929; AAM86837.1; -; Genomic DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008640; Hep_Hag.
DR InterPro; IPR008635; HIM.
DR InterPro; IPR005594; Yada_C.
DR Pfam; PF05658; Hep_Hag; 7.
DR Pfam; PF05662; HIM; 4.
DR Pfam; PF03895; Yada; 1.
KW Hypothetical protein.
SQ SEQUENCE 641 AA; 62093 MW; A5951553FE845162 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 641;
Best Local Similarity 52.9%; Pred. No. 94;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VDQKATNIPFYAPGT 17
Db 82 LMGKATYLAATISST 98

RESULT 13
O8ZHJ0_YERPE PRELIMINARY; PRT; 658 AA.
ID O8ZHJ0_YERPE
AC O8ZHJ0_YERPE (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative surface protein (Fragment).
GN OrderedLocustNames=YPO0302;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tlball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungaii K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
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RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Feltwell T., Hamlin N., Holroyd S., Jegels K., Karlyshev A.V.,  
 RA Leather S., Moline S., Oyston P.C.F., Quail M.A., Rutherford K.M.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.,  
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague."  
 RL Nature 413:523-527(2001).  
 DR EMBL: AJ141445; CAC89747.1; -; Genomic\_DNA.  
 DR PIR: AH0110; AH0110.  
 DR GO: GO:0019867; C:outer membrane; IEA.  
 DR GO: GO:0009405; P:pathogenesis; IEA.  
 DR InterPro: IPR008640; Hep\_Hag.  
 DR InterPro: IPR008635; HIM.  
 DR InterPro: IPR005594; Yada\_C.  
 DR Pfam: PF05658; Hep\_Hag; 7.  
 DR Pfam: PF05662; HIM; 4.  
 DR Pfam: PF03895; Yada; 1.  
 KM Complete proteome.  
 FT NON TER 1  
 SQ SEQUENCE 658 AA; 63875 MW; FC20411944FPEZPF CRC64;

Query Match 47.4%; Score 46; DB 2; Length 658;  
 Best Local Similarity 52.9%; Pred. No. 97;  
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIFPYTAPGT 17  
 Db 99 LINGKATNLAPATISST 115

## RESULT 14

Q68E47\_AERPU PRELIMINARY; PRT; 190 AA.  
 AC Q68E47;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=PFBA076.62;  
 OS *Aeromonas punctata* (*Aeromonas caviae*).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
 OC Aeromonadaceae; Aeromonas.  
 OX NCBI\_TaxID=648;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HGB5;  
 RA Rhodes G., Parkhill J., Bird C., Ambrose K., Jones M., Huys G.,  
 RA Swings J., Pickup R.W.;  
 RT "The complete nucleotide sequence of the conjugative tetracycline  
 RT resistance plasmid pFBA076, a member of a group of Incu plasmids with  
 RT global ubiquity."  
 RL Appl. Environ. Microbiol. 70:7497-7510(2004).  
 DR EMBL: CR376602; CAG15109.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 SQ SEQUENCE 190 AA; 21295 MW; 4790837FF3CFEBS4 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 190;  
 Best Local Similarity 47.1%; Pred. No. 38;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 DQKATNIFPYTAPGT 18  
 Db 58 DGEDASNTVATDPATE 74

## RESULT 15

O619H6\_CABRR PRELIMINARY; PRT; 279 AA.  
 AC O619H6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein CBG14280.  
 GN Name=CBG14280;

OS *Caenorhabditis briggsae*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.  
 OX NCBI\_TaxID=6238;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RG The C.briggsae Sequencing Consortium;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 DR EMBL: CAAC01000068; CAC68479.1; -; Genomic\_DNA.  
 DR SMR: O619H6; 101-178.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001766; TF\_Fork\_head.  
 DR InterPro: IPR011991; Wing\_hlx\_DNA\_bd.  
 DR Pfam: PF00250; Fork\_head; 1.  
 DR PRINTS: PR00053; FORKHEAD.  
 DR PRODOM: PD000425; TF\_Fork\_head; 1.  
 DR SMART: SM00339; FH; 1.  
 DR PROSITE: PS00657; FORK\_HEAD\_1; 1.  
 DR PROSITE: PS00658; FORK\_HEAD\_2; 1.  
 DR PROSITE: PS50039; FORK\_HEAD\_3; 1.  
 KM DNA-binding; Hypothetical protein; Nuclear protein; Transcription;  
 KM Transcription regulation.  
 SQ SEQUENCE 279 AA; 31322 MW; 0C926B95AD122D9B CRC64;

Query Match 46.4%; Score 45; DB 2; Length 279;  
 Best Local Similarity 57.1%; Pred. No. 58;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIFPYTAPG 16  
 Db 213 GAANAIFPYFNG 226

Search completed: December 12, 2005, 20:41:10  
 Job time : 100.759 secs